

ABSTRACT

OTT, OLIVER OTIS. Screening Semi-Exotic Maize Germplasm for Disease Resistance and Agronomic Traits. (Under the direction of Matthew Krakowsky and Major Goodman.)

The germplasm base of U.S. maize is narrow, with six inbred lines appearing in the pedigrees of 76% of formerly proprietary (ex-PVP) inbreds that are currently available through the North Central Plant Introduction Station in Ames, IA. Maize landraces provide one source to enhance maize diversity for many traits, both agronomic and disease-resistance traits. In conjunction with the Germplasm Enhancement of Maize Allelic Diversity project, a set of maize landrace accessions has been backcrossed to the Dupont Pioneer ex-PVP inbred line PHB47. The landrace BC₁ F₁s were evaluated for resistance to Gray leaf spot (GLS, *Cercospora zae-maydis*), Northern leaf blight (NLB, *Setosphaeria turcica*), and Southern leaf blight (SLB, *Cochliobolus heterostrophus*), and agronomic traits including: days to anthesis (DTA) and silk (DTS), plant height (PH), ear height (EH) and lodging in 2012 and 2013.

Trends in disease resistance and agronomic traits in maize populations were examined, and accessions from the Northern South America population provided the most resistance to all three diseases, followed by Middle South America, Andean, Mexican, and USA. For the agronomic traits assessed, accessions from the Northern South America population and Middle South America tended to be the latest flowering, tallest and had lowest lodging rates followed by Andean, Mexican, and USA accessions. The spatial geography of these disease and agronomic traits was examined using a Matérn spatial model. This model was used in Kriging to predict trait scores of BC₁ F₁s with a donor parent from locations that were not sampled herein. Spatial models accounted for 42, 38, 26, 37, and 47% of the variation across the Americas in DTA, DTS, PH, EH and lodging respectively. Spatial models accounted for 63, 63, and 59% of the variation across the Americas in GLS, NLB, and SLB, respectively. Phenotyping standard errors (SE) and spatial prediction SEs were similar for all traits, demonstrating the spatial model's ability to predict disease scores. This

work forms a framework from which researchers can more precisely target accessions for inclusion into a research program.

© Copyright 2014 Oliver Ott

All Rights Reserved

Screening Semi-Exotic Maize Germplasm for Disease Resistance and Agronomic Traits

by
Oliver Otis Ott

A dissertation submitted to the Graduate Faculty of
North Carolina State University
in partial fulfillment of the
requirements for the Degree of
Doctor of Philosophy

Crop Science

Raleigh, North Carolina

2014

APPROVED BY:

Matthew D. Krakowsky
Co-Chair of Advisory Committee

Major M. Goodman
Co-Chair of Advisory Committee

James B. Holland

Brian Riech

BIOGRAPHY

Oliver is from northwest Ohio where he grew up on a small family-run grain farm. He received his undergraduate degree in Plant Sciences at Cornell University, where he worked in the Lab of Rebecca Nelson. From there he moved to North Carolina State University to study maize breeding, with Major Goodman and Matthew Krakowsky. He hopes to join the ranks of the employed plant breeders.

ACKNOWLEDGMENTS

I would like to thank my two co-advisors for constant help and attention during my time in graduate school, and for allowing me to observe and participate in their applied plant breeding program. I would also like to thank the other two members of my committee, for their help with the thought processes that are required to become a crop scientist.

Special thanks to Wayne Dillard, Bill Hill, and Dale Dowden, the hardest working, kindest and overall best technicians that a graduate student could ever hope to work with.

Thank you to Monsanto Seed Company for their financial support my first year in graduate school. Thanks to Dupont Pioneer International for the James Wright graduate fellowship for the last four years of my time in graduate school. Monsanto and Dupont Pioneer also generously provided me with field space for disease trials.

The friendship and help from the other graduate students with whom I have had the opportunity to work especially Jill Recker and Zachary Jones.

I would also like to thank Cathy Herring and the staff of the Central Crops Research Station (especially Robert Parish), as well as the staff of 27 Farms in Homestead, Florida.

In conclusion Mrs. Verginia Huntley, Ms. Nancy Huntley, and Mr. Neal Huntley were all important parts of my life while I was in graduate school, providing friendship, and constant encouragement through the process.

TABLE OF CONTENTS

LIST OF TABLES	v
LIST OF FIGURES	viii
-CHAPTER I-	1
Maize Diversity and Germplasm Collections	1
Increasing the U.S.A. Maize Germplasm Base	4
Flowering Time in Maize	6
Plant and Ear Height in Maize	9
Lodging in Maize	11
Gray Leaf Spot in Maize	13
Northern Leaf Blight in Maize	16
Southern Leaf Blight in Maize	18
Kriging	19
Kriging for Use in Germplasm Utilization	25
References	28
-CHAPTER II-	38
Screening Semi-Exotic Maize Germplasm for Resistance to Gray Leaf Spot and Southern and Northern Leaf Blight	38
Abstract	39
Introduction	40
Methods and Materials	45
Germplasm	45
Disease Evaluation	45
Data Analysis	47
Results and Discussion	52
References	62
Supplemental References	133
-CHAPTER III-	135
Evaluation of Agronomic Traits in a Set of Semi-Exotic Maize Germplasm Using Population and Spatial Methods	135
Abstract	136
Introduction	137
Methods and Materials	141
Germplasm	141
Trait Evaluation	141
Data Analysis	143
Results and Discussion	147
References	155
APPENDIX	226
Appendix	227
Appendix References	263

LIST OF TABLES

-CHAPTER II-	38
Table 2.1 Worst and best performing BC ₁ F ₁ s for GLS, NLB, and SLB; DTA of each family is also noted	69
Supplemental Table 2.1 Chi square tests with Yates correction for random distribution of QTL discovered in Nested Association Mapping Population studies for Gray Leaf Spot (GLB), Northern Leaf Blight (NLB), and Southern Leaf Blight (SLB).....	76
Supplemental Table 2.2 BC ₁ F ₁ s Development	77
Supplemental Table 2.3 List of accessions used, country of origin, race name, accession name, source, and latitude, longitude, and altitude at point of collection with least square means and standard errors of GLS, NLB, SLB, and DTA.....	97
Supplemental Table 2.4 Disease ratings for check hybrids.....	117
Supplemental Table 2.5 Details of experimental units at six locations	118
Supplemental Table 2.6 Thirty one accessions for which no collection information could be found.....	119
Supplemental Table 2.7 Analysis of variance table for GLS	120
Supplemental Table 2.8 GLS analysis of variance by sources of variation	120
Supplemental Table 2.9 Analysis of variance table for NLB.....	121
Supplemental Table 2.10 NLB analysis of variance by sources of variation	121
Supplemental Table 2.11 Analysis of variance table for SLB	122
Supplemental Table 2.12 SLB analysis of variance by sources of variation	122
Supplemental Table 2.13 Tukey test for GLS scores in maize populations	124
Supplemental Table 2.14 Results from Tukey test for NLB scores in maize populations	126
Supplemental Table 2.15 Results from Tukey test for SLB scores in maize populations.....	128
Supplemental Table 2.16 Comparison of percent of variation accounted for by four different types of models.....	130
Supplemental Table 2.17 Parameter estimates for the Matérn Spatial model developed for the three diseases	131
-CHAPTER III-	135
Table 3.1 Range of performance values of BC ₁ F ₁ s for observed traits	160

Supplemental Table 3.1 Yates corrected Chi-square tests for random distribution of QTL discovered in Nested Association Mapping Population studies for Days to Anthesis (DTA) and for Days to Silk (DTS)	167
Supplemental Table 3.2 BC ₁ F ₁ Development	168
Supplemental Table 3.3 List of accessions used, country of origin, race name, accession name, source, and latitude, longitude, and altitude at point of collection with least square means and standard errors of DTA, DTS, ASI, and Lodging.	188
Supplemental Table 3.4 Agronomic ratings for check hybrids.....	208
Supplemental Table 3.5 Details of experimental units.....	209
Supplemental Table 3.6 Accessions for which no collection information could be found	210
Supplemental Table 3.7 Analysis of variance table for DTA	211
Supplemental Table 3.8 DTA analysis of variance by sources of variation.....	211
Supplemental Table 3.9 Analysis of variance table for DTS	212
Supplemental Table 3.10 DTS analysis of variance by sources of variation	212
Supplemental Table 3.11 Analysis of variance table for lodging	213
Supplemental Table 3.12 Lodging analysis of variance by sources of variation	213
Supplemental Table 3.13 Results from Tukey test for DTA scores in maize populations.....	215
Supplemental Table 3.14 Results from Tukey test for DTS scores in maize populations	217
Supplemental Table 3.15 Results from Tukey test for lodging (cm) in maize populations	219
Supplemental Table 3.16 Comparison of percent of variation accounted for by four different types of models.....	221
Supplemental Table 3.17 Parameter estimates for the Matern spatial model developed for the three diseases	222
APPENDIX	226
Appendix Table 1 Yates correctd Chi square tests for random distribution of QTL discovered in Nested Association Mapping Population studies for Plant Height (PH) and Ear Height (EH)	231
Appendix Table 2 Analysis of variance table for PH.....	232
Appendix Table 3 PH analysis of variance by sources of variation.....	232
Appendix Table 4 Analysis of variance table for EH	233
Appendix Table 5 EH analysis of variance by sources of variation.....	233

Appendix Table 6. List of accessions used country of origin, race name, accession name, source, and Latitude, Longitude, and Altitude at point of collection.	235
Appendix Table 7 Checks used in experiments, their pedigrees, year of release, and least square mean estimate of PH and EH and their standard errors	250
Appendix Table 8 Results from Tukey test for PH (cm) in maize populations	251
Appendix Table 9 Results from Tukey test for EH (cm) in maize populations	253
Appendix Table 10 Parameter estimates for the Matérn Spatial model developed for PH and EH	259
Appendix Table 11 Comparison of percent of variation accounted for by four different types of models	261
Appendix Table 12 Summary of number of accessions used from each country and the number of which are currently available from NCRPIS	262

LIST OF FIGURES

-CHAPTER I-	1
Figure 1.1 Example Semivariogram	21
Figure 1.2 Example Anisotropic Semivariogram	23
-CHAPTER II-	38
Figure 2.1 Pairwise regression of GLS, NLB, SLB, and DTA scores for the 483 BC ₁ F ₁ s screened	68
Figure 2.2 Raw point pattern data of GLS scores of BC ₁ F ₁ s at point of collection of donor landraces	70
Figure 2.3 Raw point pattern data of NLB Scores of BC ₁ F ₁ s at point of collection of donor landraces	71
Figure 2.4 Raw point pattern data of SLB Scores of BC ₁ F ₁ s at point of collection of donor landraces	72
Figure 2.5A-B 2.5A shows predicted GLS scores of BC ₁ F ₁ s with possible donor parents from locations across the Americas; 2.5B shows the standard errors of the estimates	73
Figure 2.6A-B 2.6A shows predicted NLB scores of BC ₁ F ₁ s with possible donor parents from locations across the Americas; 2.6B shows the standard errors of the estimates	74
Figure 2.7A-B 2.7A shows predicted SLB scores of BC ₁ F ₁ s with possible donor parents from locations across the Americas; 2.7B shows the standard errors of the estimates	75
Supplemental Figure 2.1 Development of genotypes used as covariates in analysis.	123
Supplemental Figure 2.2 Boxplot of WMD GLS scores by maize population [†]	125
Supplemental Figure 2.3. Boxplot of WMD NLB scores by maize population [†]	127
Supplemental Figure 2.4 Boxplot of WMD SLB scores by maize population [†]	129
Supplemental Figure 2.5 Covariance functions for Matérn models for GLS, NLB, and SLB [†]	132
-CHAPTER III-	135
Figure 3.1 Pairwise correlations DTA, DTS, ASI, and Lodging	159
Figure 3.2 Raw point pattern data of DTA scores of BC ₁ F ₁ s at point of collection of donor landraces	161
Figure 3.3 Raw point pattern data of DTS Scores of BC ₁ F ₁ s at point of collection of donor landraces	162
Figure 3.4 Raw point pattern data of lodging scores of BC ₁ F ₁ s at point of collection of donor landraces	163
Figure 3.5A-B 3.5A shows predicted DTA scores of BC ₁ F ₁ s with possible donor parents from locations across the Americas; 3.5B shows the standard errors of the estimates	164
Figure 3.6A-B 3.6A shows predictions DTS scores of BC ₁ F ₁ s with possible donor parents from locations across the Americas; 3.6B shows the standard errors of the estimates	165

Figure 3.7A-B 3.7A shows predictions Lodging scores of BC ₁ F ₁ s with possible donor parents from locations across the Americas; 3.7B shows the standard errors of the estimates	166
Supplemental Figure 3.1 Development of genotypes used as covariates in analysis.	214
Supplemental Figure 3.2 Boxplot of DTA scores by maize Sub-population [†]	216
Supplemental Figure 3.3 Boxplot of DTS scores by maize population [†]	218
Supplemental Figure 3.4 Boxplot of lodging (cm) by maize population [†]	220
Supplemental Figure 3.5 Covariance functions for Matérn models for DTA, DTS, and lodging [†]	223
APPENDIX	226
Appendix Figure 1 Pairwise regression of DTA, DTS, ASI, EH, PH, and Lodging for the 483 BC ₁ F ₁ s screened.	234
Appendix Figure 2 Boxplot of PH (cm) by maize population	252
Appendix Figure 3 Boxplot of EH (cm) by maize population	254
Appendix Figure 4 Raw point pattern data of PH measurements (cm) of BC ₁ F ₁ s at point of collection of donor landraces	255
Appendix Figure 5 Raw point pattern data of EH measurements (cm) of BC ₁ F ₁ s at point of collection of donor landraces	256
Appendix Figure 6A-B 6A shows predicted PH of BC ₁ F ₁ s with donor parents collected at un-sampled locations across the Americas; 6B shows the standard errors of the PH estimates	257
Appendix Figure 7A-B 7A shows predicted EH of BC ₁ F ₁ s with donor parents collected at un-sampled locations across the Americas; 7B shows the standard errors of the EH estimates.....	258
Appendix Figure 8 Covariance functions for the Matérn models for Plant Height and Ear Height [†]	260

-CHAPTER I-
Literature Review

Maize Diversity and Germplasm Collections

Whether called corn (*Zea mays L.*), from the old English word for grain, or maize, from the Arawac tribes who introduced it to the Spanish, maize is an integral part of billions of people's daily life. Maize is thought to have been domesticated ~10,000 years BP, in southwestern Mexico, from teosinte (Sluyter and Dominguez, 2006; Wilkes, 2004). Only recently has the hypothesis been widely accepted that the teosinte sub-species *Zea mays ssp. parviglumis* is the direct wild ancestor of maize (Matsuoka et al, 2002). Despite profound differences in ear and plant morphology, teosinte and maize are genetically very close (Doebley and Stec, 1991). The morphological features which are typical of the domestication syndrome and which have large effects on morphology are under the control of about six regions of the genome (Doebley, 2004). Subsequent to domestication, a large amount of genetic material is believed to have been introgressed into maize from teosinte, which most likely grew sympatrically with domesticated maize (Matsuoka et al, 2002). Maize and diploid teosintes have the same chromosome complement ($2n=2x =20$) and form fertile crosses, which enables this genetic exchange (Wilkes, 2004). It is thought that during this teosinte introgression period the regions associated with domestication were under intense selection pressure in order to keep plant type, but the rest of the genome was not, enabling the teosinte introgression. This period of teosinte introgression after domestication is one explanation addressing the overabundance of diversity that exists in maize and its wide range of genetic and morphological differences, compared to other domesticated crops (van Heerwaarden et al, 2011).

Teosintes have a narrow geographical distribution centered in central and southwestern Mexico, with limited populations in northern Mexico, Guatemala, and Nicaragua (Wilkes, 1967). Virtually all teosintes are endangered as a result of modern agriculture, animal husbandry practices, and narrow habitat range. In contrast, maize's growing region covered much of the New World at the time of European colonization with a great amount of morphological variability and local adaptation (Galinat, 1988). It was this great environmental adaptability and preference by humans that allowed maize to become so phenotypically diverse and to form so many distinct populations (Galinat, 1988). The total number of unique New World maize germplasm accessions of landraces exceeds 25,000, which have been categorized into some 300 races (Goodman and Brown, 1988). These accessions are maize landraces or varieties of maize that were/are grown by farmers and which have not been improved with scientific breeding methods.

Strains of maize in Latin America were collected in the 1940s through the 1960s with the aid of the National Research Council (NRC) and the Rockefeller Foundation. Collection missions were centralized in four national centers in Brazil, Colombia, Mexico, and Peru (Brieger et al, 1958; Grobman et al, 1961; Roberts et al, 1957; Wellhausen et al, 1952). The national centers are important as they form the original stock centers for the NRC-Rockefeller collections on which the races of maize were defined and described. The national centers also provide more favorable environments in which to regenerate locally adapted material and a sizable body of knowledge and experience with their national accessions, but unfortunately much of the knowledge is not easily accessible by the general public (Tabo, 2005). In order to form backup collections and ease germplasm exchange and distribution,

almost all of the national New World germplasm banks have donated samples of their holdings either to the International Maize and Wheat Improvement Center (CIMMYT) in Mexico or to the National Center for Genetic Resources Preservation (NCGRP) in Ft. Collins, Colorado, or both (Tabata, 1997).

In order to better utilize maize accessions, several germplasm enhancement projects have been undertaken worldwide. One germplasm enhancement project that has been particularly effective is the Latin American Maize Project (LAMP). LAMP was started in the mid-1980s with a \$1.5 million contribution to the U.S. Department of Agriculture (USDA) from Pioneer Hi-bred International with Pioneer's chief executive officer at the time, William L. Brown, being driving force behind the effort (Salhuana and Pollak, 2006; Salhuana et al, 1991). Approximately 12,000 Latin American accessions were evaluated in the initial stage of the project, and a set of ~300 accessions were identified and targeted for use. LAMP evaluated only half of accessions present in the germplasm banks at the time, highlighting the poor state of the remaining half, for which there was not adequate seed for evaluation. Another project that worked in conjunction with LAMP was the Latin American Maize Regeneration Project, which was a program of the National Germplasm Resources Board of the USDA that was started in 1983. The regeneration project was coordinated at different times by North Carolina State University (NCSU), NCGRP Ft. Collins, and CIMMYT, and enabled the eventual regeneration of most of the maize accessions from Latin America, including those of LAMP, starting at a time when many were on the verge of losing viability due to the limited resources and understaffing of the national programs (Pollak, 2003; Salhuana et al, 1991).

Increasing the U.S.A. Maize Germplasm Base

For many years, the introduction of tropical germplasm into the U.S.A. maize germplasm base has been proposed as a means of diversifying and potentially improving productivity of temperate maize. Melhus (1948) called for studies of Latin American maize, highlighting the fact that tropical material could provide useful variation for disease and insect resistance. Lonquist (1974) proposed developing breeding pools from both tropical and tropical-by-temperate germplasm, and noted the failure of breeders to select the best tropical parents due to little to no prior information as to the quality of the parents.

The greater amount of the work involving the introduction of tropical germplasm into the U.S.A. has been done by Major Goodman at North Carolina State University and Arnel Hallauer at Iowa State University, who have actively released temperate-adapted inbred lines with tropical or exotic pedigrees (Goodman, 1999; Goodman and Carson, 2000; Hallauer and Carena, 2008; Tarter et al, 2004). Though the groups have been active for several decades, the amount of exotic germplasm that has been integrated into U.S.A. private breeding programs remains small. In 1998, Goodman surveyed private breeding programs in the U.S.A. and found that there had been an increase in the use of exotic germplasm from less than 1% in 1984 to 2.9% in 1996 (Goodman, 1998). Moreover, only one-tenth of the exotic germplasm referred to in that study was of tropical origin. According to Goodman (1998), most exotic germplasm used in the U.S.A. has three sources: B68 and French lines F2 and F7. Inbred line B68, the only source with a tropical background, is an Iowa State inbred that was developed from backcrossing Maiz Amargo with B14 (Zuber, 1975). Tropical germplasm to this day is mostly used as a source of disease or insect resistance, introduced

mainly through backcrossing, and gauging the use of exotic germplasm with surveys of the private sector is nearly impossible as breeding companies are no longer willing to share information about germplasm due to intellectual property concerns (Mikel, 2008).

In the U.S.A., the LAMP project eventually led to the Germplasm Enhancement of Maize (GEM) project, a cooperative public and private effort initiated to expand the germplasm base of commercial maize in the U.S.A. (Salhuana et al, 1991; Pollak, 2003). Currently GEM involves the cooperation of 28 private companies (GEM, 2014). GEM functions by using exotic germplasm crossed onto donated private, temperate, elite inbred lines. These families are either then selfed from the F₁ or backcrossed to another elite line of the same heterotic group and then selfed to form semi-inbred families which are then topcrossed and tested. Superior families are initially distributed to the GEM cooperators and, after two years, to the general public through the NCRPIS in Ames, Iowa. The hope is that GEM cooperators and others then would place the GEM families in their breeding programs, would make selections within the segregating material, and would derive their own inbred lines.

While the breeding efforts through GEM are major steps forward in maize germplasm enhancement, in many aspects the programs will not have succeeded until larger percentages of exotic germplasm are being grown in production acreage across the U.S.A. Achieving this success is a formidable task for many reasons. First, exotic materials are several decades behind elite U.S.A. materials in terms of genetic improvement. In 1948, when maize breeding programs across the U.S.A. were in their second or third cycles of selection, the Rockefeller Foundation's program in Mexico, what would later become CIMMYT, was only

releasing its first hybrids (Fitzgerald, 1986). This gap has only widened due to better funding and more consistent research goals in temperate, private-sector breeding programs. The good news is that today the degree to which exotic or tropical germplasm lags behind its U.S.A. counterparts may not be as much of a problem to overcome as in the past. With the continued development of new breeding methodologies, molecular marker technologies, and statistical modeling, exotic germplasm can possibly be improved more quickly, with better efficiency and at a lower cost than before. Second, studies have been conducted examining the underlying genetic structure of maize photoperiod response, and many other adaptive traits (Coles et al, 2010; Hung et al, 2012). These studies give direction to the ways in which material can be more quickly adapted to temperate growing conditions with the use of new breeding methodologies. In the future, there is hope that breeding programs and germplasm management will become better integrated, and temperate breeding programs will be less reluctant to use new sources of germplasm.

Flowering Time in Maize

While there are many phenotypic traits of importance to maize breeders when choosing germplasm to incorporate into a breeding program, one of the most important is flowering time. Flowering time, both male (i.e., anthesis) and female (i.e., silking), plays a key role in the adaptation of maize to different environments by integrating environmental signals that control the timing for the transition from the vegetative to the reproductive growth (Colasanti and Muszynski, 2009). Flowering at the correct time allows the plant to avoid drought, prevent kernel abortion, and optimize the light interception period in order to maximize yield potential. Flowering too late prevents the formation of starch and adequate

dry down of the grain as well as wastes available light energy (Colasanti and Muszynski, 2009). The synchrony of male and female flowering, also known as the anthesis-silking interval (ASI), is also an important adaptive trait in maize as high asynchrony can result in yield losses, especially in modern uniform varieties, due in part to the potential for insufficient pollen at time of silking (Buckler et al, 2009). Asynchrony is an especially important factor in drought stress avoidance. In drought environments, female flowering often is delayed beyond the pollen producing capacity of the tassel, thereby resulting in under-fertilized ears (Bolanos and Edmeades, 1996).

Flowering time of maize landraces has been dramatically modified by domestication and subsequent migration and adaptation to growing environments all across the Americas and the world. Flowering time in teosinte is day-length dependent, in order to synchronize reproductive stages with the rainy season (Wilkes, 1967). In tropical environments, there is a wide range in flowering time and day-length sensitivity, depending on area of adaptation, both across geography and due to altitude changes. The time from planting to the mature grain stage in maize landraces ranges from 2 to 11 months (Kuleshov, 1933). In temperate environments, flowering time has changed to be almost day-length independent in order to adapt to short growing seasons, long summer days, and low temperatures (Gouesnard et al, 2002).

Flowering time is partially determined by the timing of the seedling emergence and by the vegetative to reproductive stage transition, but weather conditions and apical dominance also influence the timing of flowering. Flowering time in maize has been shown

to be a complex trait, under the control of many genes with small effects; the largest mapping project to date, which was conducted under long daylight conditions, found 36 QTL for days to anthesis (DTA) and 39 for days to silk (DTS), of which the largest effect DTS QTL allele had an additive effect of only 1.7 days (Buckler et al, 2009). Since QTL effects are so small and numerous, it is difficult to use any conclusions drawn from a QTL study for breeding by marker assisted selection (Jannink et al, 2010). Flowering time is a highly heritable trait, making phenotypic selections in breeding nurseries fairly straight forward (Buckler et al, 2009). Hallauer (1999) provides an example of the adaptation of tropical material to temperate environments, where four tropical cultivars were mass selected for earlier flowering times by selecting plants with the earliest silking dates. Hallauer (1999) notes that response to the selection for earliness was similar for each of the four tropical cultivars, and that the average response across cultivars for earlier flowering was found to be 3.3 days per cycle over six cycles, showing that selection for earliness is straight forward, albeit a long-term process.

Flowering time has effects on many other traits besides grain production. For example, plant height is often affected as flowering terminates apical growth, and the longer the plant grows vegetatively the higher the number of nodes produced; thus late flowering plants are usually taller (Salas Fernandez et al, 2009). Lodging is also affected as plants that flower later in the season also tend to senesce more slowly (Prochazkova et al, 2001). Foliar disease resistance is often affected by flowering time, especially resistance to fungi that have a necrotrophic stage in their life cycle (Wisser et al, 2006). For many traits, it is difficult to

determine the extent pleiotropic effects of flowering time have on the genetic bases of the trait itself.

Elite breeding programs currently have flowering time highly tuned to the environment that the program is targeting. Given the importance of flowering time as an adaptive trait and to the maximization of yield potential, it is crucial that flowering time not vary too much within a breeding program, to avoid wasting space and effort with lines that have no future in commercial production (Duvick et al, 2004). Flowering time constraints are one reason why breeders may be reluctant to use exotic germplasm, it has been noted even if there are desirable traits in an exotic line or family (Hawbaker et al, 1997).

Plant and Ear Height in Maize

Plant and ear heights are two other traits routinely measured when assessing agronomic acceptability. Like many traits in maize, plant height is polygenically inherited with more than 100 QTLs reported across all ten chromosomes (Peiffer et al, 2014; Wang et al, 2006) and with up to 30 QTLs reported in a single mapping experiment (Schon et al, 2004). In maize landraces grown in temperate environments, excessive plant height is often associated with photoperiod sensitivity, where the change from vegetative to reproductive growth is delayed in long day environments (Colasanti et al, 1998).

Plant height is important as taller plants produce more dry matter relative to the amount of grain produced; this lower amount of harvested matter compared to total dry matter produced can be considered a waste of energy and resources on the part of the plant. Taller plants may be of interest in the future if maize is used as a dual-purpose crop, where

grain is still harvested for food or feed, and where increased plant biomass would be an added value (Graham et al, 2007). If increased biomass becomes desirable, it will reverse the trend in plant height that has occurred in maize breeding to date. Improvement in maize yield in the U.S.A. over the last 70 years has been due to the ability of hybrids to be planted at higher plant densities, along with response to increased inputs and weed control, not to increase of yield on a per-plant basis (Duvick, 1984). These cultural and management practices have reduced the need for tall plants, which tend to produce denser canopies, providing more shade to reduce weed growth, even at low planting densities. Taller plants also tend to have a greater response to nitrogen application (Johnson et al, 1986). These attributes, however, are no longer necessary under modern cultivation practices.

Examining maize hybrids from three eras in maize production, 1930-1950, 1950-1970, and 1970-1980, Meghji et al (1984) found that ear height and plant height were both reduced from one era to the next; they also found that this was connected with reduced tendency to lodge. They suggested there was also a connection between reduced plant height and ability to yield well at high planting densities. This conclusion was supported by another study which examined the change in traits of maize hybrids released from 1930 to 1978 (Duvick, 1984). It was noted that large improvements were made in resistance to stalk lodging in hybrids from 1940 to 1950, which corresponded with a reduction in the level of mid-parent heterosis for plant height. The trend toward reduction in heterosis for plant and ear height was about 0.3 cm/year for plant height and 0.4cm/year for ear height, which were both statistically significant. This reduced heterosis for height traits was not connected with

a reduced level of grain yield heterosis, which increased significantly over the years, illustrating that grain yield is independent of plant height (Duvick, 1984).

Plant and ear heights of landraces, much like flowering time, have a great range of phenotypic values across the range of maize growing environments, with tropical germplasm from Columbia and the Yucatan in southern Mexico being the tallest (Kuleshov, 1933). Maize landraces may be of more use to breeders if high-biomass/high-plant height becomes desirable. Conversely for breeders there are serious concerns about the connection of plant height and lodging.

Lodging in Maize

With the mechanization of agriculture lodging and intactness of plants at harvest time become a great concern, as prior to this maize was tended by hand and a maize plant that lodged before harvest could still be picked, though ear quality is often affected. With mechanization came the need for all plants to be erect in order for harvest machinery to function with minimal yield loss (Li, 2014). Stalk lodging in maize is a major problem and is estimated to cause annual yield losses of 5-25 % (Kang et al, 1999; Zuber and Kang, 1978). In 1993, maize farmers in the state of Nebraska lost over \$200 million as a result of lodging due to high winds (Elmore and Ferguson, 1999).

Several physiological traits have been assessed for their use in selection for lodging resistance, including stalk compressive strength, stem diameter, pith density, and rind penetration resistance (Abedon et al, 1999; Hondroyianni et al, 2000; Thompson, 1969; Zuber and Kang, 1978). Lodging can be induced by the presence of many species of fungi and bacteria which can cause stalk rot, especially after flowering. Pathogenic organisms

decay pith tissue in lower stalks, which lowers stalk strength, thereby increasing the likelihood of lodging (Leonard and Thompson, 1976). Anderson and White (1994) evaluated several methods of identifying stalk rot and lodging resistance, to determine which traits were best for selecting against lodging . Traits that were examined included: a rind puncture test, a push over test, measurements of rind thickness, pith moisture percentage, pith density, and ratings of Anthracnose stalk rot and *Diplodia* stalk rot. Overall, they reported that the rind puncture test had the greatest correlation with lodging. Rind puncture was also one of the easier measurements to take and was non-destructive, thus enabling seed to be harvested from a tested plant, and was recommended for use in breeding nurseries (Anderson and White, 1994).

The time between flowering and senescence that is critical to the occurrence of lodging (Borrell et al, 2001). Plants that can “stay green” are more likely to stay erect; Stay-green is the general term for when senescence is delayed compared with a standard reference genotype (Thomas and Howarth, 2000). Stay-green can occur in several different ways: 1) when senescence is initiated late but then proceeds at a normal rate, 2) when senescence initiates on schedule but proceeds slowly, and 3) when chlorophyll is retained but senescence proceeds normally beneath the surface of the retained pigmentation (Thomas and Howarth, 2000). It is the second type that is of the greatest value and that has been selected for in maize improvement (Duvick, 1984). Ideally senescence can enable the drying down of the grain in the ear but can allow the rest of the plant to remain green so as to help prevent lodging.

In general, exotic material has higher rates of lodging than improved U.S.A. material, which may be one of the factors that make breeders reluctant to use exotic germplasm (Gardner, 1990). However, there is variation in maize accessions to lodging propensity (Gutiérrez et al, 2003). Currently, there is very little information available to breeders as to which accessions would be less likely to lodge and thus be the best option for working with exotic germplasm. As germplasm enhancement efforts continue, more exotic material will be assessed for agronomic traits, giving researchers better ideas as to which exotic germplasm to use.

Gray Leaf Spot in Maize

Gray leaf spot (GLS) is an important foliar disease of maize that is caused by *Cercospora zea-maydis* and its sister species *Cercospora zeina* (Crous et al, 2006; Dunkle and Levy, 2000; Wang et al, 1998). *Cercospora zea-maydis* and *Cercospora zeina* are morphologically similar but can be distinguished by physiological and phylogenetic criteria. *C. zea-maydis* and *C. zeina* are both hemibiotrophic Ascomycetes, which have a feeding pattern characterized by three stages; initial feeding which occurs on live plant tissue, subsequent inducement of necrosis, and finally necrotrophic feeding, thus exhibiting an extended latent period (Balint-Kurti et al, 2010).

GLS was first identified from specimens collected in Illinois in 1924 (Tehon and Daniels, 1925), where *C. zea-maydis* was identified. This species remained the main pathogen responsible for GLS in the U.S.A. until relatively recently. Now, *C. zeina*, considered to originate in Africa, is also known to contribute to disease, and both species are widespread in the United States (Crous et al, 2006). The fungus survives the winter on

infected maize residue from the previous growing season; this forms the source of inoculum for the next growing season. As temperatures increase in the spring, the overwintered mycelia produce spores that splash onto young maize leaves, and these spores germinate and enter the plant where they induce the first observable symptoms on the lower leaves of the plant. Reproduction and formation of secondary inoculum occurs in colonized tissue through the production of asexual spores called conidia. The sexual mating cycle of *Cercospora* species is not well known as no teleomorphs have been discovered. The onset of GLS symptoms typically occur after plants have flowered (Rupe et al, 1982). The relationship between maturity and GLS was demonstrated by planting of the same hybrid at three-week intervals and assessing GLS development throughout the season (Ward and Nowell, 1998). There is also evidence that a toxin plays a role in disease development; *C. zea-maydis* produces cercosporin, a photosensitizing perylenquinone that disrupts cell membranes in the presence of light (Dunkle and Levy, 2000).

GLS became a major problem in the U.S.A. only in the 1970s due to widespread adoption of conservation tillage and continuous maize growing systems, increasing the amount of maize debris left in the field from previous growing seasons across large portions of the maize growing regions (Ward et al, 1999). GLS infection of maize acreage increased from 7.2 to 14.9 million hectares during the 1980s and 1990s (Sparks, 1997). As of today, GLS affects maize production areas worldwide, limiting yields to a moderate extent in the U.S.A. Corn Belt and considerably in South Africa, though reported yield losses due to GLS have been as high as 50% in some U.S.A. maize fields (Ward et al, 1999).

GLS is managed through use of moderately resistant hybrids, foliar fungicides, and tillage practices which remove debris (Lipps et al, 1996; Payne and Waldron, 1983; Ward et al, 1997). Of these methods, resistant hybrids offer the best control option since crop residue management cancels benefits gained from conservation tillage, and fungicide applications are often not profitable (de Nazareno et al, 1993; Munkvold et al, 2001). In commercial hybrids, resistance to GLS is derived most often from the Lancaster side of the pedigree (Carson et al, 2002; Ulrich et al, 1990). This may be due to higher turnover rates in male inbred, which allows for more introgression of resistance sources. Some commercial hybrids with increased resistance to GLS have been developed; however all genotypes eventually show some symptoms given adequate levels of inoculum and appropriate environmental conditions (Bubeck et al, 1993; Holland and Goodman, 1995; Kraja et al, 2000).

Several studies have been conducted to assess inbred lines as potential sources of GLS resistance. In one example, Coates and White (1994) screened 1,396 inbreds for GLS, 62 of which were selected due to their high GLS resistance and correct maturity range for evaluation in hybrid combinations. Coates and White (1994) note that hybrid combinations of inbreds CI30, CI88A, DS:74:1071, H110, Mo18W, Mo11, and TEX1 were significantly more resistant than the check hybrid and may be valuable sources of GLS resistance. They also highlight several other inbred lines that could be used as sources of resistance. Pratt and Gordan (2006) note that several inbred lines from North Carolina State University display high levels of GLS resistance, including NC262, NC264, NC320, NC332, and NC354 among others. In the U.S.A. there has been a concerted effort to improve the resistance of elite germplasm, but the development of GLS resistant material has not been as comprehensive in

many areas where GLS has become endemic, or where a different species of *Cercospora* is more prevalent (Pratt and Gordan, 2006). In order to better understand the mechanisms of genetic resistance to GLS, several QTL mapping studies have been done. The largest of these studies found 16 QTL with mostly small effect sizes (Benson, 2013). The broad sense heritability of GLS has been estimated to be high at $H^2 = 73\%$, making improvement with phenotypic selection straight forward (Clements et al, 2000).

Northern Leaf Blight in Maize

Northern leaf blight (NLB) is caused by the fungus *Setosphaeria turcica* (anamorph *Exserohilum turcicum*), and is an economically damaging foliar disease of maize throughout the world, especially in temperate and highland-tropical growing environments. *S. turcica* is a hemibiotrophic Ascomycete (Levy and Pataky, 1992). This results in infection which is generally limited to leaves (White, 1999). The fungus produces asexual conidia on conidiophores that protrude directly out of lesions on the leaf surface (Knox-Davies and Dickson, 1960).

As early as the 1950s, resistance to NLB became a target of maize breeding programs due to a series of heavy NLB epidemics that occurred in the U.S.A. in the 1940s and 50s (Ferguson and Carson, 2007; Robert and Findley, 1952; Welz and Geiger, 2000). During the early 1940s, double-cross hybrids were being used, and the majority of the hybrids were highly susceptible to NLB. Farmers, who for the first time had significant amounts of money invested in quality seeds, became more aware of the presence of disease in the newly-developed maize varieties and began demanding resistant hybrids. Thus breeding programs

were initiated with polygenic resistance being the first type of resistance utilized (Jenkins and Robert, 1961)

It was in 1959 that qualitative resistance to NLB was first described in detail. Resistance was categorized into six dominant genes, *Ht1*, *Ht2*, *Ht3*, *Htm1*, *Htn1* and *NN*, which were shown to control resistance to specific races of *S. turcicum*. The *Ht1*, *Ht2*, and *Ht3* genes confer a “chlorotic lesion” type of reaction to the pathogen whereas the *Htm1* gene helps delay symptoms until after anthesis (Carson, 1995). In the 1960s and 1970s these genes were utilized in U.S.A. germplasm; the *Ht1* gene was used extensively until a race of *E. turcicum* with corresponding virulence to it was found in Hawaii in 1972 and subsequently spread to the continental U.S.A. (Smith and Kinsey, 1980). This rapid development of resistance to the *Ht1* gene made qualitative NLB resistance less appealing to most maize breeders, so the remaining major-effect genes were not widely deployed (Ferguson and Carson, 2007; Welz and Geiger, 2000). Pratt and Gordon (2006) state that deployment of major-gene resistance to NLB in the U.S.A. had been over-done, which had left U.S.A. maize germplasm vulnerable to race shifts, and thus further breeding efforts would require a combination of the *Ht* genes and quantitative resistance.

Several QTL mapping studies have been conducted to find genes that confer resistance to NLB. The largest of these studies found 29 QTL with mostly small but varying effect sizes, the largest of which is hypothesized to be *Ht1*. The overall heritability of NLB was estimated to be 77%, making improvement with phenotypic selection theoretically quite feasible (Poland et al, 2011). Though breeders in the U.S.A. have been concerned with the integration of NLB resistance into their programs, breeders in tropical environments have

placed more emphasis on quantitative resistance, partly due to different race types than in the U.S.A. Tropical breeders have been able to develop lines with high levels of resistance, thus tropical material may serve as a source of new resistance genes for temperate germplasm (Paliwal et al, 2000).

Southern Leaf Blight in Maize

Southern leaf blight (SLB), caused by *Cochliobolus heterostrophus*, is another hemibiotrophic Ascomycete (though SLB is more necrotropic compared to GLS or NLB) foliar fungal-disease of maize that occurs worldwide, but is most common and destructive in warm temperate and tropical maize growing regions (Hooker, 1972). Primary infection occurs when spores are dispersed by wind currents and water droplets. The source of new inoculum for SLB comes from overwintering mycelium on debris left in the field from the previous year (Hesseltine et al, 1971). Disease development is favored by warm moist weather conditions, and therefore it is one of the most prevalent biotic stresses in the Southeast U.S.A. and the humid tropics. *C. heterostrophus* has a short life cycle of 60 to 72 hours under ideal conditions, making it one of the faster-progressing maize pathogens. Reproduction occurs in both asexual and sexual stages, with asexual reproduction occurring repeatedly within a single growing season and providing inoculum for increased disease pressure during a growing season. The sexual stage has rarely been observed in the field, and requires a strain of the opposite mating type in order to induce sexual reproduction (Turgeon and Lu, 2000).

Three races of SLB have been characterized: O, T, and C. The most common, Race O, is responsible for the majority of the current SLB outbreaks worldwide (Carson et al,

2004). Race T is also an important race as it produces T-toxin, which is toxic only to maize with Texas male sterile cytoplasm (*cms-T*). In the 1960s and early 1970s, seed companies relied extensively on the use of *cms-T* in the production of hybrids, creating a lack of cytoplasmic diversity, which placed heavy selection pressure on Race T (Levings and Siedow, 1992). The large amount of maize acreage with T cytoplasm allowed for a large race shift to Race T SLB, resulting in the SLB epidemic of 1970-1971. This epidemic highlighted not only the dangers of the SLB, but also the dangers of genetic uniformity. The third, Race C, was first discovered in 1987 and infects only maize with C cytoplasmic male sterility (*cms-C*) maize, with most infection occurring in China (Wei, 1988).

In 1970-71 yield losses of hybrids with *cms-T* reached 50%. Today this is the exception as hybrids show yield loss from 0.7 to 0.8% for each increase of 1% in the affected leaves, with affected leaf area rarely reaching 25% (Byrnes et al, 1989; Hooker, 1972). SLB can be managed in several ways, including crop rotation and tilling maize debris under to reduce inoculum load. However, genetic resistance is the preferred control method (Carson, 1998). Maize inbred lines developed in tropical climates may provide new sources of resistance to SLB. This material often shows moderate to high quantitative resistance to SLB Race O (Pratt and Gordon, 2006). Maize landraces may be a source for resistance to SLB in conjunction with the use of improved inbreds and hybrids from the tropics.

Kriging

Kriging was first developed in the late 1950s by the South African mining engineer Danie Krige and the French mathematician Georges Matheron (Matheron, 1963). Kriging is a blanket term that covers a suite of least-squares linear regression algorithms that are

intended to predict values of a variable at location where data for the variable is not available, based on a spatial pattern of existing data (Banerjee et al, 2004). Kriging uses the data twice: the first time to estimate the spatial autocorrelation model and the second time for use in making predictions (Stein, 1999).

The most widely used method is Ordinary Kriging, generally a highly reliable estimation method (Yamamoto, 2000). This method assumes that the data set has a stationary variance but a non-stationary mean within a search radius, and accounts for local fluctuations of the mean by limiting the area to some local neighborhood (Cressie, 1988). Other types of kriging exist (Stein, 1999), but were not used herein.

Defining the local neighborhood is the first step for spatial prediction when using kriging. Local neighborhoods can be described with the use of a semivariogram. A semivariogram depicts the spatial autocorrelation of the measured sample points (Banerjee et al, 2004). This uses a basic principle of geography: the closer points are together the more alike they are likely to be. Thus measured points that are close together will generally have a smaller variance between them than those farther apart. To develop a semivariogram, the squared difference of every pair of locations could be plotted against distance, but since plotting each pair of locations quickly becomes uninterpretable in large data sets, the number of points plotted in a semivariogram is reduced by grouping pairs of locations based on their distance from one another. This grouping process is known as binning. To bin points, the distance between all pairs of points in the sample is first calculated. Secondly pairs with similar distances are placed in the same bin. For all pairs within a bin the variance is calculated, and the average of those variances is calculated. It is then divided by two to give

the semivariance value. These values are then plotted with the calculated semivariance on the y-axis, and the bin distance on the x-axis. An example semivariogram and the features that help explain a local neighborhood is given in Figure 1.1.

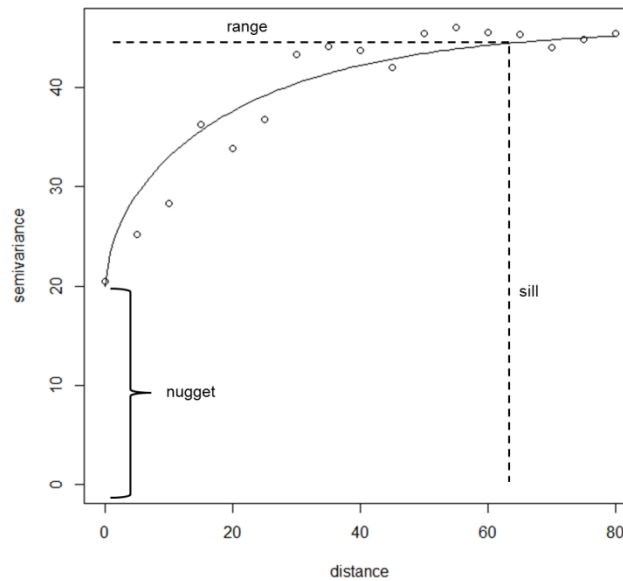


Figure 1.1 Example Semivariogram

Pairs of locations that are closer together, far left on the x-axis of the semivariogram, should have smaller variance between points. As pairs of locations become farther apart, they should become more dissimilar and have a larger variance (move up on the y-axis of the semivariogram). Noted are graphical depictions of three of the parameters used to describe the model: the nugget, sill, and range.

There are several features of the semivariogram that help explain the spatial process that data is exhibiting. The semivariance at a distance of zero in theory should be zero, because there are no differences between points that are compared to themselves. In practice, this is not the case due to measurement and ascertainment error, thus the variance at distance zero is designated as the nugget (Stein, 1999). In the example above, the semivariogram

model intercepts the y-axis at 20, thus the nugget is 20. Measurement error occurs for many reasons, including error inherent in measuring devices, measurements done at larger scales than the micro variation of the nugget effect, and natural phenomena that vary spatially over a range of scales, i.e. micro or macro scales.

Another feature of the semivariogram is the range, which is the distance from zero to the point where the model fit to the semivariogram flattens out and the semivariance becomes approximately equal to the variance of the entire population. The range defines the maximum neighborhood over which values will be estimated, to take advantage of the statistical correlation among the observations (Stein, 1999). The third feature of the semivariogram that helps define the local neighborhood is the sill, the semivariance at which the semivariogram model attains the range (the value on the y-axis). The sill minus the nugget is known as the partial sill (Stein, 1999).

These three parameters do not explain all of the spatial distribution of a variable. There can be differences in the variance between points depending on the direction from the center point. It is quite natural for the behavior of a data set to vary differently in one direction as compared to another. For example, data collected on a steeply sloping hill may vary in two directions. The first is up and down the hill where it varies quickly from the top to bottom, and the second is across the hill where it varies more slowly. This is called anisotropy and often must be accounted for in spatial models (Banerjee et al, 2004). When performing anisotropic correction in Kriging modeling, the user is essentially guiding the Kriging interpolator to use sample data points that will most accurately reflect the behavior

of the surface (Hansen, 1993). When interpolating points oriented in a north-south direction the Kriging weights can be influenced to use the parameters of one model while the points oriented in an east-west direction will be weighted using a different model. An example of an anisotropic semivariogram is given in Figure 1.2.

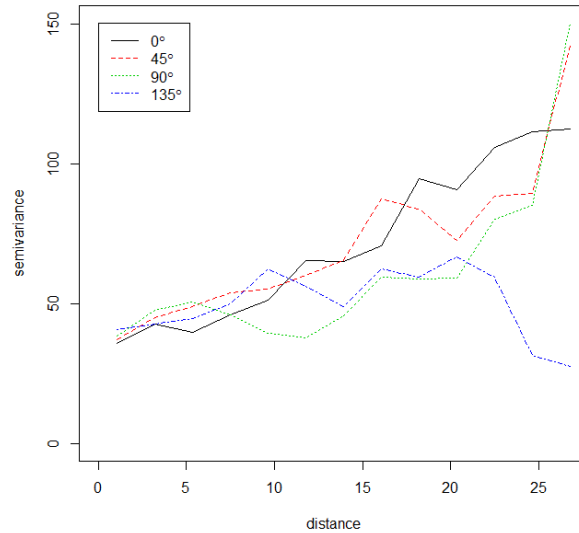


Figure 1.2 Example Anisotropic Semivariogram

Noted are four semivariograms over different angles, which are not similar, implying anisotropy correction is needed.

The four lines of the graph plot variances (the Y-axis) and their corresponding distances (the X-axis), for four different angles from the center point. The semivariogram reveals that the data in this example is anisotropic. Thus, it would be necessary to account for the directions in which the variances will be calculated. These parameters are discussed in the following section. When more than one direction is set, the angle to which these sectors will be oriented must be specified. In the above diagram, the angles are 0, 45, 90, and 135

degrees. It is unlikely to find data pairs exactly following such orientations, thus it is necessary to define an interval around exact values for which points will be considered; this interval is known as the tolerance. Once the experimental semivariogram has been generated, a model curve can be calculated which closely fits the semivariogram. It is necessary to create a model that “looks” in the direction in which the data is varying. This is done by modifying the number of directions analyzed, the angles in which they are oriented, and the degrees of tolerance afforded to each direction.

There are several different models that can be used to fit a semivariogram with varying levels of complexity. Stein (1999) recommends the Matérn model for many data sets in building spatial models. Matérn covariance functions are a very general class of covariance functions which include special cases such as the exponential and the Gaussian covariance function. With modern computing, values defining these models are calculated with the use of maximum likelihood, as calculating the model parameters directly is computational intractable. Maximum likelihood estimates are found through an iterative process to maximize the log likelihood of the model. This process can be computationally intensive, so to improve the estimation process starting values of parameters describing the spatial model are used to begin iterative process. These are often based on visual inspection of the semivariogram (Mardia and Marshall, 1984). Once models specifying the local neighborhood have been developed, the second step is predicting the unknown values. This occurs by first defining a grid over the space that is to be predicted. Once the correct model is

found, blanks in the grid are filled in by using the spatial coordinates of each cell in the grid space, with the use of any covariates which have been defined over the same grid space.

Kriging for Use in Germplasm Utilization

Though kriging originated in the mining industry, it has the potential to be used in identifying potentially useful plant genetic resources. Plant accessions conserved in germplasm banks are obvious places to look for useful traits, but given the immense size of these collections finding individual accessions with a given trait can be difficult and extremely costly. In the case of maize, there are over 27,000 unique maize accessions worldwide, the evaluation of which is next to impossible due to constraints on the number of trial locations, field space, and monetary concerns of many programs (Ortiz et al, 2010; Taba, 2005). What is needed is a method of efficiently selecting a limited number of accessions to screen with a greater probability of capturing useful variation than if material were selected at random or through the use of techniques that do not focus on the sought-after trait.

Core collections have often been proposed as a way to work with a subset of accessions that represent the diversity across a crop species. There are numerous examples of methodologies to develop core collections, which in practice tend towards limiting the size of the subset to around 10% of the original collection size (Brown, 1989). However, much core collection research seems to focus on methods to establish core collections (Hu et al, 2000; Malosetti and Abadie, 2001; Odong et al, 2013; Ortiz et al, 1998) or the analysis of the diversity held within core collections (Fu et al, 2005; Glaszmann et al, 2010; Tohme et al, 1996). It has also been noted that the method used to develop a core set may need to change based on evaluation criteria (Odong et al, 2013). There appears to be a lack of evidence

showing that core collections have had a significant impact on the utilization of genetic resources (Street et al, 2013).

Spatial analysis could provide another method to improve the efficiency with which specific traits are identified from genetic resource collections; this is based on the premise that traits displayed by accessions follow useful spatial patterns. Spatial patterns may in part reflect the selection pressures of the environment from which an accession was originally sampled (Mackay et al, 1990, 2005). Many traits can be linked to climatic parameters that are dependent on geography. Endresen (2010) demonstrated how eco-geographic data from the collection sites of 14 Nordic barley landraces (*Hordeum vulgare L.*) were successfully correlated to morphological traits using multilinear modeling techniques.

Spatial analysis has been noted for its potential usefulness in the collection of germplasm for many species, as it may aid in targeting collection trips to distinct environments which then may maximize the amount of genetic and phenotypic variation collected for traits of breeding importance. Spatial data can be useful as it may provide a better understanding of existing collections and how these collections could be best utilized for plant improvement projects (Greene, 1996). For example spatial models can be developed to ascertain the amount of loss in genetic variation in primitive varieties and wild species based on the distribution of germplasm and key demographic factors across the landscape, or over different time points. Another example of its usefulness could be in the analysis of genetic vulnerability of cultivated crops by examining the distribution of cultivars in a region or country (Greene, 1996).

Spatial analysis can also be used to better understand and effectively use existing germplasm collections. Ecogeographic representation of collections can be assessed by correlating collection sites on maps such as climate, soil, topography and ecosystem, to gain insight to the forces that may have affected the degree of selection of different traits. Morphological descriptors or genetic variation can be linked with environmental attributes. Use of spatial data can also assist researchers in selecting potentially useful material from the collection (Steiner, 1996). It is hoped that by using spatial methods accessions can be identified that originate in environments having similar agronomic attributes.

Using spatial analysis, we hope to better predict agronomic and disease traits of maize landraces using a set of semi-exotic BC₁ F₁s. The underlying hypothesis is that trait variation between BC₁ F₁s can be modeled using the point of collection, altitude of collection point, and genetic data to increase prediction accuracy. From this, we hope to identify accessions that would be most likely to carry a trait of interest.

References

- Abedon BG, Darrah LL, Tracy WF, 1999. Developmental changes associated with divergent selection for rind penetrometer resistance in the MoSCSSS maize synthetic. *Crop Sci* 39:108-114
- Anderson B, White D, 1994. Evaluation of methods for identification of corn genotypes with stalk rot and lodging resistance. *Plant Dis* 78:590-593
- Balint-Kurti PJ, Yang J, Van Esbroeck G, Jung J, Smith ME, 2010. Use of a maize advanced intercross line for mapping of QTL for northern leaf blight resistance and multiple disease resistance. *Crop Sci* 50:458-466
- Banerjee S, Gelfand AE, Carlin BP, 2004. Hierarchical modeling and analysis for spatial data. Chapman & Hall/CRC Press, Boca Raton
- Benson J, 2013. Resistance to gray leaf spot of maize: Underlying genetic architecture and associated mechanisms. Cornell University Dissertation, <http://hdlhandle.net/1813/34022> (accessed June 18, 2014)
- Bolanos J, Edmeades G, 1996. The importance of the anthesis-silking interval in breeding for drought tolerance in tropical maize. *Field Crops Res* 48:65-80
- Borrell A, Hammer G, Oosterom E, 2001. Stay-green: A consequence of the balance between supply and demand for nitrogen during grain filling. *Ann Appl Biol* 138:91-95
- Brieger FG, Gurgel JTA, Paterniani E, Blumenschein A, Alleoni MR, 1958. Races of maize in Brazil and other eastern South American countries. National Academy of Science-National Research Council Washington, DC, USA
- Brown A, 1989. Core collections: A practical approach to genetic resources management. *Genome* 31:818-824
- Bubeck, D, Goodman MM, Beavis W, Grant D, 1993. Quantitative trait loci controlling resistance to gray leaf spot in maize. *Crop Sci* 33:838-847
- Buckler ES, Holland JB, Bradbury PJ, Acharya CB, Brown PJ, Browne C, Ersoz E, Flint-Garcia S, Garcia A, Glaubitz JC, Goodman MM, Harjes C, Guill K, Kroon DE, Larsson S, Lepak NK, Li H, Mitchell SE, Pressoir G, Peiffer JA, Rosas MO, Rocheford TR, Romay MC, Romero S, Salvo S, Villeda HS, da Silva HS, Sun Q, Tian F, Upadaya N, Ware D, Yates H, Yu J, Zhang Z, Kresovich S, McMullen MD, 2009. The genetic architecture of maize flowering time. *Science* 325:714-718

- Byrnes K, Pataky J, White D, 1989. Relationships between yield of three maize hybrids and severity of southern leaf blight caused by race O of *Bipolaris maydis*. Plant Dis 73:834-840
- Carson M, 1995. A new gene in maize conferring the "chlorotic halo" reaction to infection by *Exserohilum turcicum*. Plant Dis 79:717-720
- Carson M, 1998. Aggressiveness and perennation of isolates of *Cochliobolus heterostrophus* from North Carolina. Plant Dis 82:1043-1047
- Carson M, Goodman MM, Williamson S, 2002. Variation in aggressiveness among isolates of *Cercospora* from maize as a potential cause of genotype-environment interaction in gray leaf spot trials. Plant Dis 86:1089-1093
- Carson M, Stuber C, Senior M, 2004. Identification and mapping of quantitative trait loci conditioning resistance to southern leaf blight of maize caused by *Cochliobolus heterostrophus* race O. Phytopath 94:862-867
- Clements MJ, Dudley J, White D, 2000. Quantitative trait loci associated with resistance to gray leaf spot of corn. Phytopath 90:1018-1025
- Coates ST, White DG, 1994. Sources of resistance to gray leaf spot of corn. Plant Dis 78:1153-1155
- Colasanti J, Muszynski M, 2009. The maize floral transition. pp41-55. In: Handbook of maize: its biology. Bennetzen J, Hake S, eds. Springer, NY
- Colasanti J, Yuan Z, Sundaresan V, 1998. The indeterminate gene encodes a zinc finger protein and regulates a leaf-generated signal required for the transition to flowering in maize. Cell 93:593-603
- Coles ND, McMullen MD, Balint-Kurti PJ, Pratt RC, Holland JB, 2010. Genetic control of photoperiod sensitivity in maize revealed by joint multiple population analysis. Genetics 184:799-812
- Cressie N, 1988. Spatial prediction and ordinary Kriging. Math Geol 20:405-421
- Crous PW, Groenewald JZ, Groenewald M, Caldwell P, Braun U, Harrington TC, 2006. Species of *Cercospora* associated with grey leaf spot of maize. Stud Mycol 55:189-197
- De Nazareno N, Lipps P, Madden L, 1993. Effect of levels of corn residue on the epidemiology of gray leaf spot of corn in Ohio. Plant Dis 77:67-70

- Doebley J, 2004. The genetics of maize evolution. *Annu Rev Genet* 38:37-59
- Doebley J, Stec A, 1991. Genetic analysis of the morphological differences between maize and teosinte. *Genetics* 129:285-295
- Dunkle LD, Levy M, 2000. Genetic relatedness of African and United States populations of *Cercospora zae-maydis*. *Phytopath* 90:486-490
- Duvick D, J Smith, Cooper M, 2004. Long-term selection in a commercial hybrid maize breeding program. *Plant Breed Rev* 24:109-152
- Duvick DN, 1984. Genetic contributions to yield gains of US hybrid maize, 1930 to 1980, pp15-48. In: *Genetic Contributions to Yield Gains of Five Major Crop Plants*. Fehr WR ed. CSSA Spec. Publ. 7. CSSA and ASA, Madison, WI.
- Elmore RW, Ferguson RB, 1999. Mid-season stalk breakage in corn: Hybrid and environmental factors. *J Prod Agric* 12:293-299
- Endresen DTF, 2010. Predictive association between trait data and ecogeographic data for nordic barley landraces. *Crop Sci* 50:2418-2430
- Ferguson L, Carson M, 2007. Temporal variation in *Setosphaeria turcica* between 1974 and 1994 and origin of races 1, 23, and 23N in the United States. *Phytopath* 97:1501-1511
- Fitzgerald D, 1986. Exporting American agriculture: The Rockefeller Foundation in Mexico, 1943-53. *Soc Stud Sci* 16:457-483
- Fu YB, Peterson GW, Williams D, Richards KW, Fetch JM, 2005. Patterns of AFLP variation in a core subset of cultivated hexaploid oat germplasm. *Theor Appl Genet* 111:530-539
- Galinat WC, 1988. The origin of corn, pp1-31. In: *Corn and Corn Improvement 3rd ed.* Sprague GF, Dudley JW eds. American Society of Agron, Madison, WI
- Gardner FP, Valle R, and McCloud DE, 1990. Yield characteristics of ancient races of maize compared to a modern hybrid. *Agron J* 82: 864-868.
- Glaszmann J, Kilian B, Upadhyaya H, Varshney R, 2010. Accessing genetic diversity for crop improvement. *Curr Opin Plant Biol* 13:167-173
- Germplasm Enhancement of Maize Website, 2014. www.publiciastate.edu/~usda-gem. (accessed 17 June 2014)

- Goodman MM, 1999. Broadening the genetic diversity in maize breeding by use of exotic germplasm, pp139-148. In: International Symposium on the Genetics and Exploitation of Heterosis in Crops. Coors JG, Pandey S eds. ASA, CSSA, and SSSA, Madison, WI.
- Goodman MM, Brown WL, 1988. Races of Corn. pp33-79. In: Corn and Corn Improvement. 3rd ed. Sprague GF, Dudley JW eds. Agronomy Monograph 18. ASA, CSSA, and SSSA, Madison, WI.
- Goodman MM, 1998, Research policies thwart potential payoff of exotic germplasm, Diversity 14:30-35
- Goodman MM, Carson ML, 2000. Reality vs. myth: Corn breeding, exotics, and genetic engineering. Annual Corn Sorghum Research Conference Proc. 55: 140-172.
- Gouesnard B, Rebourg C, Welcker C, Charcosset A, 2002. Analysis of photoperiod sensitivity within a collection of tropical maize populations. Genet Resour Crop Evol 49:471-481
- Graham RL, Nelson R, Sheehan J, Perlack R, Wright LL, 2007. Current and potential US corn stover supplies. Agron J 99:1-11
- Greene SL, and Hart TC, 1996. Plant genetic resource collections: an opportunity for the evolution of global data sets. Proceedings of the Third International Conference on Integrating GIS and Environmental Modeling. National Center for Geographic Information and Analysis, Santa Barbara, CA.
- Grobman A, Salhuana W, Sevilla R, with Mangelsdorf PC, 1961. Races of maize in Peru. National Academy of Sciences- National Research Council, Washington, DC, USA
- Gutiérrez L, Franco J, Crossa J, Abadie T, 2003. Comparing a preliminary racial classification with a numerical classification of the maize landraces of Uruguay. Crop Sci 43:718-727
- Hallauer A, 1999. Conversion of tropical germplasm for temperate area use. Illinois Corn Breeders' School 35:20-36
- Hallauer AR, Carena MJ, 2008. Maize breeding, pp1-98 In: Handbook of Plant Breeding: Cereals. Carena MJ ed. Springer, NY.
- Hansen R, 1993. Interpretive gridding by anisotropic Kriging. Geophysics 58:1491-1497
- Hesseltine CW, Ellis JJ, Shotwell OL, 1971. *Helminthosporium*: Secondary metabolites, southern leaf blight of corn, and biology. J Agric Food Chem 19:707-717

- Holland JB, Goodman MM, 1995. Combining ability of tropical maize accessions with US germplasm. *Crop Sci* 35:767-773
- Hondroyianni E, Papakosta D, Gagianas A, Tsatsarelis K, 2000. Corn stalk traits related to lodging resistance in two soils of differing salinity. *Maydica* 45:125-133
- Hu J, Zhu J, and Xu H, 2000. Methods of constructing core collections by stepwise clustering with three sampling strategies based on the genotypic values of crops. *Theor Appl Genet* 101:264-268
- Hung H, Shannon LM, Tian F, Bradbury PJ, Chen C, Flint-Garcia SA, McMullen MD, Ware D, Buckler ES, Doebley JF, Holland JB, 2012. ZmCCT and the genetic basis of day-length adaptation underlying the postdomestication spread of maize. *PNAS* 109:1913-1921
- Jannink JL, Lorenz AJ, Iwata H, 2010. Genomic selection in plant breeding: From theory to practice. *Brief Funct Genomics* 9:166-177
- Jenkins MT, Robert AL, 1961. Further genetic studies of resistance to *Helminthosporium turcicum* pass. in maize by means of chromosomal translocations. *Crop Sci* 1:450-455
- Johnson E, Fischer K, Edmeades G, Palmer A, 1986. Recurrent selection for reduced plant height in lowland tropical maize. *Crop Sci* 26:253-260
- Kang MS, Din AK, Zhang Y, Magari R, 1999. Combining ability for rind puncture resistance in maize. *Crop Sci* 39:368-371
- Knox-Davies P, Dickson J, 1960. Cytology of *Helminthosporium turcicum* and its ascigerous stage, *Trichometasphaeria turcica*. *Am J Bot* 47:328-339
- Kraja A, Dudley JW, White DG, 2000. Identification of tropical and temperate maize populations having favorable alleles for disease resistance. *Crop Sci* 40:948-954
- Kuleshov N, 1933. World's diversity of phenotypes of maize. *J Amer Soc Agron* 25:688-700
- Leonard K, Thompson D, 1976. Effects of temperature and host maturity on lesion development of *Colletotrichum graminicola* on corn. *Phytopath* 66:635-639
- Levings III CS, Siedow JN, 1992. Molecular basis of disease susceptibility in the Texas cytoplasm of maize. *Plant Mol Biol* 19:135-147
- Levy Y, Pataky J, 1992. Epidemiology of northern leaf blight on sweet corn. *Phytoparasitica* 20:53-66

- Li K, Yan J, Li J, and Xianhong Y, 2014. Genetic architecture of rind penetrometer resistance in two maize recombinant inbred line populations. *BMC Plant Biology* 14:152
- Lipps P, Thomison P, Pratt R, 1996. Reaction of corn hybrids to gray leaf spot. *Annual Corn Sorghum Research Conference Proc.* 51:163-180
- Lonnquist J, 1974. Consideration and experiences with recombinations of exotic and corn belt maize germplasm. *Annual Corn Sorghum Research Conference Proc.* 29:102-117
- Mackay M, von Bothmer R, Skovmand B, 2005. Conservation and utilization of plant genetic resources—future directions. *Czech J Genet Plant Breed* 41:335-344
- Mackay M, Srivastava J, Damania A, 1990. Strategic planning for effective evaluation of plant germplasm, pp21-25. In: *Strategic planning for effective evaluation of plant germplasm Wheat genetic resources: Meeting diverse needs.* Strivastava JP, Damania AB eds. John Wiley & Sons, NY
- Malosetti M, Abadie T, 2001. Sampling strategy to develop a core collection of Uruguayan maize landraces based on morphological traits. *Genet Resour Crop Evol* 48:381-390
- Mardia KV, Marshall R, 1984. Maximum likelihood estimation of models for residual covariance in spatial regression. *Biometrika* 71:135-146
- Matheron G, 1963. Principles of geostatistics. *Economic Geology* 58:1246-1266
- Matsuoka Y, Vigouroux Y, Goodman MM, Sanchez J, Buckler E, Doebley J, 2002. A single domestication for maize shown by multilocus microsatellite genotyping. *PNAS* 99:6080-6084
- Meghji M, Dudley J, Lambert R, Sprague G, 1984. Inbreeding depression, inbred and hybrid grain yields, and other traits of maize genotypes representing three eras. *Crop Sci* 24:545-549
- Melhus LE, 1948. Exploring the maize germplasm of the tropics. *Annual Corn Sorghum Research Conference Proc.* 3:7-19.
- Mikel MA, 2008. Genetic diversity and improvement of contemporary proprietary North American dent corn. *Crop Sci* 48:1686–1695
- Munkvold G, Martinson C, Shriver J, Dixon P, 2001. Probabilities for profitable fungicide use against gray leaf spot in hybrid maize. *Phytopath* 91:477-484

- Odong T, Jansen J, van Eeuwijk F, van Hintum T, 2013. Quality of core collections for effective utilization of genetic resources review, discussion and interpretation. *Theor Appl Genet* 126:289-305
- Ortiz R, Ruiz-Tapia E, Mujica-Sanchez A, 1998. Sampling strategy for a core collection of Peruvian quinoa germplasm. *Theor Appl Genet* 96:475-483
- Ortiz R, Taba S, Tovar VHC, Mezzalama M, Xu Y, Yan J, Crouch JH, 2010. Conserving and enhancing maize genetic resources as global public goods—a perspective from CIMMYT. *Crop Sci* 50:13-28
- Paliwal RL, Granados G, Lafitte HR, Violic AD, Marathée JP, 2000. Tropical maize: improvement and production. FAO, Rome, Italy
- Payne G, Waldron J, 1983. Overwintering and spore release of *Cercospora zeaе-maydis* in corn debris in North Carolina. *Plant Dis* 67:87-89
- Peiffer JA, Romay MC, Gore MA, Flint-Garcia SA, Zhang Z, Millard MJ, Gardner CA, McMullen MD, Holland JB, Bradbury PJ, Buckler ES, 2014. The genetic architecture of maize height. *Genetics* 196:1337-1356
- Poland JA, Bradbury PJ, Buckler ES, Nelson RJ, 2011. Genome-wide nested association mapping of quantitative resistance to northern leaf blight in maize. *PNAS* 108:6893-6898
- Pollak LM, 2003. The history and success of the public–private project on germplasm enhancement of maize (GEM). *Adv Agron* 78:45-87
- Pratt RC, Gordon SG, 2006. Breeding for resistance to maize foliar pathogens. *Plant Breed Rev* 27:119-173
- Prochazkova D, Sairam R, Srivastava G, Singh D, 2001. Oxidative stress and antioxidant activity as the basis of senescence in maize leaves. *Plant Sci* 161:765-771
- Robert A, Findley W, 1952. Diseased corn leaves as a source of infection and natural epidemics of *Helminthosporium turcicum*. *Plant Dis Rep* 36:9-10
- Roberts LM, Grant UJ, R. Ramírez E, Hatheway WH, Smith DL, with Mangelsdorf PC, 1957. Races of maize in Colombia. National Academy of Sciences, National Research Council, Washington, DC, USA
- Rupe J, Siegel M, Hartman J, 1982. Influence of environment and plant maturity on gray leaf spot of corn caused by *Cercospora zeaе-maydis*. *Phytopath* 72:1587-1591

- Salas Fernandez MG, Becraft PW, Yin Y, Lübberstedt T, 2009. From dwarves to giants? Plant height manipulation for biomass yield. *Trends Plant Sci* 14:454-461
- Salhuana W, Pollak L, 2006. Latin american maize project (LAMP) and germplasm enhancement of maize (GEM) project: Generating useful breeding germplasm. *Maydica* 51:339-355
- Salhuana W, Jones Q, Sevilla R, 1991. The Latin American maize project: Model for rescue and use of irreplaceable germplasm. *Diversity* 7:40-42
- Schon CC, Utz HF, Groh S, Truberg B, Openshaw S, Melchinger AE, 2004. Quantitative trait locus mapping based on resampling in a vast maize testcross experiment and its relevance to quantitative genetics for complex traits. *Genetics* 167:485-498
- Sluyter A, Dominguez G, 2006. Early maize (*Zea mays* L) cultivation in Mexico: Dating sedimentary pollen records and its implications. *PNAS* 103:1147-1151
- Smith D, Kinsey J, 1980. Further physiologic specialization in *Helminthosporium turcicum*. *Plant Dis* 64:779-781
- Sparks V, 1997. Managing gray leaf spot with hybrid resistance and patented technology. *Annual Corn Sorghum Research Conference Proc.* 52:299-311
- Stein ML, 1999. *Interpolation of spatial data: Some theory for Kriging.* Springer, New York
- Steiner JJ and Greene SL, 1996. Proposed ecological descriptors and their utility for plant germplasm collections. *Crop Sci.* 36:439-451
- Street K, Hamilton RS, Tay D, Taba S, Mackay M, 2013. Mining germplasm banks for photosynthetic improvement—wheat, rice, potato, legumes and maize, pp112-129. In: *Applying Photosynthesis Research to Improvement of Food Crops.* Gready JE, Dwyer SA, Evans JR eds. Australian Centre for International Agricultural Research proceedings, Canberra, Australia
- Taba S, 1997. Latin American maize germplasm regeneration and conservation: Proceedings of a workshop held at CIMMYT June 4-6, 1996. pp1-74. In: *Maize program special report CIMMYT, DF, Mexico*
- Taba S, 2005. Preliminary breeder core subsets and prebreeding. pp9-25. In: *Latin American maize germplasm conservation: Regeneration, in situ conservation, core subsets, and prebreeding.* Taba S ed. A special publication, CIMMYT, El Batán, Texcoco, México.

- Tarter J, Goodman MM, Holland JB, 2004. Recovery of exotic alleles in semiexotic maize inbreds derived from crosses between Latin American accessions and a temperate line. *Theor Appl Genet* 109:609-617
- Tehon L, Daniels E, 1925. Notes on the parasitic fungi of Illinois. *Mycologia* 17:240-249
- Thomas H, Howarth CJ, 2000. Five ways to stay green, *J Exp Bot* 51 Spec No:329-337
- Thompson D, 1969. Selection for stalk quality in corn. Annual Corn Sorghum Research Conference Proc. 24:7-14
- Tohme J, Gonzalez D, Beebe S, Duque MC, 1996. AFLP analysis of gene pools of a wild bean core collection. *Crop Sci* 36:1375-1384
- Turgeon BG, Lu S, 2000. Evolution of host specific virulence in *Cochliobolus heterostrophus*, pp93-126. In: Fungal pathology. Kronstad JW ed. Kluwer Academic Publishers, Dordrecht, TheNetherlands.
- Ulrich J, Hawk J, Carroll R, 1990. Diallel analysis of maize inbreds for resistance to gray leaf spot. *Crop Sci* 30:1198-1200
- van Heerwaarden J, Doebley J, Briggs WH, Glaubitz JC, Goodman MM, Sanchez- Gonzalez J, Ross-Ibarra J, 2011. Genetic signals of origin, spread, and introgression in a large sample of maize landraces. *PNAS* 108:1088-1092
- Wang J, Levy M, Dunkle LD, 1998. Sibling species of *Cercospora* associated with gray leaf spot of maize. *Phytopath* 88:1269-1275
- Wang Y, Yao J, Zhang Z, Zheng Y, 2006. The comparative analysis based on maize integrated QTL map and meta-analysis of plant height QTLs. *Chinese Science Bulletin* 51:2219-2230
- Ward J, Nowell D, 1998. Integrated management practices for the control of maize grey leaf spot. *Integrated Pest Management Reviews* 3:177-188
- Ward J, Laing M, Nowell D, 1997. Chemical control of maize grey leaf spot. *Crop Protection* 16:265-271
- Ward JM, Stromberg EL, Nowell DC, Nutter Jr FW, 1999. Gray leaf spot: A disease of global importance in maize production. *Plant Dis* 83:884-895
- Wei J, Lui K, Chen J, Luo P, and Lee-Stadelmann OY, 1988. Pathological and physiological identification of race C of *Bi-polaris maydis* in China. *Phytopath* 78:550-554.

- Wellhausen EJ, Roberts LM, E. Hernández X, with Mangelsdorf PC, 1952. Races of maize in Mexico: Their origin, characteristics and distribution. Bussey Institution of Harvard University, Cambridge, Massachusetts, USA
- Welz H, Geiger H, 2000. Genes for resistance to northern corn leaf blight in diverse maize populations. *Plant Breeding* 119:1-14
- White DG, 1999. Compendium of corn diseases, 3rd ed. Amer Phytopathological Soc Press, St. Paul, Minn.
- Wilkes G, 2004. Corn, strange and marvelous: But is a definitive origin known. pp3-63. In: Corn: Origin, history, technology, and production. Smith CW, Betrán J, Runge ECA eds. Wiley & Sons, Inc. NJ
- Wilkes, HG 1967. Teosinte: The closest relative of maize. Bussey Institution of Harvard Univ, Cambridge MA
- Wisser RJ, Balint-Kurti PJ, Nelson RJ, 2006. The genetic architecture of disease resistance in maize: A synthesis of published studies. *Phytopath* 96:120-129
- Yamamoto JK, 2000. An alternative measure of the reliability of ordinary kriging estimates. *Math Geol* 32:489-509
- Zuber M, 1975. Corn germplasm base in the US--is it narrowing, widening, or static? Annual Corn Sorghum Research Conference Proc. 30:277-286
- Zuber M, Kang M, 1978. Corn lodging slowed by sturdier stalks. *Crops and Soils* 30:13-15

-CHAPTER II-

Screening Semi-Exotic Maize Germplasm for Resistance to Gray Leaf Spot and Southern and Northern Leaf Blight

Prepared for submission to Maydica

O. O. Ott^{1*}, B. J. Riech², M.M. Goodman¹, J. B. Holland^{1,3}, M. D. Krakowsky^{1,3}

¹Department of Crop Science, NC State University, Raleigh, NC, USA 27695

²Department of Statistics, NC State University, Raleigh, NC, USA 27695

³USDA-ARS. Plant Science Research Unit, Raleigh, NC, USA 27695

*Corresponding author: E-mail:oliver.o.ott@gmail.com

Keywords: maize, Gray leaf spot, Northern leaf blight, Southern leaf blight, accessions, Spatial analysis, Kriging

Abstract

Gray leaf spot (GLS, *Cercospora zea-maydis*), Northern leaf blight (NLB, *Setosphaeria turcica*), and Southern leaf blight (SLB, *Cochliobolus heterostrophus*) are foliar diseases of maize which perennially effect maize yield potential across the world and are most effectively managed with genetic resistance. One potential source of this genetic resistance is maize landraces. In conjunction with the Germplasm Enhancement of Maize Allelic Diversity project, a set of maize landrace accessions has been backcrossed to the DuPont Pioneer ex-Plant Variety Protection inbred line PHB47. The landrace single back crosses BC₁ F₁s were evaluated for GLS, NLB and SLB in 2012 and 2013, and accessions were identified which could be used as sources of disease resistance. Trends in disease resistance in maize populations were examined, and accessions from the Northern South America population provided the most resistance to all three diseases, followed by Middle South America, Andean, Mexican, and USA. The spatial geography of these traits was examined using a Matérn spatial model. This model was used in Kriging to predict disease scores of BC₁ F₁s with potential donor parent accessions with collection locations from across the Americas. The spatial model accounted for 63, 63, and 59% of the variation across the Americas in GLS, NLB, and SLB respectively. Phenotyping standard errors (SE) and spatial prediction SEs were similar, demonstrating the spatial model's ability to predict disease scores. This forms a framework from which researchers can more precisely target germplasm accessions for inclusion into a research program.

Introduction

Gray leaf spot (GLS) caused by *Cercospora zae-maydis* and its sister species *Cercospora zeina*, Northern leaf blight (NLB) caused by the fungi *Setosphaeria turcica* (anamorph *Exserohilum turcicum*), and Southern leaf blight (SLB), caused by *Cochliobolus heterostrophus*, are all important foliar diseases of maize (*Zea mays* L.; Dunkle and Levy, 2000; Horwitz et al, 2013; Perkins and Pedersen, 1987; Wang et al, 1998). These diseases perennially affect maize in the U.S.A. and the world (Balint-Kurti et al, 2008; Zwonitzer et al, 2010). These three foliar pathogens are similar to one another as they are hemibiotrophic ascomycete fungi and share similar pathogenesis characteristics. These diseases vary considerably in the timing of their life cycle; SLB is the most aggressive with a reinfection cycle of just a few days, while the reinfection cycle is approximately two weeks for NLB, and three weeks for GLS, the least aggressive of the three (Beckman and Payne, 1982; Belcher et al, 2012; Jennings and Ullstrup, 1957).

GLS was first identified from specimens collected in Illinois in 1924 (Tehon and Daniels, 1925). The species which was first discovered, *C. zae-maydis*, remained the main pathogen responsible for GLS in the United States until relatively recently. Now *C. zeina*, considered to originate in Africa, is also known to contribute to GLS, with both species having a wide distribution in the United States (Crous et al, 2006). GLS became a major problem in the U.S.A. in the 1970's due to widespread adoption of conservation tillage and continuous maize growing systems, which increased the amount of maize debris left in the field from previous growing seasons. GLS infection of maize acreage increased from 7.2 to 14.9 million hectares during the 1980's and 1990's (Sparks, 1997). Today, GLS has spread to

maize-growing areas worldwide, limiting yields to a moderate extent in the U.S.A. Corn Belt and considerably in Africa (Ward et al, 1999). In 1995, reported yield losses due to GLS were as high as 50% in some U.S.A. maize fields (Ward et al, 1999).

Like GLS, NLB is a disease with worldwide distribution, especially in the humid high-altitude tropics. NLB first became a target of maize breeding programs after a series of heavy NLB epidemics occurred in the U.S.A. in the 1940's and 50's (Ferguson and Carson, 2007). In the early 1940's, farmers, who for the first time had significant amounts of money invested in hybrid seed, became more aware of the presence of disease in the newly developed maize hybrids (Jenkins and Robert, 1952, 1961; Welz and Geiger, 2000). It was in 1959 that qualitative resistance to NLB was first described in detail. Resistance has been shown to be conferred in part by six dominant genes, *Ht1*, *Ht2*, *Ht3*, *Htm1*, *Htm2* and *NN*, which were shown to control resistance to specific races of *S. turcica* (Pratt and Gordon 2006). In the 1960s and 1970s these genes were utilized in U.S.A. germplasm; the *Ht1* gene, which had the largest effect, was utilized extensively until a race with virulence was found in Hawaii in 1972. That race subsequently spread to the continental U.S.A. (Smith and Kinsey, 1980). This rapid development of resistance to the *Ht1* gene made qualitative NLB resistance less appealing to most maize breeders, so the remaining major-effect genes were not widely deployed (Ferguson and Carson, 2007; Welz and Geiger, 2000). Pratt and Gordon (2006) state that deployment of major gene resistance to NLB in the U.S.A. had been over-done, which had left U.S.A. maize germplasm vulnerable to race shifts, and thus further breeding efforts would require a combination of the *Ht* genes and quantitative resistance.

SLB is another damaging maize disease, especially in the Southeast U.S.A., but also in the lowland tropics. SLB is the pathogen responsible for the 1970-71 corn epidemic (Tatum, 1971). In the 1960s and early 1970s, seed companies relied extensively on the use of cytoplasmic male sterility in the form of cms-T for production of hybrids, creating a lack of cytoplasmic diversity. It was later found that the same point mutation in the mitochondria which conferred male sterility also conferred susceptibility to *C. heterostrophus* race T (Dewey et al, 1988). This susceptibility placed heavy selection on race T of SLB, resulting in the SLB epidemic of 1970-71 (Levings and Siedow, 1992). While the 50% yield loss which cms-T hybrids suffered in 1970-71 is the exception, even non cms-T hybrids with moderate genetic resistance to SLB show yield loss from 0.7 to 0.8% for each increase of 1% in the affected leaf area (Byrnes et al, 1989; Hooker, 1972).

Control of these diseases can come from altered cultural practices, the application of fungicides, or with the use of genetic resistance (Perkins and Pedersen, 1987; Ullstrup, 1972; Ward et al, 1999). Unfortunately, there is limited genetic resistance to these three diseases in elite U.S.A. germplasm (Goodman, 1999). The preference to use elite material, rather than exotic germplasm, has led to a narrowing of the genetic base of U.S.A. maize. Troyer (2004) points out that five popular, widely adapted, turn of the century cultivars account of 87% of the background of today's U.S.A. hybrid maize. Currently a relatively small number of inbred lines make up a majority of breeding germplasm in the U.S.A., with six lines (B73, A632, Mo17, PH207, Oh43, and B37) contributing to 76% of the pedigrees of former Plant Variety Protection lines (ex-PVPs) assessed by Nelson et al (2008); the majority of these inbred lines are not sources of disease resistance. Currently there is concern that this

narrowing of the germplasm pool may limit flexibility and ability to respond to new pests or pathogens (Goodman, 1999). To broaden the genetic base of corn germplasm, many programs have evaluated exotic materials and used them in breeding programs (Hallauer, 1978). Unfortunately, progress in the use of exotic material in elite breeding programs has been slow. For example, in 1996 private breeding programs in the U.S.A. were surveyed as to their use of exotic germplasm. It was found that there had been only a slight increase in the use of exotic germplasm from less than 1% in 1984 to almost 3% in 1996 (Goodman, 1998).

In order to widen the maize gene pool in the U.S.A., the Germplasm Enhancement of Maize (GEM) project was implemented by the United States Department of Agriculture Agricultural Research Service (USDA-ARS), in collaboration with both public and private research scientists (Pollak, 2003). Currently GEM involves the cooperation of 28 private cooperators (GEM, 2014). Germplasm accessions which have been selected for their potential usefulness as parents, based on agronomics, are crossed with proprietary inbreds or inbreds that have recently come off plant variety protection (ex-PVPs) to create new sources of breeding material. To date, a relatively small number of maize landraces (~25) have been used in GEM releases. This fact led to concern that a large amount of genetic diversity may be under-sampled due to the emphasis put on agronomic quality when choosing exotic germplasm for use in GEM. In an effort to represent more racial diversity, GEM implemented an Allelic Diversity (AD) project with a goal of developing adapted sources of germplasm representing a majority of the ~300 races of maize. The accessions used to represent the races of maize are those already in the collections at NCSU, largely the typical accessions of each race as listed by the Committee on Preservation of Indigenous Strains of

Maize (Clark, 1956). In order to sample the allelic diversity of maize landraces, accessions are backcrossed, without selection, to the ex-PVP inbred line, PHB47 (PI 601009). The Allelic Diversity project plans to develop inbred or double haploid lines from these BC₁ F₁s, which could be used as a genetic tool for allele mining or QTL mapping (Krakowsky et al, 2008).

The BC₁ F₁s produced by the Allelic Diversity project themselves provide a germplasm resource which, when phenotyped, may provide direction as to which landraces may be most useful for a given research objective. These BC₁ F₁s can be informative due to the essentially random dispersal of the genes underlying resistance to GLS, NLB, and SLB across the maize genome. This is important as it would be difficult to generalize from BC₁ F₁s for traits that are controlled by few genes that are not randomly dispersed due to the potential for high plant to plant variability. Genes controlling GLS, NLB, and SLB in maize were found to be randomly dispersed in the maize genome, based on results from the nested association mapping (NAM) population (Supplemental Table 2.1; Benson, 2013; Kump et al, 2011; Poland et al, 2011). Thus, screening of a BC₁ F₁ bulk conceptually examines a random sample of the genes from the landrace that control a given trait.

Another reason the BC₁ F₁s are use full as it allows disease to be assessed in a common experiment; range of flowering time would be too great to screen accessions themselves and get meaningful estimates of disease resistance in the same environment. By using backcross lines, flowering time was compressed, and so too was the variation in disease resistance. It is hoped that the BC₁ F₁s are predictive of the disease resitance of the accession. Such screening has the potential to identify landraces that have accumulated

multiple resistance alleles at the QTL loci sampled, providing the best targets for incorporation into breeding programs.

Methods and Materials

Germplasm

To develop AD BC₁ F₁s used herein, maize landrace accessions were backcrossed to the DuPont Pioneer ex-PVP inbred line PHB47 (PI 601009). One to eighteen plants from the landrace were crossed either as male or female to PHB47 to develop the F₁ hybrid. A large proportion of F₁s were produced in off-season nurseries due to photoperiod sensitivity in tropical landraces. Supplemental Table 2.2 provides the numbers of plants used to produce F₁s and BC₁ F₁s and the location where a given F₁ was produced. Once F₁s were produced, 3 to 26 plants from the F₁ were used to develop the BC₁ F₁s in summer and winter nurseries in Clayton, NC and Homestead, FL, respectively, from 2005 to 2012. A balanced bulk was then made from the BC₁ seed for these experiments, thus BC₁ F₁ bulks were used for screening. Supplemental Table 2.3 presents a full list of landraces included in this study with country of origin, race name, accession name, landrace seed source, collection coordinates, and altitude of collection.

Disease Evaluation

Four hundred and sixty-eight BC₁ F₁s were evaluated in 2012, with 483 BC₁ F₁s evaluated in 2013. The BC₁ F₁s were evaluated for GLS in 2012 and 2013 at both the Piedmont Research Station in Salisbury, NC and the Wood Farm in Andrews, NC, the latter in cooperation with Dupont Pioneer (Johnston, IA). These environments have been used previously for disease screening studies and are conducive to GLS development, as they have moderate temperatures and long periods of leaf wetness, due to both adequate rainfall and

heavy morning dews (Bubeck et al, 1993; Zwonitzer et al, 2010). These same sets of BC₁ F₁s were evaluated in three environments for NLB in 2012 and 2013 at the DuPont Pioneer Research Station in Windfall, IN and in 2013 at the Monsanto (St. Louis, MO) Research Station in Thomasboro, IL. These locations were chosen as they are currently used by their respective companies for NLB testing and no proven NLB environments exist within the system of North Carolina Department of Agriculture/North Carolina State University research farms. BC₁ F₁s were evaluated over three environments for SLB at the NCSU Central Crops Research Station, Clayton, NC, in 2012 and 2013 and at the DuPont Pioneer Research Station in Cairo, GA in 2013. Both of these locations were good for SLB development due to high temperatures and moderate moisture and have been used previously in SLB screening (Zwonitzer et al, 2010).

Trials at all locations were laid out using an augmented replications within sets design. BC₁ F₁s were grouped into four sets by flowering time (collected on the accessions in crossing nurseries) with two replications of each set planted adjacently. Six checks were included in each rep, five of which were F₁ hybrids which spanned the breadth of resistance to these three diseases, including PHB47 x NC296, HBA1 x PHB47, Pioneer 33M54, Pioneer 3394, and PHB47 x DJ7. The sixth check was the recurrent parent PHB47; the available pedigree and release information of checks is presented in Supplemental Table 2.4.

Experimental units consisted of single row plots, and dimensions and seed densities are provided in Supplemental Table 2.5. Plots were maintained using the cultivation practices common to each of the trial locations. At the DuPont Pioneer Research Station in Cairo, GA, and NCSU Central Crops Research Station, Clayton, NC, trials were grown under irrigated

conditions, while the Piedmont Research Station in Salisbury, NC, Wood Farm in Andrews, NC, DuPont Pioneer Research Station in Windfall, IN, and Monsanto Research Station in Thomasboro, IL were rain fed.

Inocula for SLB for North Carolina locations were provided by Syngenta Seeds Inc. (Stanton, MN). For GLS at North Carolina locations inocula was again provided by Syngenta Seeds, with the addition of inocula produced by Peter Balint-Kurti of the USDA-ARS, while NLB or SLB inoculum was provided by Dupont Pioneer and Monsanto at their respective locations. Experiments were inoculated at the V5-V7 growth stage (Chung et al, 2010). Visual disease ratings were taken on a plot basis, i.e., the visual average of all plants in a plot, on a 1-9 scale, with 1 designated as susceptible, and 9 designated as resistant (Bubeck et al, 1993). The initial ratings were taken approximately two weeks after the peak flowering time, with subsequent ratings occurring at 10 to 14 day intervals. Ratings were not taken if plant senescence was judged to be too advanced in order prevent confusion between disease and plant senescence. GLS was rated twice at both Salisbury, NC and Andrews, NC in 2012, and three times at both locations in 2013. NLB was rated once at Windfall, IN in 2012 and 2013 and twice at Thomasboro, IL in 2013. SLB was rated twice in 2012 and three times in 2013 at Clayton, NC and once in Cairo, GA in 2013. As GLS, NLB, and SLB are known to be affected by maturity, days to anthesis (DTA, as the number of days from planting to pollen shed of 50% of plants in a row) was recorded for use in data analysis at Andrews, NC and Clayton, NC in 2012 and at Andrews, NC, Clayton, NC, and Thomasboro, IL in 2013.

Data Analysis

The least squared mean (LSM) of DTA was first calculated for use as a covariate, using ASReml v. 3.0 software (Gilmour et al, 2009). The model included each BC₁ F₁ bulk as a fixed effect, and random effects included environment, sets within environment, replications within sets within environment, and field range (row) and plot (column) as position effects within environment (Brownie et al, 1993), and the interaction of BC₁ F₁ family and environment. For analysis of disease traits, the Weighted Mean Disease (WMD) was estimated from repeated disease assessments in environments that had more than one rating taken during the growing season (Balint-Kurti et al, 2008). Higher WMD values signify increased resistance. The model to estimate WMD LSM included BC₁ F₁ bulk and DTA (as a covariate) as fixed effects, with the same random effects as in the above model. In order to separate effects of the six checks from the experimental lines dummy variables were added to the data set as outlined in Piepho et al (2006), which allowed for comparisons of checks to one another and experimental BC₁ F₁s to one another.

Once LSM of BC₁ F₁s were estimated, trends within maize landrace populations were examined. Maize landrace population analysis was previously conducted on 945 accessions by Vigouroux et al (2008), of which 347 were included in this study and were firmly placed in a population. Vigouroux et al (2008) divided accessions using individual plant neighbor-joining based upon the log-transformed proportion of shared alleles between individuals, to develop a hierarchical tree of maize populations. Vigouroux et al (2008) identified nine populations of maize, but our sampling across populations was not uniform across the nine populations, leaving little power to detect differences in under-sampled populations. Thus, populations with fewer than 25 accessions were merged with the populations in which they

are most closely nested based on the hierarchical tree. Caribbean accessions were placed in the Northern South America population (NSA; n=52), to which they are closely related. Southwest U.S.A., Northern U.S.A., and Chilean accessions (many Chilean materials trace their ancestry to U.S.A. sources) were merged to form a USA population (n=40). Southeast U.S.A. accessions (many of which were brought to Brazil after the American Civil War (Brieger et al, 1958)) were merged with the Middle South America population (MSA; n=48). The Mexican (MEX; n=114) and Andean (AND; n=92) populations were kept intact as they were well sampled. Thus for our purposes, five populations were examined for trends in disease resistance. The mean LSM of BC₁ F₁s with a donor parent within each of the populations were examined. A Tukey HSD test was conducted to determine if there were significant differences in average disease scores between maize populations using R v. 2.15.2 (R Core team, 2013).

To better predict the potential usefulness of a landrace collected at locations not represented in this study, the spatial distribution of resistance to these three diseases was examined. This analysis utilized the spatial coordinates of the collection locations of accessions. The great majority of the landraces had coordinates provided by Vigouroux et al (2008). For those that did not, coordinates were determined in three ways. First, the International Center for Maize and Wheat Improvement (CIMMYT) was contacted for information on collection locations (Kevin Pixley, personal communication). Second, collection data was used which had been compiled by José de Jesús Sánchez-González at the University of Guadalajara (personal communication). If no accession collection data could be found, then the approximate collection location was used, as noted by the publications of the

Committee on Preservation of Indigenous Strains of Maize (Brieger et al, 1958; Brown, 1960; Grant et al, 1963; Grobman et al, 1961; Hatheway, 1957; Ramírez et al, 1960; Roberts et al, 1957; Timothy et al, 1961; 1963; Wellhausen et al, 1952; 1957). The accessions with estimated collection locations are noted in Supplemental Table 2.6. In cases where no collection altitude was listed, altitude was estimated by using GPS Visualizer (www.gpsvisualizer.com/elevation), once collection coordinates had been obtained.

To predict the disease scores of BC₁ F₁s across the Americas at locations outside this study, a Matérn spatial model was developed for each disease using latitude, longitude, and altitude using Ordinary Kriging with the geoR package of R v 2.15.2 (Cressie, 1992; Ribeiro Jr and Diggle, 2001). Model parameters were calculated using maximum likelihood. Once a spatial model for each disease was developed, Ordinary Kriging was done to predict the disease scores for BC₁ F₁s of accessions outside those used here. Locations which were farther than 5 degrees (~560 km) from the closest sampled data point herein were not predicted.

In an attempt to improve prediction accuracy, genotypic data for 96 simple sequence repeat markers (SSRs) was used as a covariate. Vigouroux et al (2008), genotyped 951 maize landraces of which 351 were part of this disease screening study. Several steps were required to develop this genotype data so that it could be used as a covariate in the analysis. First the allele frequency matrix for the 351 landraces with data from Vigouroux et al (2008) that were used herein was generated using PowerMarker V3.25 (Liu and Muse, 2005). Next this allele frequency matrix was used to calculate a Pearson correlation matrix for the markers from the 351 landraces. From this correlation matrix eigenvectors were calculated using R 2.15.2 (R

Core Team, 2013). In total, 91 eigenvectors had eigenvalues over one. As it was computationally difficult to use all 91 eigenvectors in spatial analysis, the number of eigenvectors to be used was reduced. This was done by placing all 91 eigenvectors in a linear model as independent variables, with each disease as the dependent variable, and eliminating eigenvectors using backwards stepwise selection to minimize the Bayesian information criterion (BIC; Schwarz, 1978).

Once a reduced set of eigenvectors for each disease had been selected, the values for the 132 accessions which had phenotypic data, but lacked genotypic data, were imputed using spatial methods, as there was a significant association between latitude and longitude and the values of the eigenvectors. Imputation was done by fitting a Matérn spatial model with a maximum likelihood function, using collection-point latitude, longitude, and altitude of the accessions (Matérn, 1986). This Matérn spatial model was then used to predict the values of the reduced set of eigenvectors at the 132 locations where genotypic data were not available using Ordinary Kriging with the geoR package of R v 2.15.2 (Cressie, 1992; Ribeiro Jr and Diggle, 2001). These predicted eigenvectors were then merged with the real eigenvectors. This allows us to use a full data set with eigenvectors, latitude, longitude, and altitude as predictors in the spatial model. A visual representation of this is given in Supplemental Figure 2.1.

To predict the disease scores of BC₁ F₁s across the Americas at locations outside this study, a Matérn spatial model was developed for each disease using specific eigenvector covariates, latitude, longitude, and altitude. Model parameters were calculated using maximum likelihood with the geoR package of R v 2.15.2. After maximum likelihood

estimation was conducted, each of the eigenvalue covariates was examined to determine if they were still significant when using the spatial model. This was done by calculating the standardized Z-statistic for the genetic covariates, using the beta for each eigenvector and its standard error, and removing covariates which had absolute Z-values of less than 1.96. Once a spatial model for each disease was developed, Ordinary Kriging was done to predict the disease scores for BC₁F₁s of accessions outside those used here. Locations which were farther than 5 degrees (~560 km) from the closest sampled data point herein were not predicted.

The predictive ability of both models (without genotypic data and those which had genotypic data included) was tested using five rounds of five-fold cross validation. This was done by randomly dividing that data into five parts, five different times. A model was estimated using four fifths of the data using the same Matérn spatial model methodology as was used for the entire data set. The resulting model was then used to estimate the disease scores for the remaining one fifth of the data. These estimates were then correlated with the observed phenotypes to test prediction accuracy. This was done five times in total using a different four fifths of the data each time. Total accuracy of prediction was defined as the average square of correlation coefficient between predicted values and observed phenotypes for the disease traits in the five validation samples.

Results and Discussion

In this study, a large number of geographically diverse maize landraces have been sampled for their potential use as sources of resistance to GLS, NLB, and SLB. In screening trials, the BC₁F₁ effects were significant ($p < 0.001$) for all three diseases. A list of the ten

best and worst performing BC₁ F₁s for each disease is provided in Table 2.1. A full table of the disease scores and standard errors of the BC₁ F₁s assessed is given in Supplemental Table 2.3, while the ANOVA tables for the analysis of the three diseases are provided in Supplemental Tables 2.7-2.12.

Overall, the BC₁ F₁s showed a large amount of variation for each of the diseases, with some showing levels of resistance similar to the resistant checks: PHB47 x NC296, DKHBA1 x PHB47, and Pioneer 33M54. Disease scores and standard errors of checks are provided in Table 2.2. Many of the BC₁ F₁s were significantly better than the recurrent parent PHB47, with 95, 87 and 91% of BC₁ F₁s being significantly different than PHB47 at $p < 0.05$.

There were also several accession that were not significantly different than the resistant checks. Individual accessions that would especially be of use to researchers targeting temperate material include: Argentine Pop (PI217404), Mexican June (PI221889), White Dent (PI311232 and PI221885), and Gourd Seed (PI217405). These accessions are the good sources of resistance for all three diseases, and would be somewhat adapted to temperate growing conditions. Note that many of these accessions were collected in the Southeast U.S.A., an area from which most accessions are very poor agronomically. Accessions that could be of use in a tropical program, or integrated into a temperate breeding program through crossing and/or selection, include VEN 891 (Tuxpeno), TOL 399 (Yucatan), SAN 347 (Puya Grande), CHS 159 (Tehua), and CHS 53 (Olotillo). These accessions from lowland tropical environments in Colombia, Venezuela, and southern Mexico are the best performing accessions in the entire study and would be of the most use

in areas with longer growing seasons. In Andean environments, accessions which would be useful include: NAR 315 (Capiro), ECU 877 (Cubano Cateto), ECU 855 (Yunquillano forma Andaqui), PIU 96 (Morochillo), and BOV 716 (Yungueno). Hailing from Colombia, Ecuador, Peru, and Boliva, these provide resistance to all three diseases and would be more adapted to a high-altitude growing environment.

The pairwise phenotypic correlations of the diseases were moderate and significant at $p < 0.001$, with $r^2 = 0.70$ between GLS and NLB, $r^2 = 0.48$ between GLS and SLB, and $r^2 = 0.51$ between SLB and NLB. Plots of pair-wise correlations of the disease traits in the $BC_1 F_1$ s are given in Figure 2.1. The correlation between GLS and NLB found in this study is similar to the correlation ($r^2 = 0.72$) found when assessing a set of public inbreds to these three diseases (Wisser et al, 2011). In that same study, the correlations between SLB/ GLS and SLB/NLB were both found to be 0.71, which differs from what was found in this set of $BC_1 F_1$ s. This may be due to the fact that Wisser et al (2011) examined the disease scores of inbreds, some of which may have been selected for resistance to multiple diseases during the breeding process.

In examining GLS disease scores by donor parent population, the population with the highest mean GLS score was Northern South America (NSA) at 5.2 (a rating of 9 is complete resistance) followed by Middle South America (MSA) at 4.9, Andean (AND) at 4.8, Mexican (MEX) at 4.6, and United States/Canada (USA) at 3.2. Population means of NLB scores are simmular with NSA at 6.13, AND at 5.71, MSA at 5.3, MEX at 5.18, and USA at 2.9. Rankings of donor parent by population for SLB are much the same as with the other

diseases, with NSA at 5.3, AND at 4.8, MSA at 4.8, MEX at 4.8, and USA at 3.7. (See Supplemental Tables 2.13-2.15 and Supplemental Figures 2.2-2.4 for full results).

With a Tukey HSD $\alpha=0.05$ value of 0.22, three SLB sets were formed (Supplemental Table 2.15). Accessions from NSA are significantly better than AND, MSA and MEX, which are not significantly different from each other; and donor parents from the USA are significantly more susceptible than any of the other populations. This can be seen in the boxplot of SLB scores in Supplemental Figure 2.4.

When examining distribution of disease resistance for each of the maize populations, landraces which formed part of the Northern South America population were shown to be the best sources of resistance for all three of the diseases, followed by Middle South America, Andean, Mexican, and USA. Overall, though, the population of origin does not tell a very precise picture of disease resistance, as there is a large amount of variation in disease scores for all three diseases within each population.

To examine the spatial distribution of disease resistance across the Americas, the disease scores of the BC₁ F₁s at the point of collection of the donor accessions were placed on maps (Figures 2.2-2.4). These show spatial trends in the disease data, which were further explored with predictions at unsampled locations. Kriging maps developed as a result of spatial prediction of GLS scores predict BC₁ F₁s with a donor parent collected in areas in Central America, Northern South American, and the Caribbean tend to be the most disease resistant as can be seen on the map in Figure 2.5A. As the collection locations move further from the equator there is a trend toward greater disease susceptibility of donor landraces. Of interest is the tendency for reduced resistance in accessions collected at high altitude

locations, as can be seen for collections made in high-altitude areas of Peru and Bolivia. This may be due to cooler and/or dryer high-altitude environments, where disease pressure is not as high as in the lowlands.

Cross-validation of the spatical models without genotypic data indicated the spatial model accounted for 63% of the variation in GLS in the BC₁ F₁s. The inclusion of the genotypic data did not improve the amount of variation accounted for, which remained the same at 63% .Moreover, prediction standard errors (SEs) are of similar magnitude to the standard errors of the experimental phenotypes. Phenotyping SEs range from 0.49 to 0.58 as can be seen in Figure 2.5B, while prediction SEs for GLS ranged from 0.40 to 0.62.

The prediction map of NLB resistance is comparable to that of GLS with areas around the equator showing donor parents that confer the most resistance (Figure 2.6A). Overall the NLB spatial model without genotypic data accounts of 60% of the variation across the Americas based on cross validation. With the inclusion of gentytic data the predtiction accuracy rose to 63%, with prediction SEs ranging from 0.68 to 0.90 as seen in Figure 2.6B. These are higher than the SEs of the phenotypic estimates which had a range of 0.47 to 0.58.

The prediction map of SLB disease scores is similar to those of GLS and NLB, with the most resistant accessions originating in Northern South America, and the most susceptible from Chile and the USA, as seen in Figure 2.7A. The spatial model without genotype data accounted for 50% of the variation, with inclusion accurary rose to 59%. SLB prediction SEs ranged from 0.41 to 0.54 (Figure 2.7B). This is only slight increase when compared to the SEs of the phenotypes which ranged from 0.30 to 0.40. This indicates an

equivalent level in the ability to predict disease scores in BC₁ F₁s as to phenotype them. Supplemental Table 2.16 gives the amount of variation different types of models Ordinary Least Squares, and Spatial methods account for, with and without the genetic covariates. Parameter estimates for the spatial models for each disease can be seen in Supplemental Table 2.17. One interesting point of parameter estimates of spatial models is that kriging defines and models the disease scores at a local neighborhood, thus the parameter estimates for latitude, longitude, and altitude are close to zero and do not appear significant in the spatial analysis. The covariance functions for the three Matérn models for GLS, NLB, and SLB are given in Supplemental Figure 2.5, and give an indication as to how the correlation of disease resistance between points decreases as the distance between points increases.

For all three diseases, the percentage of variation across the Americas associated with spatial models was greater than the percent of variation due to family means captured using ordinary least squares. This prediction accuracy was aided by the inclusion of genotypic data which differed between disease models. For GLS the 3rd and 38th eigenvectors were ultimately used, for NLB the 2nd, 3rd, and 10th eigenvectors, and for SLB the 3rd, 23rd and 63rd. Eigenvector three was significant for all three diseases, and thus it may play a role in explaining the population structure of the maize landraces as it pertains to disease resistance. These specific eigenvectors are only useful in the development of the prediction models. It is difficult to assign biological significance to them as the genotypes used as covariates are from a single plant from each landrace, and that single plant did not contribute to the BC₁ F₁ lines that were screened here, giving little credence to further inferences.

Overall predictive analysis for GLS, NLB, and SLB show areas nearest the equator and in coastal regions were predicted to have the most disease resistance. Predictions further from the equator and at the highest elevations show lower amounts of disease resistance. There is great similarity in how resistance for these three diseases is distributed, reinforced by both similarities in disease susceptibility in populations and the moderate to high correlations between disease scores in pair-wise comparisons of these diseases. This hints at a common biological basis for disease resistance. There are several reasons why resistance for different diseases can occur in the same germplasm. The first may be the connection between flowering time and disease. The most resistant BC₁ F₁s also tend to be the latest flowering in our temperate environments. In order to account for the effects of flowering, DTA was included as a covariate in LSM estimation. DTA was a significant covariate ($p < 0.001$) for all three diseases, as seen in Supplemental Tables 2.7, 2.9, and 2.11. DTA is significantly ($p < 0.001$) phenotypically correlated with all of these diseases, with r^2 of 0.59, 0.70, 0.42 with GLS, NLB, and SLB respectively (Figure 2.1).

The effects of flowering time may be especially important for these diseases as they are hemibiotrophic necrotrophs. This means that the pathogen can take advantage of the natural senescence of the plant to increase rates of colonization. Therefore, later flowering lines which senesce later would be more difficult to colonize. In this study, DTA ranged ~12 days overall, thus the earliest-flowering lines were partly senesced at the last disease rating. DTA of all lines is given in Supplemental Table 2.3. Nevertheless, some families (e.g., Pollo (CUN 443), Costeño (ATL 328), Nal Tel ATB (GUA 111) and Tuxpeño Norteño (CHH

287)), showed both high levels of disease resistance and earlier flowering, implying that other mechanisms for disease resistance exist.

A second reason for the similar disease resistance distributions across geographies may be due environments that are similar in climate that are conducive to disease development around the equator and in the lowland tropics. Thus, resistance for all of these diseases may have been strongly selected for in these areas. To date there has been very little research done surveying the prevalence of maize diseases in tropical areas. Buddenhagen (1985) noted that NLB, SLB and GLS were all diseases widely distributed across the entire American tropics, but he was not able to give the status of any of the pathogens on a finer geographic scale. Buddenhagen (1985) also noted that, unlike the U.S.A., where maps of areas of prevalence to many diseases have been made, there is no publicly available information on the assessment of maize diseases in the tropics. Even though comprehensive surveys of maize diseases in the tropics have not been done, GLS, NLB, and SLB are all diseases being screened in breeding nurseries in the tropics, which gives some indication as to their presence in these areas (Latterell and Rossi, 1983; Renfro, 1985).

A possible third explanation for the similarity in trends in disease resistance is Multiple Disease Resistance (MDR; Nene, 1988; Zwonitzer et al, 2010). MDR hypothesizes that the mechanism, whether it be single or multi-gene/allele in action, which provides resistance to one or two diseases may condition resistance to another disease. MDR could take the form of physical barriers to fungal colonization, priming the immune response or influencing pathogen detoxification pathways (Wisser et al, 2011). Further work could provide experimental validation by screening accessions not included in this study and

validating disease predictions. More work could be done examining how the amount of variation in disease resistance changed during the backcrossing process to shed light on the degree of variation in disease resistance in the accessions themselves. Other potential research directions may examine trends in disease resistance levels for different types of maize pathogens or for pathogens that are much more locally distributed, to give us a better picture of the cause of the underlying genetic structure of disease resistance across populations and geographies.

Beyond these maize diseases, the spatial methodologies used in this study could also be used for other traits and other crop species to identify accessions that are more likely to be of use for researchers, given the traits and crop of interest. When used in conjunction with a germplasm bank, spatial methodologies could allow a researcher to create their own core collections that would be tailored to their specific objectives. Spatial methods have the potential to be useful, as many traits can be linked to climatic parameters that are dependent on geography. Such spatial patterns may in part reflect the selection pressures of the environment from which an accession was originally sampled (Mackay et al, 1990, 2005). For example, Endresen et al (2010) demonstrated how ecological and geographic data from the collection sites of 14 Nordic barley landraces (*Hordeum vulgare L.*) were correlated with morphological traits. This type of ecological and geographic data fits in well with the spatial methods used in this study, and in many cases climate data are freely available (e.g., <http://iridl.ldeo.columbia.edu/>).

In this study; a set of semi-exotic BC₁ F₁s were screened for their resistance to three major foliar diseases, with the intent to expand inference to maize accessions not sampled in

this study by the use of population and spatial analysis. Disease resistance within maize populations was found to have a large range, making conclusions as to the disease resistance level of an entire population difficult. Inferences made using spatial methods were more encouraging. With a relatively small amount of genetic and location data, good predicted accuracy was obtained, given the vast area over which the accessions were collected. Predictive models could be further improved with the addition of other types of variables including climate data, other types of genotypic data, and information about production systems.

Using spatial methods to make predictions about accessions may be beneficial for several reasons; first, it would produce sets of accessions more likely to have a given trait of interest. This may reduce the size of screening efforts and the cost to a researcher. Second, it may help reduce the amount of seed requested from the germplasm bank by researchers, by generating more targeted germplasm requests (Mark Millard, personal communication). Seed distribution and regeneration of seed is a large burden on germplasm bank resources. With the use of spatial methods, smaller and more refined sets of landraces may suffice to achieve research aims. Third, spatial methods may provide a method by which previous studies, which have assessed or made crosses with accessions, can be unified into a single predictive platform. This would leverage information that has already been collected but not been fully exploited and lay out a framework to enable full exploitation of the resources that germplasm banks offer.

References

- Balint-Kurti PJ, Wisser R, Zwonitzer JC, 2008. Use of an advanced intercross line population for precise mapping of quantitative trait loci for gray leaf spot resistance in maize. *Crop Sci* 48:1696-1704
- Beckman PM, Payne GA, 1982. External growth, penetration, and development of *Cercospora zea-maydis* in corn leaves. *Phytopath* 72:810-815
- Belcher AR, Zwonitzer JC, Santa Cruz J, Krakowsky MD, Chung C, Nelson R, Arellano C, Balint-Kurti PJ, 2012. Analysis of quantitative disease resistance to southern leaf blight and of multiple disease resistance in maize, using near-isogenic lines. *Theor. Appl. Genet.* 124:433-445
- Benson J, 2013. Resistance to gray leaf spot of maize: Underlying genetic architecture and associated mechanisms. Cornell University Dissertation. <http://hdl.handle.net/1813/34022> (accessed June 18, 2014)
- Brieger FG, Gurgel JTA, Paterniani E, Blumenschein A, Alleoni MR, 1958. Races of maize in Brazil and other eastern South American countries. National Academy of Science-National Research Council Washington, DC, USA
- Brown WL, 1960. Races of maize in the West Indies. National Academy of Sciences. National Research Council, Washington, DC, USA
- Brownie C, Bowman DT, Burton JW, 1993. Estimating spatial variation in analysis of data from yield trials: a comparison of methods. *Agron J* 85:1244-1253
- Bubeck D, Goodman MM, Beavis W, Grant D, 1993. Quantitative trait loci controlling resistance to gray leaf spot in maize. *Crop Sci* 33:838-847
- Buddenhagen I, 1985. Maize disease in relation to maize improvement in the tropics. *Relazioni E Monografie Agrarie Subtropicali E Tropicali Nuova Serie*. Brandolini A, Salamini F eds. 100:243-276
- Byrnes K, Pataky J, White D, 1989. Relationships between yield of three maize hybrids and severity of southern leaf blight caused by race O of *Bipolaris maydis*. *Plant Dis* 73:834-840
- Chung C, Jamann T, Longfellow J, Nelson R, 2010. Characterization and fine-mapping of a resistance locus for northern leaf blight in maize bin 8.06. *Theor Appl Genet* 121:205-227

- Clark J, 1956. Collection, preservation and utilization of indigenous strains of maize. *Econ Bot* 10:194-200
- Cressie N, 1992. Statistics for spatial data. *Terra Nova* 4:613-617
- Crous PW, Groenewald JZ, Groenewald M, Caldwell P, Braun U, Harrington TC, 2006. Species of *Cercospora* associated with grey leaf spot of maize. *Stud Mycol* 55:189-197
- Dewey RE, Siedow JN, Timothy DH, Levings III CS, 1988. A 13-kilodalton maize mitochondrial protein in *E coli* confers sensitivity to *Bipolaris maydis* toxin. *Science* 239:293-295
- Dunkle LD, Levy M, 2000. Genetic relatedness of African and United States populations of *Cercospora zea-maydis*. *Phytopath* 90:486-490
- Endresen DTF, 2010. Predictive association between trait data and ecogeographic data for Nordic barley landraces. *Crop Sci* 50:2418-2430
- Ferguson L, Carson M, 2007. Temporal variation in *Setosphaeria turcica* between 1974 and 1994 and origin of races 1, 23, and 23N in the United States. *Phytopath* 97:1501-1511
- Germplasm Enhancement of Maize Website, 2014. www.publiciastate.edu/~usda-gem. (accessed 17 June 2014)
- Gilmour AR, Gogel B, Cullis B, Thompson R, 2009. ASReml user guide release 3.0. VSN International Ltd. Hemel Hempstead, UK
- Goodman MM, 1998. Research policies thwart potential payoff of exotic germplasm, *Diversity* 14:30-35
- Goodman MM, 1999. Broadening the genetic diversity in maize breeding by use of exotic germplasm, pp139-148. In: *The Genetics and Exploitation of Heterosis in Crops*. Coors JG, Pandey S, Gerdes JT eds. ASA-CSSA-SSSA, Madison, WI
- Grant UJ, Hatheway WH, Timothy DH, Cassalet DC, Roberts LM, 1963. Races of maize in Venezuela. National Academy of Sciences. National Research Council, Washington, DC, USA
- Grobman A, Salhuana W, Sevilla R, with Mangelsdorf PC, 1961. Races of maize in Peru. National Academy of Sciences. National Research Council, Washington, DC, USA
- Hallauer AR, 1978. Potential of exotic germplasm for maize improvement, pp229-247. In: *Maize Breeding and Genetics*. Waldon DB ed. John Wiley & Sons, New York

- Hatheway WH, 1957. Races of maize in Cuba. National Academy of Sciences. National Research Council, Washington, DC, USA
- Hooker A, 1972. Southern leaf blight of corn—present status and future prospects. *J Environ Qual* 1:244-249
- Horwitz BA, Condon BJ, Turgeon BG, 2013. *Cochliobolus heterostrophus*: A *Dothideomycete* pathogen of maize, pp213-228. In: Genomics of soil-and plant-associated fungi. Horwitz BA, Mukherjee PK, Mukherjee M, Kubicek CP eds. Springer, NY
- Jenkins MT, Robert AL, 1952. Inheritance of resistance to the leaf blight of corn caused by *Helminthosporium turcicum*. *Agron J* 44:136-140
- Jenkins MT, Robert AL, 1961. Further genetic studies of resistance to *Helminthosporium turcicum* Pass. in maize by means of chromosomal translocations. *Crop Sci* 1:450-455
- Jennings P, Ullstrup A, 1957. A histological study of 3 *Helminthosporium* leaf blights of corn. *Phytopath* 47:707-714.
- Krakovsky MD, Holley R, Deutsch J, Rice J, Blanco MH, Goodman MM, 2008. Maize allelic diversity project. Maize Genetics Conference Abstracts. 50th Maize Genetics Conference. Washington D.C. Feb 27 - Mar 2, 2008.
- Kump KL, Bradbury PJ, Wisser RJ, Buckler ES, Belcher AR, Oropeza-Rosas MA, Zwonitzer JC, Kresovich S, McMullen MD, Ware D, Balint-Kurti PJ, Holland JB, 2011. Genome-wide association study of quantitative resistance to southern leaf blight in the maize nested association mapping population. *Nat Genet* 43:163-168
- Latterell F, Rossi A, 1983. Gray leaf spot of corn: A disease on the move. *Plant Dis* 67:842-847
- Levings III CS, Siedow JN, 1992. Molecular basis of disease susceptibility in the Texas cytoplasm of maize. *Plant Mol Biol* 19:135-147
- Liu K, Muse SV, 2005. PowerMarker: An integrated analysis environment for genetic marker analysis. *Bioinformatics* 21:2128-2129
- Mackay M, von Bothmer R, Skovmand B, 2005. Conservation and utilization of plant genetic resources—future directions. *Czech J Genet Plant Breed* 41:335-344
- Mackay M, Srivastava J, Damania A, 1990. Strategic planning for effective evaluation of plant germplasm, pp21-25. In: Strategic planning for effective evaluation of plant

germplasm Wheat genetic resources: Meeting diverse needs. Strivastava JP, Damania AB eds. John Wiley & Sons, NY

Matérn B, 1986. *Spatial Variation: Meddelanden fran Statens Skogsforskningsinstitut*, Vol. 49, pp. 1–144, Ed. 2. Springer, Berlin.

Nelson PT, Coles ND, Holland JB, Bubeck DM, Smith OSC, Goodman MM, 2008. Molecular characterization of maize inbreds with expired US plant variety protection. *Crop Sci* 48:1673-1685

Perkins J, Pedersen W, 1987. Disease development and yield losses associated with northern leaf blight on corn. *Plant Dis* 71:940-943

Piepho H, Williams E, Fleck M, 2006. A note on the analysis of designed experiments with complex treatment structure. *Hort Sci* 41:446-452

Poland JA, Bradbury PJ, Buckler ES, Nelson RJ, 2011. Genome-wide nested association mapping of quantitative resistance to northern leaf blight in maize. *PNAS* 108:6893-6898

Pollak LM, 2003. The history and success of the public–private project on germplasm enhancement of maize (GEM). *Adv Agron* 78:45-87

Pratt RC, Gordon SG, 2006. Breeding for resistance to maize foliar pathogens. *Plant Breed Rev* 27:119

R Core Team, 2013. *R: A Language and environment for statistical computing*. R Foundation for Statistical Computing. Vienna, Austria, www.r-project.org

Ramírez ER, Timothy DH, Díaz BE, Grant UJ, with GE Nickerson C, Anderson E, Brown W, 1960. *Races of maize in Bolivia*. National Academy of Sciences, National Research Council, Washington, DC, USA

Renfro B, 1985. Breeding for disease resistance in tropical maize and its genetic control. *Relazioni E Monografie Agrarie Subtropicali E Tropicali Nuova Serie*. Brandolini A, Salamini F eds. 100: 341-366

Ribeiro Jr PJ, Diggle PJ, 2001. *geoR: A package for geostatistical analysis*. *R News* 1:14-18

Roberts LM, Grant UJ, R. Ramírez E, Hatheway WH, Smith DL, with Mangelsdorf PC, 1957. *Races of maize in Colombia*. National Academy of Sciences, National Research Council, Washington, DC, USA

- Schwarz G, 1978. Estimating the dimension of a model. *Annals of Statistics* 6:461-464
- Smith D, Kinsey J, 1980. Further physiologic specialization in *Helminthosporium turcicum*. *Plant Dis* 64:779-781
- Street K, Hamilton RS, Tay D, Taba S, Mackay M, 2013. Mining germplasm banks for photosynthetic improvement—wheat, rice, potato, legumes and maize, pp112-129. In: *Applying Photosynthesis Research to Improvement of Food Crops*. Gready JE, Dwyer SA, Evans JR eds. Australian Centre for International Agricultural Research proceedings, Canberra, Australia
- Tatum LA, 1971. The southern corn leaf blight epidemic. *Science* 171:1113-1116
- Tehon L, Daniels E, 1925. Notes on the parasitic fungi of Illinois. *Mycologia* 17:240-249
- Timothy DH, Hatheway WH, Grant UJ, Torregroza CM, Sarria VD, Varela AD, 1963. Races of maize in Ecuador. National Academy of Sciences, National Research Council, Washington, DC, USA
- Timothy DH, Peña VB, R. Ramírez E, with Brown WL, Anderson E, 1961. Races of maize in Chile. National Academy of Sciences, National Research Council, Washington, DC, USA
- Tohme J, Gonzalez D, Beebe S, Duque MC, 1996. AFLP analysis of gene pools of a wild bean core collection. *Crop Sci* 36:1375-1384
- Troyer AF, 2004. Background of US hybrid corn II. *Crop Sci* 44:370-380
- Ullstrup A, 1972. The impacts of the southern corn leaf blight epidemics of 1970-1971. *Annu Rev Phytopathology* 10:37-50
- Vigouroux Y, Glaubitz JC, Matsuoka Y, Goodman MM, Sánchez J, Doebley J, 2008. Population structure and genetic diversity of New World maize races assessed by DNA microsatellites. *Am J Bot* 95:1240-1253
- Wang J, Levy M, Dunkle LD, 1998. Sibling species of *Cercospora* associated with gray leaf spot of maize. *Phytopath* 88:1269-1275
- Ward JM, Stromberg EL, Nowell DC, Nutter Jr FW, 1999. Gray leaf spot: A disease of global importance in maize production. *Plant Dis* 83:884-895

Wellhausen EJ, Fuentes OA, Hernández-Corzo A, with Mangelsdorf PC, 1957. Races of maize in Central America. National Academy of Sciences, National Research Council, Washington, DC, USA

Wellhausen EJ, Roberts LM, E. Hernández X, with Mangelsdorf PC, 1952. Races of maize in Mexico: Their origin, characteristic and distribution. Bussey Institution of Harvard University, Cambridge, Massachusetts, USA

Welz H, Geiger H, 2000. Genes for resistance to northern corn leaf blight in diverse maize populations. *Plant Breeding* 119:1-14

Wisser RJ, Kolkman JM, Patzoldt ME, Holland JB, Yu J, Krakowsky M, Nelson RJ, Balint-Kurti PJ, 2011. Multivariate analysis of maize disease resistances suggests a pleiotropic genetic basis and implicates a GST gene. *PNAS USA* 108:7339-7344

Zwonitzer JC, Coles ND, Krakowsky MD, Arellano C, Holland JB, McMullen MD, Pratt RC, Balint-Kurti PJ, 2010. Mapping resistance quantitative trait loci for three foliar diseases in a maize recombinant inbred line population-evidence for multiple disease resistance? *Phytopath* 100:72-79

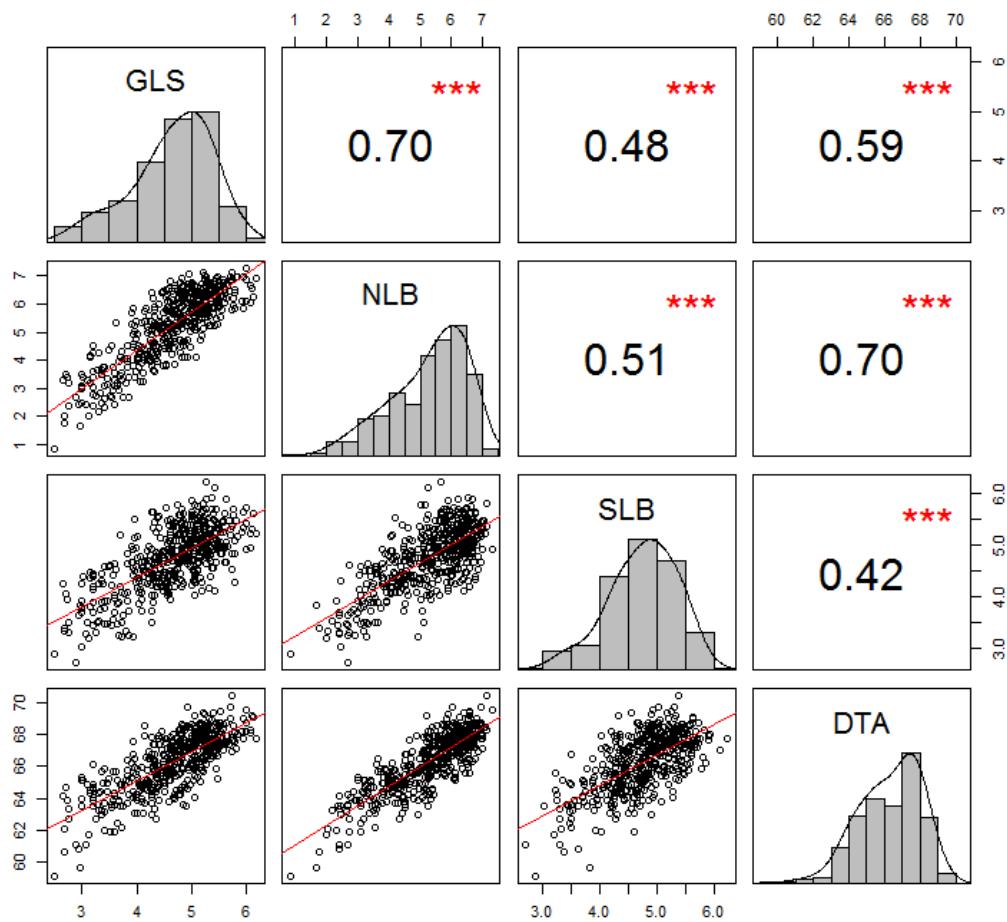


Figure 2.1 Pairwise regression of GLS, NLB, SLB, and DTA scores for the 483 BC₁ F₁s screened

Upper diagonal indicates significance (***) level of pairwise linear regression and pairwise r^2 . Diagonal shows distribution of scores for each trait. Below diagonal shows the pairwise linear regressions and scatter of points.

Table 2.1 Worst and best performing BC₁F₁s for GLS, NLB, and SLB; DTA of each family is also noted

Rank	Race	Accession	GLS [†]	DTA	Race	Accession	NLB [†]	DTA	Race	Accession	SLB [†]	DTA
483	Gaspe Flint	PI 401757	2.50	59	Gaspe Flint	PI 401757	0.84	59	Shoshone	PI 213769	2.70	61
482	Navajo	PI 218163	2.66	64	Cristalino Chico	CHI 324	1.68	60	Gaspe Flint	PI 401757	2.87	59
481	Bear Isl. Chippewa	PI 213801	2.67	61	Bear Isl. Chippewa	PI 213801	1.77	61	Cristalino Blanco	ARZM 19074	3.01	64
480	Araucano	CHI 320	2.67	62	Cristalino Amarillo	AR 21004	2.01	62	Cristalino Amarillo	AR 21004	3.19	62
479	Tesuque Pueblo	PI 218137	2.70	65	Araucano	CHI 320	2.03	62	Dulce de Jalisco	JAL 304	3.21	66
478	Havasupai	P I317675	2.74	64	Winnebago	PI 213772	2.18	63	Curagua	CHI 314	3.22	65
477	Winnebago	PI 213774	2.75	63	Longfellow	PI 214195	2.31	62	Curagua Grande	CHI 303	3.24	64
476	San Lorenzo Pueblo	PI 218135	2.76	63	Cristalino Amarillo	ARZM 19070	2.36	64	Sac And Fox	PI 217411	3.25	64
475	Shoshone	PI 213769	2.88	61	Winnebago	PI 213774	2.39	63	Seneca Hominy Corn	PI 401754	3.28	61
474	Longfellow Flint	PI 217408	2.94	61	Seneca Hominy Corn	PI 401754	2.41	61	Winnebago	PI 213774	3.29	63
	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮
10	Chococeno	CHO 340	5.94	69	Amagaceno	HUI 317	6.96	69	Morochillo	PIU 96	5.75	68
9	Puya Grande	SAN 347	5.95	68	Cariaco	VEN 639	6.96	68	Costeno	ATL 314	5.79	66
8	Puya Grande	VEN 345	5.98	69	Oloton	GUA 383	6.97	67	Tuson	BAI IIIB	5.80	67
7	Olotillo	CHS 53	5.99	69	Salpor Tardio	GUA 485	6.98	68	Negrito	VEN 870	5.83	68
6	Yucatan	TOL 399	5.99	68	Puya Grande	SAN 347	6.99	68	Comun	NAR 330	5.87	66
5	Cristal	SP XI	6.06	68	Tuson	CUB 67	7.02	68	Tuson	TRN 10	5.91	68
4	Cristal	SP X	6.07	68	Capio	ANT 348	7.08	68	Comun	VEN 881	5.91	68
3	Huanuco	HCO 128B	6.09	69	Negrito	VEN 870	7.13	68	Cateto Nortista	GIN I	5.94	68
2	Tehua	CHS 29	6.11	69	Tehua	CHS 159	7.13	70	Yunquillano forma Andaqui	ECU 710	6.12	67
1	Tuxpeno	VEN 891	6.17	68	Olotillo	CHS 53	7.29	69	Andaqui	CAQ 307	6.24	68

[†]GLS, NLB, and SLB disease was rated on a 1 to 9 scale with 9 being completely resistant

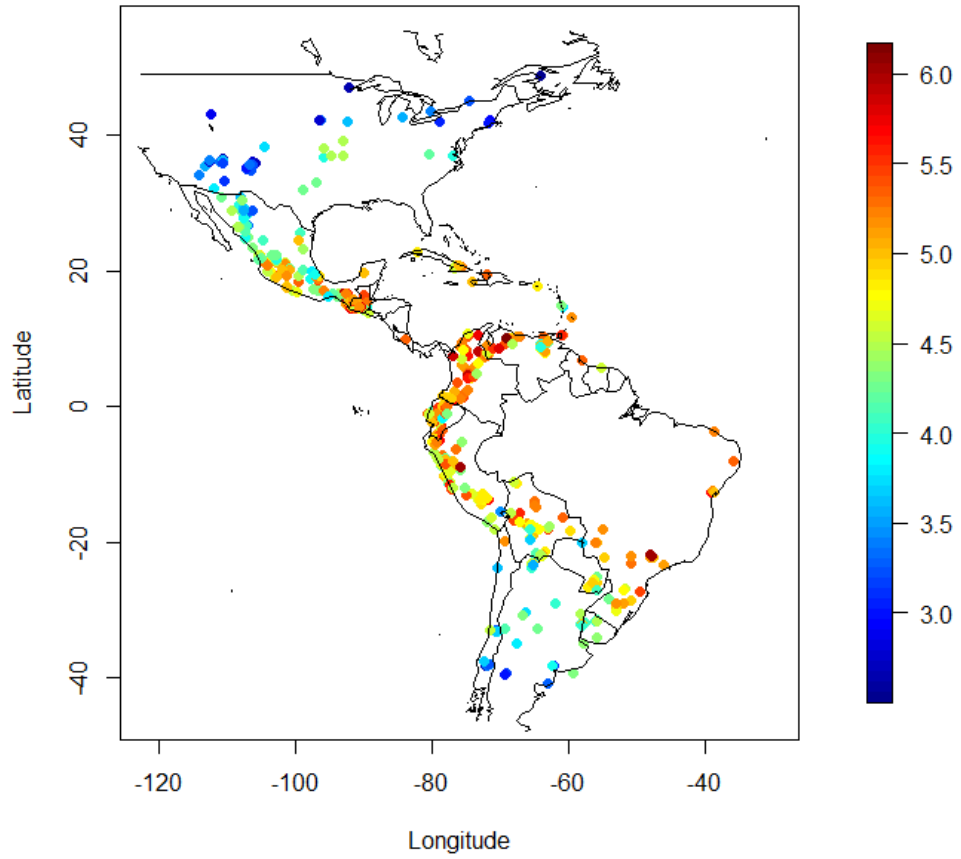


Figure 2.2 Raw point pattern data of GLS scores of BC₁ F₁s at point of collection of donor landraces

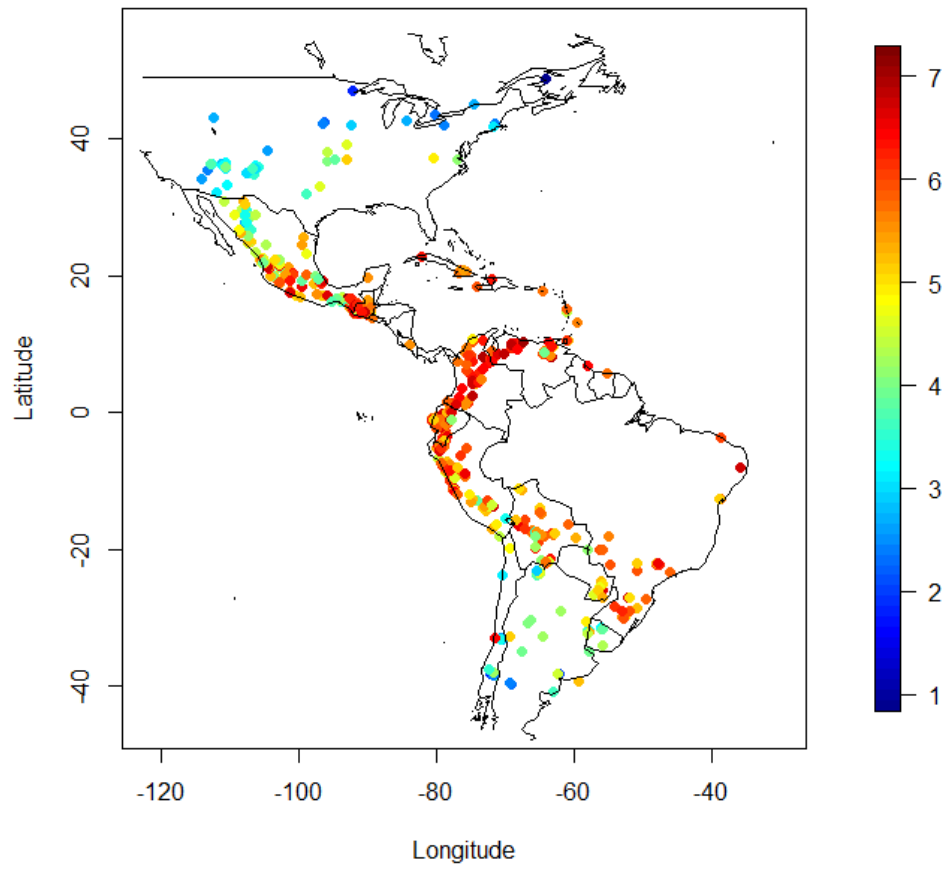


Figure 2.3 Raw point pattern data of NLB Scores of $BC_1 F_1$ s at point of collection of donor landraces

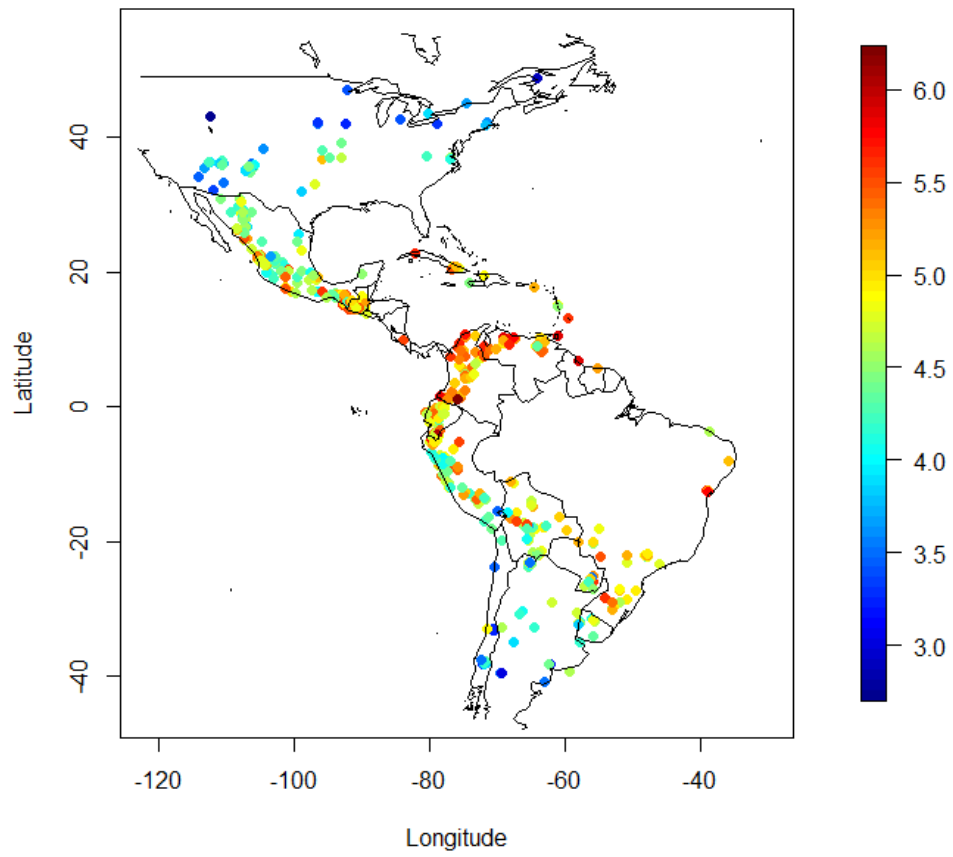


Figure 2.4 Raw point pattern data of SLB Scores of BC₁ F₁s at point of collection of donor landraces

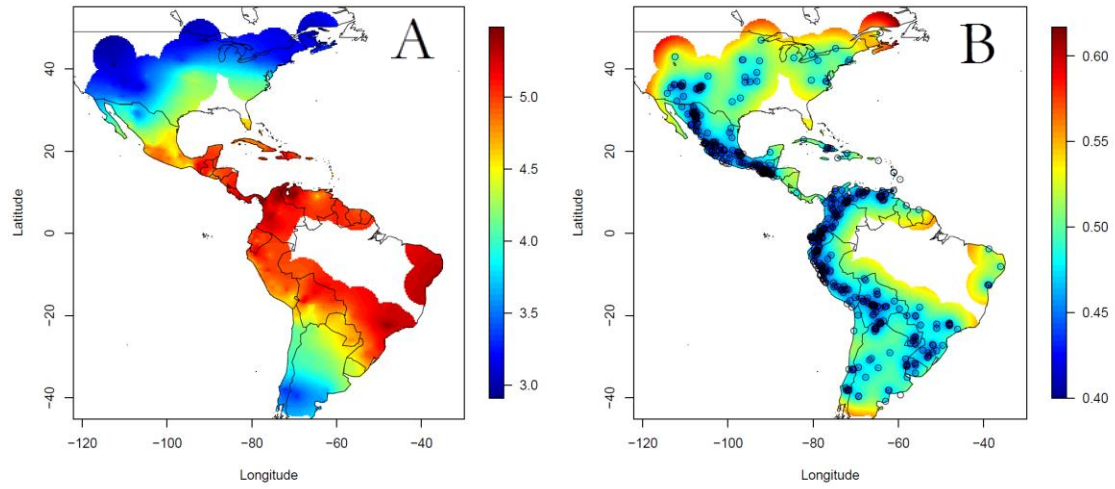


Figure 2.5A-B 2.5A shows predicted GLS scores of $BC_1 F_1$ s with possible donor parents from locations across the Americas; 2.5B shows the standard errors of the estimates

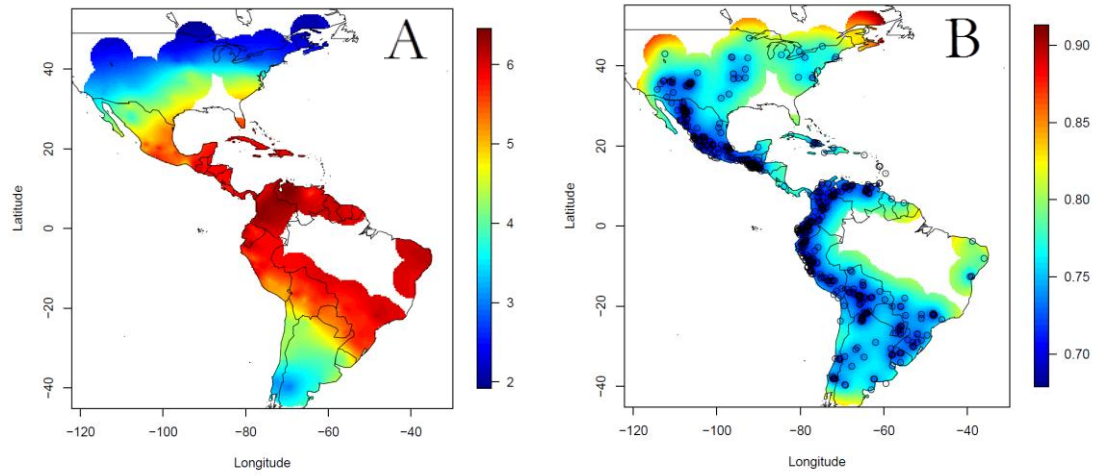


Figure 2.6A-B 2.6A shows predicted NLB scores of $BC_1 F_1$ s with possible donor parents from locations across the Americas; 2.6B shows the standard errors of the estimates

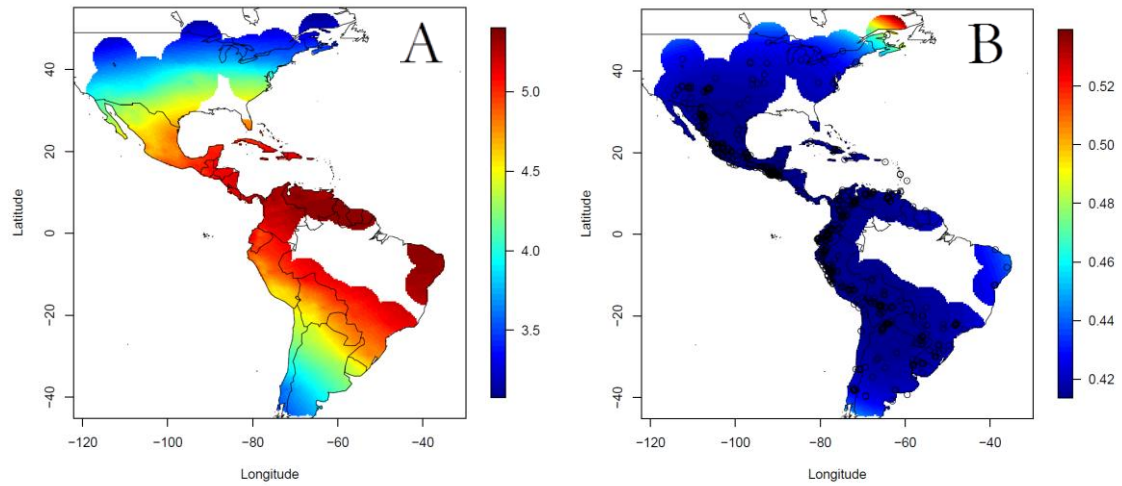


Figure 2.7A-B 2.7A shows predicted SLB scores of $BC_1 F_1$ s with possible donor parents from locations across the Americas; 2.7B shows the standard errors of the estimates

Supplemental Table 2.1 Chi square tests with Yates correction for random distribution of QTL discovered in Nested Association Mapping Population studies for Gray Leaf Spot (GLB), Northern Leaf Blight (NLB), and Southern Leaf Blight (SLB)

Chromosome	Proportion of Genome	Observed # of QTL GLS	Expected # of QTL GLS	GLS Chi square [†]
1	0.14	3	2.24	0.71
2	0.11	2	1.76	0.31
3	0.11	1	1.76	0.04
4	0.10	1	1.60	0.01
5	0.11	3	1.76	1.72
6	0.08	2	1.28	1.16
7	0.10	1	1.60	0.01
8	0.09	2	1.44	0.78
9	0.08	0	1.28	0.48
10	0.07	1	1.12	0.13
Total	1	16	16	5.34
w/9 df crit = 16.91				
Chromosome	Proportion of Genome	Observed # of QTL NLB	Expected # of QTL NLB	NLB Chi square [†]
1	0.14	6	4.06	1.47
2	0.11	6	3.19	3.43
3	0.11	2	3.19	0.15
4	0.10	3	2.90	0.12
5	0.11	2	3.19	0.15
6	0.08	3	2.32	0.60
7	0.10	2	2.90	0.06
8	0.09	2	2.61	0.00
9	0.08	1	2.32	0.29
10	0.07	2	2.03	0.11
Total	1	29	29	6.38
w/9 df crit = 16.91				
Chromosome	Proportion of Genome	Observed # of QTL SLB	Expected # of QTL SLB	SLB Chi square [†]
1	0.14	4	4.58	0.00
2	0.11	3	3.57	0.00
3	0.11	6	3.56	2.43
4	0.10	3	3.23	0.02
5	0.11	3	3.51	0.00
6	0.08	2	2.51	0.00
7	0.10	3	3.09	0.05
8	0.09	2	2.97	0.07
9	0.08	4	2.63	1.33
10	0.07	2	2.33	0.01
Total	1	32	32	3.92
w/9 df crit = 16.91				

[†]Note: first, using the NAM map, the proportion of the genome for each chromosome was calculated (McMullen et al, 2009). Next, the numbers of QTL observed from the NAM mapping studies were counted on each chromosome (Benson, 2013; Kump et al, 2011; Poland et al, 2011). The expected number of QTL on each chromosome was calculated proportional to each chromosome's proportion of the genome. The observed QTL counts per chromosome were compared to expected counts with a Chi square test, with 9 df.

Supplemental Table 2.2 BC₁ F₁s Development

Country, Race, and Accession of each landrace used are given. Plant Number and Year F₁ is the number of plants that were used to make the F₁, inside parentheses the year that cross was made. Plant Number and Year BC₁ is the number of plants that were used to make the BC₁, and inside parentheses the year that cross was made. Location of F₁ Production gives the location and year where F₁s were made. F₁s were made by GEM project personnel in both Clayton, NC (CLY) and Homestead, FL (FL) or in locations donated with in kind support from Dupont Pioneer in Hawaii, and Syngenta in Puerto Rico.

Country	Race	Accession [†]	Plant Number and (Year) F ₁	Plant Number and (Year) BC ₁	Location and (Year) of F ₁ Production
Argentina	Amargo	ARZM 03014	5 (10) + 9 (11)	12 (12)	CLY (10) + CLY (11)
Argentina	Bola Blanca	ARG 532 (USDA)	4 (07)	8 (08)	Pioneer (07)
Argentina	Calchaqui Small White	ARG 2420 (USDA)	8 (07)	12 (08)	Pioneer (07)
Argentina	Camelia	ARZM 03025	8 (10)	12 (11)	CLY (10)
Argentina	Canario de Formosa	ARZM 06016	12 (10)	12 (11)	CLY (10)
Argentina	Canario de Ocho	ARG VI	8 (08)	12 (09)	Pioneer (08)
Argentina	Capia Blanco	ARG 499 (USDA)	7 (08)	12 (09)	Pioneer (08)
Argentina	Capia Rosado	ARG 460 (USDA)	5 (07)	10 (08)	Pioneer (07)
Argentina	Cateto Sulino	ARG I	8 (10)	12 (11)	CLY (10)
Argentina	Chulpi	ARG 484 (USDA)	7 (08)	12 (09)	Syngenta (08)
Argentina	Cravo	ARZM 05071	12 (10)	12 (11)	CLY (10)
Argentina	Cristal Sulino	ARG III	12 (10)	12 (11)	CLY (10)
Argentina	Cristalino Amarillo	AR 21004	1 (06)	9 (07)	Pioneer (06)
Argentina	Cristalino Amarillo	ARZM 19070	7 (08)	12 (09)	Syngenta (08)
Argentina	Cristalino Blanco	ARZM 19074	7 (08)	12 (09)	Syngenta (08)
Argentina	Cristalino Colorado	ARZM 16021	12 (10)	12 (11)	CLY (10)
Argentina	Cuarentino	ARG 486 (USDA)*	9 (10)	12 (11)	CLY (10)
Argentina	Culli	ARG 471 (USDA)	12 (07)	12 (08)	Pioneer (07)
Argentina	Dentado Amarillo	ARZM 16062	12 (10)	12 (11)	CLY (10)

Supplemental Table 2.2 Continued

Country	Race	Accession [†]	Plant Number and (Year) F ₁	Plant Number and (Year) BC ₁	Location and (Year) of F ₁ Production
Argentina	Dentado Blanco	ARZM 03056	12 (10)	12 (11)	CLY (10)
Argentina	Dentado Blanco Rugoso	ARZM 01149	12 (10)	12 (11)	CLY (10)
Argentina	Dulce	ARZM 20005B	12 (11)	12 (12)	CLY (11)
Argentina	Marron	ARG 468 (USDA)	10 (11)	16 (12)	FL (11)
Argentina	Oke	ARG 539 (USDA)	6 (07)	12 (08)	Pioneer (07)
Argentina	Pisincho	ARG 481 (USDA)*	12 (10)	12 (11)	CLY (10)
Argentina	Pisingallo	ARZM 13095	7 (08)	11 (09)	Syngenta (08)
Barbados	Tuson	BARBGP 2*	8 (10)	10 (11)	FL (10)
Bolivia	Altiplano	BOV 903	2 (06)	6 (07)	Pioneer (06)
Bolivia	Argentino	BOV 920	8 (07)	12 (08)	Pioneer (07)
Bolivia	Aysuma	BOV 331	4 (06)	5 (07)	Pioneer (06)
Bolivia	Camba	BOV 1131	7 (06)	9 (07)	Pioneer (06)
Bolivia	Cateto	BOV 1083	9 (09)	12 (10)	FL (09)
Bolivia	Cateto	BOV 317	7 (08)	12 (09)	Pioneer (08)
Bolivia	Chake-Sara	BOV 520	3 (07) + 3 (08)	6 (09)	Pioneer (07) + Pioneer (08)
Bolivia	Checchi	BOV 320	7 (08)	12 (09)	Syngenta (08)
Bolivia	Checchi	BOV Comp.	8 (09)	12 (10)	FL (09)
Bolivia	Cholito	BOV 309	3 (06)	5 (07)	Pioneer (06)
Bolivia	Chuspillu	BOV 883	4 (09) + 7 (10)	4 (10) + 5 (11) + 4 (11)	Syngenta (09) + FL (10)
Bolivia	Coroico	BOV 1064	8 (06)	15 (07)	Pioneer (06)
Bolivia	Coroico Amarillo	BOV 405	9 (07)	12 (08)	Pioneer (07)
Bolivia	Coroico Blanco	BOV 406	6 (07)	10 (08)	Pioneer (07)
Bolivia	Cubano Dentado	BOV 440	14 (09)	12 (10)	FL (09)
Bolivia	Cubano Dentado	BOV 585	10 (07)	10 (08)	Pioneer (07)
Bolivia	Enano	BOV 1032	2 (06)	5 (07)	Pioneer (06)
Bolivia	Huilcaparu	BOV 685	5 (10)	8 (11)	FL (10)

Supplemental Table 2.2 Continued

Country	Race	Accession [†]	Plant Number and (Year) F ₁	Plant Number and (Year) BC ₁	Location and (Year) of F ₁ Production
Bolivia	Huilcaparu Moteado	BOV Comp.	5 (07)	5 (08)	Pioneer (07)
Bolivia	Karapampa	BOV 978	5 (06)	7 (07)	Pioneer (06)
Bolivia	Kcello	BOV 325	9 (09)	5 + 8 (10)	FL (09)
Bolivia	Kcello	BOV 848	9 (09)	12 (10)	FL (09)
Bolivia	Kcello	BOV 948	6 (06)	5 (07)	Pioneer (06)
Bolivia	Morado	BOV 567	1 (06)	7 (07)	Pioneer (06)
Bolivia	Ninuelo	BOV 1088	13 (07)	7 (08)	Pioneer (07)
Bolivia	Paru	BOV Comp.	6 (09)	3 (10)	FL (10)
Bolivia	Patillo Grande	BOV 649	2 (06)	6 (07)	Pioneer (06)
Bolivia	Perola	BOV 711	3 (06)	4 (07)+ 8 (08)	Pioneer (06)
Bolivia	Pisankalla	BOV 344	6 (06)	4 (07)	Pioneer (06)
Bolivia	Pisankalla	BOV 864	6 (10)	12 (11)	CLY (10)
Bolivia	Pisankalla	BOV 965	5 (10)	17 (11)	CLY (10)
Bolivia	Pojoso Chico	BOV 800	8 (06)	6 (07)	Pioneer (06)
Bolivia	Pororo	BOV 583	14 (09)	11 (10)	FL (09)
Bolivia	Pororo	BOV 806	7 (10)	13 (11)	CLY (10)
Bolivia	Uchuquilla	BOV 318	1 (06)	5 (07)	Pioneer (06)
Bolivia	Uchuquilla	BOV 954	13 (09)	12 (10)	FL (09)
Bolivia	Yungueno	BOV 362	3 (06)	4 (07)	Pioneer (06)
Bolivia	Yungueno	BOV 716	7 (07)	7 (08)	Syngenta (07)
Brazil	Avati Pichinga	BR 2760 (USDA)	16 (09)	15 (11)	FL (09)
Brazil	Avati Pichinga	BR 2776 (USDA)	5 (10)	15 (11)	CLY (10)
Brazil	Avati Pichinga Ihu	BR 2830 (USDA)	10 (07)	3 (08)	Pioneer (07)
Brazil	Caingang	PR III	18 (09)	12 (10)	FL (09)
Brazil	Caingang	SP XIII	4 (09)	15 (10)	FL (09)
Brazil	Caraja	1692 (USDA)	7 (07)	10 (08)	Pioneer (07)

Supplemental Table 2.2 Continued

Country	Race	Accession [†]	Plant Number and (Year) F ₁	Plant Number and (Year) BC ₁	Location and (Year) of F ₁ Production
Brazil	Cateto	BA II	8 (09)	12 (10)	FL (09)
Brazil	Cateto	CE I	6 (10)	22 (11)	FL (10)
Brazil	Cateto Assis Brasil	RGS XIV	12 (08)	12 (09)	Pioneer (08)
Brazil	Cateto Grande	MT IV	12 (09)	12 (11)	FL (09)
Brazil	Cateto Nortista Precoce	SUR I	9 (08)	12 (09)	Pioneer (08)
Brazil	Cravo Paulista	SP I	1 (08) + 2 (09)	7 (10)	Pioneer (08) +Pioneer (09)
Brazil	Cravo Riograndense	RGS VII	6 (07)	12 (08)	Pioneer (07)
Brazil	Cristal	SP X	7 (07)	11 (08)	Pioneer (07)
Brazil	Cristal	SP XI	7 (09)	12 (10)	FL (09)
Brazil	Cristal Inter. Perola	1115 (USDA)	6 (08)	12 (09)	Syngenta (08)
Brazil	Cristal Paraguay Paulista	2334 (USDA)	2 (08) + 4 (09)	12 (10)	Syngenta (08) +FL (09)
Brazil	Dente Branco Paulista	SP V	6 (07)	11 (08)	Syngenta (07)
Brazil	Dente Branco R. G.	SC II	10 (09)	12 (10)	FL (09)
Brazil	Dente Paulista	SP IV	7 (07)	11 (08)	Syngenta (07)
Brazil	Dente R. G. Liso	RGS VI	11 (09)	12 (10)	FL (09)
Brazil	Dente R. G. Liso	SC I	6 (07)	10 (08)	Syngenta (07)
Brazil	Dente R. G. Rugoso	RGS II	11 (09)	12 (10)	FL (09)
Brazil	Dourados Saboro	BR 50 (USDA)	9 (09)	12 (10)	Pioneer (09)
Brazil	Entrelacado	MT VI	6 blk (09)	12 (10)	Pioneer (09)
Brazil	Hickory King	RGS IX*	6 (10)	15 (11)	CLY (10)
Brazil	Moroti	MT I	7 (09)	13 (10)	FL (09)
Brazil	Moroti	PE I	4 (06)	5 (07)	Pioneer (06)
Brazil	Moroti Precoce	BOL I	5 (09)	12 (10)	Pioneer (09)
Brazil	Semi Dente Paulista	SP IX	15 (09)	12 (10)	FL (09)
Brazil	Semi Dente R. G.	RGS XV	9 (09)	12 (10)	Pioneer (09)
Brazil	Tuson	BAI III	5 (10)	21 (11)	FL (10)

Supplemental Table 2.2 Continued

Country	Race	Accession [†]	Plant Number and (Year) F ₁	Plant Number and (Year) BC ₁	Location and (Year) of F ₁ Production
Brazil	Tuson	BAI IIB	2 (10) + 8 (11)	12 (12)	FL (10) + CLY (11)
Chile	Araucano	CHI 320*	6 (06)	4 (07)+ 8 (08)	Pioneer (06)
Chile	Capia Chico Chileno	CHI 382*	7 (06)	4 (07)+ 8 (08)	Pioneer (06)
Chile	Cristalino Chico	CHI 324	7 (10)	15 (11)	CLY (10)
Chile	Cristalino Chileno	CHI 156	7 (07)	12 (08)	Pioneer (07)
Chile	Cristalino Grande	CHI 323*	12 (11)	12 (12)	CLY (11)
Chile	Curagua	CHI 301*	4 (10)	10 (11)	CLY (10)
Chile	Curagua	CHI 314*	7 (06)	4 (07)+ 8 (08)	Pioneer (06)
Chile	Curagua Grande	CHI 303	4 (06)	5 (07)	Pioneer (06)
Chile	Dentado Comercial	CHI 326*	7 (10)	12 (11)	CLY (10)
Chile	Dulce Evergreen	CHI 332*	5 (10)	16 (11)	CLY (10)
Chile	Dulce Golden Bantam	CHI 335*	6 (10)	26 (11)	CLY (10)
Chile	Harinoso Tarapaqueno	CHI 421	4 (11)	11 (12)	CLY (11)
Colombia	Amagaceno	ANT 343*	5 (07)	11 (08)	Syngenta (07)
Colombia	Amagaceno	HUI 317*	5 (07)	10 (08)	Pioneer (07)
Colombia	Andaqui	CAQ 307*	2 (06)	7 (07)	Pioneer (06)
Colombia	Andaqui	CAQ 333*	10 (09)	12 (10)	Pioneer (09)
Colombia	Cabuya	SAN 316*	2 (06)	7 (07)	Pioneer (06)
Colombia	Cacao	SAS 327*	4 (07)	10 (08)	Pioneer (07)
Colombia	Cacao	SAS 335*	4 (10)	7 (11)	FL (10)
Colombia	Capio	ANT 348*	2 (07)	5 (08)	Pioneer (07)
Colombia	Capio	ANT 354	2 (10)	7 (11)	FL (10)
Colombia	Capio	NAR 315	3 (06)	6 (07)	Pioneer (06)
Colombia	Caqueteno	CAQ 305*	5 (08)	12 (09)	Pioneer (08)
Colombia	Cariaco	COR 338*	8 (10)	7 (11)	FL (10)
Colombia	Chococeno	CHO 340	2 (07) + 1 (08)	5 (09)	Pioneer (07) + Pioneer (08)

Supplemental Table 2.2 Continued

Country	Race	Accession [†]	Plant Number and (Year) F ₁	Plant Number and (Year) BC ₁	Location and (Year) of F ₁ Production
Colombia	Clavo	NAR 329*	2 (07) + 3 (10)	7 (11)	Pioneer (07) + FL (10)
Colombia	Comun	NAR 330*	8 (08)	8 (10)	Ames (08)
Colombia	Comun	VAL 374*	7 (06)	4 (07)+ 8 (08)	Pioneer (06)
Colombia	Comun	CAU 454*	4 (06)	5 (07)	Pioneer (06)
Colombia	Costeno	ANT 394*	7 (07)	12 (08)	Pioneer (07)
Colombia	Costeno	ATL 314*	7 (07)	6 (08)	Syngenta (07)
Colombia	Costeno	ATL 328*	5 (10)	13 (11)	FL (10)
Colombia	Costeno	COR 320*	9 (10)	15 (11)	FL (10)
Colombia	Guirua	MAG 469*	4 (07)	4 (08)	Pioneer (07)
Colombia	Harin. Dent.	NAR 326*	5 (10)	12 (11)	FL (10)
Colombia	Imbricado	NAR 389	8 (10)	6 (11)	FL (10)
Colombia	Montana	NAR 625*	5 (06)	8 (07)	Pioneer (06)
Colombia	Pira	CUN 327*	8 (10)	9 (11)	FL (10)
Colombia	Pira	CUN 480*	8 (10)	8 (11)	FL (10)
Colombia	Pira	TOL 405	4 (07)	10 (08)	Pioneer (07)
Colombia	Pollo	CUN 424	10 (05)	4 (08)	Syngenta (05)
Colombia	Pollo	CUN 443*	12 (10)	14 (11)	FL (10)
Colombia	Puya	MAG 355*	7 (07)	12 (08)	Pioneer (07)
Colombia	Puya Grande	SAN 347*	10 (09)	20 (10)	FL (09)
Colombia	Sabanero	ANT 423*	8 (08)	12 (10)	Ames (08)
Colombia	Sabanero	CUN 342*	5 (06)	7 (07)	Pioneer (06)
Colombia	Sabanero	CUN 367	7 (06)	4 (07)	Pioneer (06)
Colombia	Sabanero	SAN 329	4 (07)	10 (08)	Pioneer (07)
Colombia	Yucatan	TOL 389*	3 (06)	7 (07)	Pioneer (06)
Colombia	Yucatan	TOL 399*	8 (09)	12 (10)	FL (09)
Costa Rica	Huesillo	CRI 370*	8 (11)	11 (12)	FL (11)

Supplemental Table 2.2 Continued

Country	Race	Accession [†]	Plant Number and (Year) F ₁	Plant Number and (Year) BC ₁	Location and (Year) of F1 Production
Cuba	Argentino	CUB 113*	11 (09)	12 (10)	Pioneer (09)
Cuba	Chandelle	CUB 54*	6 (09)	12 (10)	FL (09)
Cuba	Chandelle	CUB 68	9 (05)	12 (09)	Syngenta (05)
Cuba	Cuban Flint	CUB 63*	11 (11)	11 (12)	FL (11)
Cuba	Maiz Criollo	CUB 136*	9 (09)	12 (10)	Pioneer (09)
Cuba	Tuson	CUB 67*	4 (10)	9 (11)	CLY (10)
Ecuador	Blanco Blandito	ECU 523	4 (07)	7 (08)	Pioneer (07)
Ecuador	Blanco Harinoso Dentado	ECU 640	2 (07) + 4 (10)	11 (11)	Pioneer (07) + FL (10)
Ecuador	Candela	ECU 344*	7 (09)	11 (10)	FL (09)
Ecuador	Candela	ECU 531	4 (06)	4 (07)	Pioneer (06)
Ecuador	Candela	ECU 699	1 (06)	3 (07)	Pioneer (06)
Ecuador	Canguil	ECU 500	6 (08)	13 (09)	Syngenta (08)
Ecuador	Canguil Grueso	ECU 443	7 (10)	9 (11)	FL (10)
Ecuador	Canguil Grueso	ECU 447	12 (07)	12 (08)	Pioneer (07)
Ecuador	Chillo	ECU 411	4 (07)	7 (08)	Pioneer (07)
Ecuador	Chillo	ECU 458	5 (07)	10 (08)	Pioneer (07)
Ecuador	Chillo	ECU 480B	11 (10)	9 (11)	FL (10)
Ecuador	Cholito	ECU 718	2 (06)	7 (07)	Pioneer (06)
Ecuador	Chulpi Chico	ECU 424	9 (09)	10 (11)	Syngenta (09)
Ecuador	Clavito	ECU 884	7 (06)	7 (07)	Pioneer (06)
Ecuador	Conico Dentado	ECU 427	2 (07) + 4 (09)	2 (10) + 7 (11)	Pioneer (07) + Syngenta (09)
Ecuador	Cubano Amarillo Duro	ECU 326	10 (09)	12 (10)	FL (09)
Ecuador	Cubano Amarillo Duro	ECU 327	3 (06)	3 (07)+ 7 (08)	Pioneer (06)
Ecuador	Cubano Amarillo Duro	ECU 698	12 (09)	12 (10)	FL (09)
Ecuador	Cubano Amarillo Duro	ECU 957	13 (09)	12 (10)	FL (09)
Ecuador	Cubano Cateto	ECU 877	11 (09)	12 (10)	FL (09)

Supplemental Table 2.2 Continued

Country	Race	Accession [†]	Plant Number and (Year) F ₁	Plant Number and (Year) BC ₁	Location and (Year) of F1 Production
Ecuador	Cubano Tuson	ECU 542	7 (08)	12 (09)	Syngenta (08)
Ecuador	Cubano Tuson	ECU 660	6 (10)	16 (11)	FL (10)
Ecuador	Cubano Tuson	ECU 764	10 (10)	14 (11)	FL (10)
Ecuador	Enano Gigante	ECU Comp.	2 (06)	6 (07)	Pioneer (06)
Ecuador	Gallina	ECU 329	2 (09) + 7 (10)	8 (11)	Pioneer (09) + FL (10)
Ecuador	Huandango	ECU 735	2 (07)	3 (09)	Pioneer (07)
Ecuador	Mishca	ECU 321	6 (06)	10 (07)	Pioneer (06)
Ecuador	Morochon	ECU 454B	7 (06)	5 (07)	Pioneer (06)
Ecuador	Patillo	ECU 417	8 (07)	11 (08)	Pioneer (07)
Ecuador	Pojoso Chico Ecuatorian	ECU 522	14 (07)	12 (08)	Pioneer (07)
Ecuador	Racimo de Uva	ECU 517	9 (07)	5 (08)	Pioneer (07)
Ecuador	Tusilla	ECU 569	5 (07)	10 (08)	Pioneer (07)
Ecuador	Tuxpeno	ECU 942	8 (10)	12 (11)	FL (10)
Ecuador	Uchima	ECU 681	1 (06)	7 (07)	Pioneer (06)
Ecuador	Yungueno	ECU 572	7 (08)	12 (09)	Syngenta (08)
Ecuador	Yunquillano forma Andaqui	ECU 710	1 (06)	8 (07)	Pioneer (06)
Ecuador	Yunquillano forma Andaqui	ECU 853	6 (08)	12 (09)	Syngenta (08)
Ecuador	Yunquillano forma Andaqui	ECU 855	3 (08)	8 (10)	Pioneer (08)
El Salvad	Amarillo Salvadoreno	Comp.	6 (09) + 5 (09)	12 (10)	FL (09)+PR09
Guatemala	Comiteco	GUA 418	7 (09)	8 (10)	FL (09)
Guatemala	Comiteco	GUA 515	12 (07)	12 (08)	Pioneer (07)
Guatemala	Comiteco	GUA 546	2 (05)	5 (08)	Syngenta (05)
Guatemala	Dzit Bacal	GUA 131	5 (06)	8 (07)	Pioneer (06)
Guatemala	Imbricado	GUA 493	3 (10)	18 (11)	FL (10)
Guatemala	Imbricado	GUA 922	3 (10)	16 (11)	FL (10)
Guatemala	N de Chimaltenango	GUA 369	5 (10)	12 (11)	FL (10)

Supplemental Table 2.2 Continued

Country	Race	Accession [†]	Plant Number and (Year) F ₁	Plant Number and (Year) BC ₁	Location and (Year) of F ₁ Production
Guatemala	N de Chimaltenango	GUA 590	9 (09)	6 (10)	Syngenta (09)
Guatemala	N de T Caliente	GUA 159	12 (05)	8 (08)	Syngenta (05)
Guatemala	N de T Fria	GUA 522	2 (08)	7 (09)	Pioneer (08)
Guatemala	Nal Tel ATB	GUA 111	11 (09)	12 (10)	FL (09)
Guatemala	Nal Tel ATB	GUA 220	12 (05)	12 (08)	Syngenta (05)
Guatemala	Nal Tel ATB	GUA 281	4 (10)	19 (11)	CLY (10)
Guatemala	Nal Tel BTA	GUA 20	5 (11)	12 (12)	FL (11)
Guatemala	Nal Tel BTB	GUA 145*	14 (09)	12 (10)	FL (09)
Guatemala	Nal Tel BTB	GUA 280	9 (09)	12 (10)	FL (09)
Guatemala	Nal Tel BTB	GUA 765*	7 (10) +10 (10)	23 (11)	CLY (10) + FL (10)
Guatemala	Oloton	GUA 383	12 (05)	12 (08)	Syngenta (05)
Guatemala	Quicheno Early	GUA 162	11 (09) + 6 (09)	12 (10)	FL (09) + Syngenta (09)
Guatemala	Quicheno Late	GUA 863	1 (08) + 4 (10)	12 (11)	Syngenta (08) + FL (10)
Guatemala	Quicheno Late	GUA 877	4 (10)	9 (11)	FL (10)
Guatemala	Salpor	GUA 476	6 (08)	11 (09)	Syngenta (08)
Guatemala	Salpor Tardio	GUA 485	6 (07)	8 (08)	Syngenta (07)
Guatemala	San Marceno	GUA 506	7 (07)	2 (08)	Syngenta (07)
Guatemala	San Marceno	GUA 724	11 (05)	12 (08)	Syngenta (05)
Guatemala	Serrano	GUA 940	2 (09)	7 (11)	FL (10)
Guatemala	Tepecintle	GUA 597	13 (09)	18 (10)	FL (09)
Guatemala	Tepecintle	GUA 65	8 (07)	12 (08)	Pioneer (07)
Guatemala	Tepecintle	GUA 651	13 (09)	12 (10)	FL (09)
Guatemala	Tepecintle	GUA 79	7 (09)	12 (10)	FL (09)
Guatemala	Tuxpeno	GUA 456	6 (07)	12 (08)	Pioneer (07)
Guyana	Cateto Nortista	GIN I	8 (07)	12 (08)	Pioneer (07)
Haiti	Chandelle	HTI 14	7 (09)	12 (10)	FL (09)

Supplemental Table 2.2 Continued

Country	Race	Accession [†]	Plant Number and (Year) F ₁	Plant Number and (Year) BC ₁	Location and (Year) of F ₁ Production
Haiti	Haitian Yellow	HTI 1	11 (09)	12 (10)	FL (09)
Martinica	Early Carribean	Martinica 9	5 (09)	7 (07)	Pioneer (06)
Martinica	Unassigned	Martinica 12	2 (06)	12 (10)	FL (09)
Mexico	Apachito	CHH 138*	5 (10)	16 (11)	CLY (10)
Mexico	Apachito	CHH 166*	9 (10)	17 (11)	FL (10)
Mexico	Apachito	CHH 180*	8 (10)	25 (11)	FL (10)
Mexico	Apachito	CHH 182	6 (10)	12 (11)	Syngenta (09)
Mexico	Apachito	CHH 207	13 (10)	14 (11)	CLY (10)
Mexico	Arrocillo Amarillo	PUE 91	6 (10)	14 (11)	FL (10)
Mexico	Arrocillo Amarillo	VER 311*	7 (10)	12 (11)	FL (10)
Mexico	Azul	ACC 70-2	12 (09)	12 (10)	FL (09)
Mexico	Azul	CHH 158*	9 (10)	15 (11)	FL (10)
Mexico	Azul	CHH 220	8 (10)	22 (11)	FL (10)
Mexico	Azul	CHH 218	7 (07)	12 (09)	Pioneer (07)
Mexico	Bofo	DGO 123	2 (06)	4 (07)+ 6 (08)	Pioneer (06)
Mexico	Bofo	NAY 191*	11 (09)	18 (10)	FL (09)
Mexico	Bofo	NAY 203	8 (09)	20 (10)	FL (09)
Mexico	Bolita	OAX 44	7 (09)	11 (10)	FL (09)
Mexico	Cacahuacintle	MEX 7	6 (07)	4 (08)	Syngenta (07)
Mexico	Cacahuacintle	PUE 552*	8 (10)	13 (11)	FL (10)
Mexico	Celaya	GTO 36*	5 (07)	7 (08)	Syngenta (07)
Mexico	Celaya	GTO 69	8 (10)	15 (11)	FL (10)
Mexico	Celaya	GTO 88	9 (10)	15 (11)	CLY (10)
Mexico	Chalqueno	HGO 7	3 (08) + 4 (09)	7 (10)	Syngenta (08) + Syngenta (09)
Mexico	Chapalote	SIN 2*	11 (09)	12 (10)	Pioneer (09)
Mexico	Chapalote	SIN 6	8 (10)	15 (11)	FL (10)

Supplemental Table 2.2 Continued

Country	Race	Accession [†]	Plant Number and (Year) F ₁	Plant Number and (Year) BC ₁	Location and (Year) of F ₁ Production
Mexico	Chapalote	SIN 65	5 (10)	11 (11)	FL (10)
Mexico	Conejo	GRO 17	6 (10)	16 (11)	FL (10)
Mexico	Conejo	GRO 129	6 (10)	14 (11)	FL (10)
Mexico	Conejo	GRO 157	12 (10)	16 (11)	FL (10)
Mexico	Conico	PUE 48	12 (08)	10 (09)	Syngenta (08)
Mexico	Conico	PUE 116	15 (05)	12 (08)	Syngenta (05)
Mexico	Conico Norteno	ZAC 12	4 (09)	11 (10)	FL (09)
Mexico	Conico Norteno	ZAC 161*	1 (06)	6 (07)	Pioneer (06)
Mexico	Coscomatepec	VER 110*	5 (10)	10 (11)	FL (10)
Mexico	Coscomatepec	VER 110B*	5 (10)+4 (11)	12 (12)	FL (10) + FL (11)
Mexico	Cristalino de Chihuahua	CHH 128*	10 (10)	7 (11)	FL (10)
Mexico	Cristalino de Chihuahua	CHH 154*	9 (10)	19 (11)	FL (10)
Mexico	Cristalino de Chihuahua	CHH 254	6 (10)	16 (11)	CLY (10)
Mexico	Dulce de Jalisco	JAL78	4 +7 (10)	2 (11)	CLY (10) + FL (10)
Mexico	Dulce de Jalisco	JAL304	1 (10)	3 (11)	CLY (11)
Mexico	Dulcillo del Noroeste	SIN 34	5 (10)	8 (11)	FL (10)
Mexico	Dulcillo del Noroeste	SIN 79	6 (10)	16 (11)	FL (10)
Mexico	Dulcillo del Noroeste	SON 57*	4 (06)	7 (07)	Pioneer (06)
Mexico	Dzit Bacal	VER 96	3 (10)	10 (11)	FL (10)
Mexico	Elotero de Sinaloa	NAY 32*	5 (10)	9 (11)	FL (10)
Mexico	Elotero de Sinaloa	NAY 46	10 (10)	19 (11)	FL (10)
Mexico	Elotero de Sinaloa	SIN 17	8 (10)	16 (11)	FL (10)
Mexico	Elotes Occidentales	DGO 236*	7 (07)	12 (08)	Pioneer (07)
Mexico	Elotes Occidentales	GTO 191*	4 (10)	12 (11)	FL (10)
Mexico	Elotes Occidentales	NAY 29	7 (09)	10 (10)	Syngenta (09)
Mexico	Elotes Occidentales	NAY 38	4 (10)	11 (11)	CLY (10)

Supplemental Table 2.2 Continued

Country	Race	Accession [†]	Plant Number and (Year) F ₁	Plant Number and (Year) BC ₁	Location and (Year) of F ₁ Production
Mexico	Elotes Occidentales	ZAC 210*	2 (10)	5 (11)	FL (10)
Mexico	Gordo	CHH 131*	10 (05)	10 (08)	Syngenta (05)
Mexico	Gordo	CHH 160*	9 (10)	24 (11)	FL (10)
Mexico	Gordo	CHH 214*	5 (10)	12 (11)	CLY (10)
Mexico	Gordo	CHH 256*	5 (10)	14 (11)	CLY (10)
Mexico	Harinoso de Ocho	NAY 24	7 (07)	4 (08)	Syngenta (07)
Mexico	Jala	JAL44*	6 (07)	8 (08)	Syngenta (07)
Mexico	Jala	NAY 130	6 (10)	8 (11)	FL (10)
Mexico	Mixteco	OAX 569	6 (10)	12 (11)	FL (10)
Mexico	Motozinteco	CHS 650	2 (10)	10 (11)	FL (10)
Mexico	Motozinteco	CHS 650B	10 (10+11)	12 (12)	FL (10) + FL (11)
Mexico	Mushito	MIC 317*	8 (09)	12 (10)	FL (09)
Mexico	Mushito	MIC 371	10 (10)	9 (11)	FL (10)
Mexico	Nal-Tel	CAM 48	8 (10)	11 (11)	FL (10)
Mexico	Negrito	OAX 26*	8 (11)	4 (11)	CLY (11)
Mexico	Olotillo	CHS 53	2 (10)	9 (11)	CLY (11)
Mexico	Olotillo	CHS 81	14 (09)	18 (10)	FL (09)
Mexico	Oloton	CHS 684	3 (10)	7 (11)	FL (10)
Mexico	Onaveno	SON 24*	6 (06)	6 (07)	Pioneer (06)
Mexico	Onaveno	SON 114	8 (10)	26 (11)	FL (10)
Mexico	Palomero de Jalisco	JAL154*	12 (09)	12 (10)	FL (09)
Mexico	Palomero Tipo Chihuahua	CHH 148*	10 (10)	13 (11)	FL (10)
Mexico	Palomero Tipo Chihuahua	CHH 201*	5 (10)	26 (11)	CLY (10)
Mexico	Palomero Toluqueno	VER 35*	7 (08)	12 (09)	Syngenta (08)
Mexico	Pepitilla	GRO 3*	10 (07)	10 (08)	Pioneer (07)
Mexico	Raton	CHH 191*	1 (06) + 3 (07)	12 (08)	Pioneer (06) + Pioneer (07)

Supplemental Table 2.2 Continued

Country	Race	Accession [†]	Plant Number and (Year) F ₁	Plant Number and (Year) BC ₁	Location and (Year) of F ₁ Production
Mexico	Raton	NLE 9*	7 (10)	14 (11)	CLY (10)
Mexico	Raton	TAM 25*	11 (10)	16 (11)	CLY (10)
Mexico	Reventador	NAY 15*	10 (09)	12 (10)	FL (09)
Mexico	Reventador	NAY 39	10 (07)	7 (08)	Pioneer (07)
Mexico	Serrano de Jalisco	JAL133*	3 (10)	11 (11)	CLY (10)
Mexico	Serrano de Jalisco	JAL146	12 (10)	10 (11)	FL (10)
Mexico	Serrano Mixe	OAX 565	2 (10)	12 (11)	FL (10)
Mexico	Tablilla de Ocho	JAL301	4 (09)	12 (10)	FL (09)
Mexico	Tablilla de Ocho	NAY 185	10 (07)	9 (08)	Pioneer (07)
Mexico	Tablilla de Ocho	ZAC 187	13 (05)	10 (08)	Syngenta (05)
Mexico	Tabloncillo	JAL102	4 (10)	13 (11)	CLY (10)
Mexico	Tabloncillo	JAL103*	5 (09)	3 (10)	Pioneer (09)
Mexico	Tabloncillo	JAL103B*	9 (11)	7 (12)	FL (11)
Mexico	Tabloncillo Perla	NAY 12	13 (09)	10 (10)	FL (09)
Mexico	Tabloncillo Perla	NAY 16	3 (10) + 3 (10)	15 (11)	CLY (10) + FL (10)
Mexico	Tehua	CHS 29	5 (07)	12 (08)	Pioneer (07)
Mexico	Tehua	CHS 159	2 (09) + 2 (10)	14 (11)	FL (09) + FL (10)
Mexico	Tepecintle	CHS 76	9 (09)	19 (10)	FL (09)
Mexico	Tuxpeno	VER 143*	7 (08)	12 (09)	Syngenta (08)
Mexico	Tuxpeno Norteno	CHH 121	5 (10)	16 (11)	FL (10)
Mexico	Tuxpeno Norteno	CHH 287*	3 (06)	9 (08)	Syngenta (07)
Mexico	Tuxpeno Norteno	TAM 3*	2 (10)	14 (11)	FL (10)
Mexico	Vandeno	GRO 96	5 (07)	12 (08)	Pioneer (07)
Mexico	Zamorano Amarillo	GTO 1	3 (10)	23 (11)	CLY (10)
Mexico	Zamorano Amarillo	MIC 66*	12 (10)	8 (11)	FL (10)
Mexico	Zapalote Chico	CHS 662	3 (10)	13 (11)	FL (10)

Supplemental Table 2.2 Continued

Country	Race	Accession [†]	Plant Number and (Year) F ₁	Plant Number and (Year) BC ₁	Location and (Year) of F ₁ Production
Mexico	Zapalote Chico	OAX 48	8 (10) + 2 (10)	22 (11)	CLY (10) + FL (10)
Mexico	Zapalote Chico	OAX 50	12 (10)	12 (11)	CLY (10)
Mexico	Zapalote Chico	OAX 70	10 (10)	15 (11)	CLY (10)
Mexico	Zapalote Grande	CHS 104	9 (10)	16 (11)	CLY (10)
Mexico	Zapalote Grande	CHS 224	5 (08)	12 (09)	Pioneer (08)
Mexico	Zapalote Grande	CHS 236	9 (10)	14 (11)	FL (10)
Mexico	Zapalote Grande	CHS 521	9 (10)	21 (11)	FL (10)
Paraguay	Avati Moroti Guapi	PAG 139 (USDA)	7 (07)	12 (08)	Pioneer (07)
Paraguay	Avati Moroti Ti	PAG124 (USDA)	8 (07)	12 (08)	Pioneer (07)
Paraguay	Cateto Sabugo Grosso	PAG 422 (USDA)	6 (08)	12 (09)	Syngenta (08)
Paraguay	Semi Dente Paulista	PAG I*	8 (07)	12 (08)	Pioneer (07)
Paraguay	Moroti Guapi	PAG VI-A	7 (08)	12 (09)	Syngenta (08)
Peru	Alazan	LBQ 18	13 (09)	10 (10)	FL (09)
Peru	Alazan	LIB 34	6 (07)	12 (08)	Pioneer (07)
Peru	Aleman	HCO 38*	10 (10)	12 (11)	FL (10)
Peru	Amarillo Huancabamba	PIU 17B	2 (07)	3 (08)	Pioneer (07)
Peru	Amarillo Huancabamba	PIU 38B*	5 (07)	7 (08)	Pioneer (07)
Peru	Ancashino	ANC 102*	1 (06)	4 (07)	Pioneer (06)
Peru	Arequipeno	ARQ 1*	8 (07)	12 (08)	Pioneer (07)
Peru	Arizona	LIB 2*	8 (07)	12 (08)	Pioneer (07)
Peru	Arizona	LIB 16	11 (09)	19 (10)	FL (09)
Peru	Blanco Ayabaca	PIU 119	7 (06)	4 (07)+ 8 (08)	Pioneer (06)
Peru	Chancayano Blanco	LIM 45*	3 (08) + 1 (09)	3 (11) + 8 (11)	Pioneer (08) + FL (09)
Peru	Chancayano Pintado	LIM 46*	8 (10)	9 (11)	FL (10)
Peru	Chaparreno	ARQ34*	5 (08)	10 (09)	Pioneer (08)
Peru	Chulpi	LIM 66*	1 (06)	6 (07)	Pioneer (06)

Supplemental Table 2.2 Continued

Country	Race	Accession [†]	Plant Number and (Year) F ₁	Plant Number and (Year) BC ₁	Location and (Year) of F ₁ Production
Peru	Chuncho	CUZ 112*	3 (10)	10 (11)	FL (10)
Peru	Colorado	LIB 8*	11 (11)	12 (12)	FL (11)
Peru	Confite Morocho	AYA 20	7 (09)	12 (10)	Syngenta (09)
Peru	Confite Puneno	APC 56	7 (09)	9 (10)	Syngenta (09)
Peru	Confite Puntigudo	CAJ 27	7 (10)	9 (11)	FL (10)
Peru	Confite Puntigudo	CUZ 13	7 (06)	5 (07)	Pioneer (06)
Peru	Coruca	TAC 1*	6 (07)	12 (08)	Pioneer (07)
Peru	Cubano Amarillo	UCA 8*	11 (09)	12 (10)	Pioneer (09)
Peru	Cuzco Cristalino Amaril	CUZ 363	7 (07)	7 (08)	Syngenta (07)
Peru	Cuzco Gigante	CAJ 17	7 (09)	12 (11)	Syngenta (09)
Peru	Granada	ANC 57	6 (09)	12 (11)	Syngenta (09)
Peru	Huachano	LIM 43*	7 (07)	10 (08)	Pioneer (07)
Peru	Huancavelicano	HVC 179*	7 (08)	6 (09)+ 8 (09)	Syngenta (08)
Peru	Huanuco	HCO 128B*	1 (08) + 5 (10)	12 (11)	Pioneer (08) + FL (10)
Peru	Huarmaca	PIU 72*	8 (07)	10 (09)	Pioneer (07)
Peru	Huayleno	ANC 180x181	5 (07)	3 (08)	Pioneer (07)
Peru	Huayleno	ANC 291*	1 (06)	5 (07)	Pioneer (06)
Peru	Jora	ANC 1*	6 (07)	10 (08)	Pioneer (07)
Peru	Kculli	HVC 137	8 (11)	12 (12)	FL (11)
Peru	Maranon	LIB 63B	5 (06)	8(07)	Pioneer (06)
Peru	Mochero	LBQ 5*	9 (06)	6 (07)	Pioneer (06)
Peru	Morado Canteno	Lima 55*	1 (06)	4 (07)	Pioneer (06)
Peru	Morochillo	PIU 96*	6 (09)	7 (10)	FL (09)
Peru	Morocho	APC 67*	7 (06)	9 (07)	Pioneer (06)
Peru	Morocho	APC 77*	1 (06)	7 (07)	Pioneer (06)
Peru	Morocho Cajabambino	LIB 62*	4 (07)	4 (09)	Syngenta (07)

Supplemental Table 2.2 Continued

Country	Race	Accession [†]	Plant Number and (Year) F ₁	Plant Number and (Year) BC ₁	Location and (Year) of F ₁ Production
Peru	Pagaladroga	PIU 2	3 (08) + 8 (09)	12 (10)	Pioneer (08) + Syngenta (09)
Peru	Pardo	LIM 19*	3 (10)	11 (11)	FL (10)
Peru	Paro	CUZ 76	7 (06)	12 (07)	Pioneer (06)
Peru	Perla	ANC 23*	6 (06)	6 (07)	Pioneer (06)
Peru	Perla	ANC 24*	11 (09)	12 (10)	FL (09)
Peru	Perla	LIM 50*	10 (09)	21 (10)	FL (09)
Peru	Piricinco	SM 8*	6 (07)	10 (08)	Pioneer (07)
Peru	Pisccorunto	APC 13	7 (09)	2 (10)	Syngenta (09)
Peru	Pisccorunto	APC 13B	6 (11)	16 (12)	FL (11)
Peru	Rabo de Zorro	ANC 325*	9 (07)	12 (08)	Pioneer (07)
Peru	Rienda	CAJ 80	2 (06)	6 (07)	Pioneer (06)
Peru	San Geronimo Huancaveli	JUN 164	4 (07)	12 (08)	Pioneer (07)
Peru	Sarco	ANC 184	1 (06)	5 (07)	Pioneer (06)
Peru	Shajatu	ANC 117	2 (07) + 4 (08)	12 (09)+ 10 (09)	Pioneer (07) + Pioneer (08)
Trinidad	Tuson	TRN 1	9 (10)	22 (11)	FL (10)
Trinidad	Tuson	TRN 10	7 (07)	9 (08)	Syngenta (07)
Uruguay	Cateto Sulino	URG IV	7 (10)	12 (11)	CLY (10)
Uruguay	Cateto Sulino Escuro	URG V	9 (10)	15 (11)	CLY (10)
Uruguay	Cateto Sulino Grosso	URG III	7 (10)	12 (11)	CLY (10)
Uruguay	Dentado Branco	URZM 13010	12 (10)	12 (11)	CLY (10)
Uruguay	Semi-Dentado Rugoso	URZM 13052	12 (10)	12 (11)	CLY (10)
USA	Apache	PI 213731	7 (11)	7 (11)	CLY (11)
USA	Argentine Pop	PI 217404*	5 (10)	16 (11)	CLY (10)
USA	Bear Isl. Chippewa	PI 213801*	1 (10)	7 (11)	CLY (11)
USA	Cherokee	PI 213744*	8 (10)	12 (11)	CLY (10)
USA	Cochiti Pueblo	PI 218151*	10 (10)	17 (11)	CLY (10)

Supplemental Table 2.2 Continued

Country	Race	Accession [†]	Plant Number and (Year) F ₁	Plant Number and (Year) BC ₁	Location and (Year) of F ₁ Production
USA	Domingo Pueblo	PI 218130*	6 (10)	15 (11)	CLY (10)
USA	Gaspe Flint	PI 401757*	6 (10)	4 (11)	CLY (10)
USA	Gourd Seed	PI 217405*	7 (10)	14 (11)	CLY (10)
USA	Gourd Seed	PI 414183*	10 (10)	12 (11)	CLY (10)
USA	Havasupai	PI 317675*	7 (10)	15 (11)	CLY (10)
USA	Havasupai	PI 317679*	6 (10)	14 (11)	CLY (10)
USA	Hopi	PI 213733*	8 (10)	23 (11)	CLY (10)
USA	Hualapai	PI 213741*	11 (11)	9 (11)	CLY (11)
USA	Isleta-Tiwa	PI 218148*	7 (10)	16 (11)	CLY (10)
USA	Jemez Pueblo	PI 218173*	6 (10)	13 (11)	CLY (10)
USA	Laguna Pueblo	PI 218169*	6 (10)	13 (11)	CLY (10)
USA	Laguna Pueblo	PI 218170*	6 (10)	13 (11)	CLY (10)
USA	Longfellow Flint	PI 217408*	6 (10)	25 (11)	CLY (10)
USA	Longfellow	PI 214195*	12 (10)	15 (11)	CLY (10)
USA	Mexican June	PI 221889*	4 (10)	14 (11)	CLY (10)
USA	Mexican June	PI 311243*	10 (10)	16 (11)	CLY (10)
USA	Moencopi Pueblo	PI 218175*	6 (10)	18 (11)	CLY (10)
USA	Moencopi Pueblo	PI 218177*	4 (10)	15 (11)	CLY (10)
USA	Mohave	PI 218187*	6 (10)	12 (11)	CLY (10)
USA	Mohawk Round Nose	PI 483087*	5 (10)	24 (11)	CLY (10)
USA	N.W. Dent	PI 217480*	7 (10)	26 (11)	CLY (10)
USA	Navajo	PI 218163*	11 (11)	8 (11)	CLY (11)
USA	Northeast Flint	WLB	6 (10)	16 (11)	CLY (10)
USA	Papago-Pimans	PI 217410*	7 (10)	21 (11)	CLY (10)
USA	Pueblo 12-Row Hopi Koko	PI 503564*	7 (10)	20 (11)	CLY (10)
USA	Quapaw Red	PI 213757*	10 (10)	12 (11)	CLY (10)

Supplemental Table 2.2 Continued

Country	Race	Accession [†]	Plant Number and (Year) F ₁	Plant Number and (Year) BC ₁	Location and (Year) of F ₁ Production
USA	Sac And Fox	PI 217411*	4 (10)	23 (11)	CLY (10)
USA	San Lorenzo Pueblo	PI 218135	4 (10)	21 (11)	CLY (10)
USA	Santo Domingo Pueblo	PI 218143*	5 (10)	13 (11)	CLY (10)
USA	Seneca Hominy Corn	PI 401754*	1 (10)	7 (11)	CLY (11)
USA	Shoshone	PI 213769*	2 (10)	9 (11)	CLY (11)
USA	Smut Nose	PI 222490*	4 (10)	16 (11)	CLY (10)
USA	Supergold Pop	PI 222648*	9 (10)	12 (11)	CLY (10)
USA	Tennessee Red Cob	PI 311235*	11 (10)	12 (11)	CLY (10)
USA	Tesuque Pueblo	PI 218137*	6 (10)	15 (11)	CLY (10)
USA	White Dent	PI 221885*	11 (10)	12 (11)	CLY (10)
USA	White Dent	PI 311232*	7 (10)	16 (11)	CLY (10)
USA	Winnebago	PI 213772*	3 (10)	17 (11)	CLY (10)
USA	Winnebago	PI 213774*	3 (10)	8 (11)	CLY (11)
USA	Zia Pueblo	PI 218139*	4 (10)	15 (11)	CLY (10)
U.S. Virgin Islands	St. Croix	IVC 2*	9 (09)	19 (10)	FL (09)
Venezuela	Araguito	VEN 568	1 (09) + 8 (10)	23 (11)	Pioneer (09) + FL (10)
Venezuela	Araguito	VEN 628	12 (10)	13 (11)	FL (10)
Venezuela	Araguito	VEN 678	1 (06)	6 (07)	Pioneer (06)
Venezuela	Araguito	VEN 760	3 (10)	12 (11)	FL (10)
Venezuela	Cacao	VEN 630	3 (06)	9 (07)	Pioneer (06)
Venezuela	Canilla	VEN 693	4 (07)	10 (08)	Pioneer (07)
Venezuela	Cariaco	VEN 408	13 (09)	9 (10)	FL (09)
Venezuela	Cariaco	VEN 631	5 (10)	9 (11)	FL (10)
Venezuela	Cariaco	VEN 639	9 (05)	6 (08)	Syngenta (05)
Venezuela	Chandelle	VEN 409	9 (07)	12 (08)	Pioneer (07)

Supplemental Table 2.2 Continued

Country	Race	Accession [†]	Plant Number and (Year) F ₁	Plant Number and (Year) BC ₁	Location and (Year) of F ₁ Production
Venezuela	Chandelle	VEN 460	15 (09)	20 (10)	FL (09)
Venezuela	Chirimito	VEN 703*	8 (07)	10 (08)	Pioneer (07)
Venezuela	Comun	VEN 448	12 (09)	11 (10)	FL (09)
Venezuela	Comun	VEN 881	13 (09)	7 + 5 (10)	FL (09)
Venezuela	Costeno	VEN 775	8 (05)	8 (08)	Syngenta (05)
Venezuela	Cuba Yellow Flint	VEN 331	4 (07)	12 (08)	Syngenta (07)
Venezuela	Cuba Yellow Flint	VEN 650	6 (10)	11 (11)	FL (10)
Venezuela	Guaribero	VEN 653	11 (07)	12 (08)	Pioneer (07)
Venezuela	Guaribero	VEN 733	14 (09)	13 (10)	FL (09)
Venezuela	Huevito	VEN 396	4 (07)	5 (08)	Pioneer (07)
Venezuela	Huevito	VEN 445	14 (09)	21 (10)	FL (09)
Venezuela	Negrito	VEN 426	12 (09)	10 (10)	FL (09)
Venezuela	Negrito	VEN 673	15 (09)	19 (10)	FL (09)
Venezuela	Negrito	VEN 870	12 (05)	10 (08)	Syngenta (05)
Venezuela	Pira	VEN 457	12 (09)	11 (10)	FL (09)
Venezuela	Pollo	VEN 310	1 (09) + 5 (10)	12 (11)	CLY (09) + FL (10)
Venezuela	Puya	VEN 946	7 (08)	12 (09)	Pioneer (08)
Venezuela	Puya Grande	VEN 345	10 (09)	21 (10)	FL (09)
Venezuela	Puya Grande	VEN 651	5 (08)	12 (09)	Pioneer (08)
Venezuela	Tuson	VEN 405	4 (07)	9 (08)	Syngenta (07)
Venezuela	Tuxpeno	VEN 598	6 (09)	14 (10)	FL (09)
Venezuela	Tuxpeno	VEN 692	7 (07)	11 (08)	Syngenta (07)
Venezuela	Tuxpeno	VEN 891	10 (09)	16 (10)	FL (09)

Notes:

†Most accessions were collected during the 1940s and 1950s; additional Mexican accessions were collected during the 1960s and 1970s by E. Hernández X. and R. Ortega P. Data on altitude, Latitude and Longitude were obtained from Vigouroux et al (2008), from the Original Strains of Corn Vol I and Vol II (NSF-NRC, 1954) and from the studies of the accessions published by the National Academy of Sciences and Harvard (Brieger et al, 1958; Brown, 1960; Grant et al, 1963; Grobman et al, 1961; Hatheway, 1957; Ramírez et al, 1960; Roberts et al, 1957; Timothy et al, 1961; Timothy et al, 1963; Wellhausen et al, 1952; Wellhausen et al, 1957). Most eastern South American accessions -the collections with Roman numerals- (Brazil, Paraguay, Uruguay, Guianas, some Argentine and a few Bolivian accessions) are actually bulk samples of several accessions, and data shown are means of the accessions (Paterniani and Goodman, 1977). Also occasionally seed from a given accession was sampled twice by the Goodman group at different times. These two samples were labeled sample A and B, these are not different accessions. Accessions labeled with an (USDA) indicate accessions from Brazil which were once held in storage at Glenn Dale, MD, but not from the NRC. They were increased by MMG and are now deposited with the NCRPIS at Ames, Iowa. It is also noted that accessions noted with an asterisk (*) are those currently available from NCRPIS, unfortunately these number only 170 of the accessions used in this study.

Supplemental Table 2.3 List of accessions used, country of origin, race name, accession name, source, and latitude, longitude, and altitude at point of collection with least square means and standard errors of GLS, NLB, SLB, and DTA.

Disease was scored on a 1 to 9 scale with 9 being resistant. DTA was scored as number of days after planting till 50% of plants in row showed pollen shed, higher numbers indicated later flowering.

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	GLS	GLS SE	NLB	NLB SE	SLB	SLB SE	DTA	DTA SE
Argentina	Amargo	ARZM 03014	NCRPIS	-32.2	-58.1	20	4.04	0.58	4.52	0.55	3.86	0.36	65.0	2.09
Argentina	Bola Blanca	ARG 532 (USDA)	NCRPIS	-23.2	-65.4	2287	4.00	0.49	4.93	0.47	4.76	0.30	63.9	2.05
Argentina	Calchaqui Small White	ARG 2420 (USDA)	NCRPIS	-32.7	-64.7	895	4.27	0.50	4.29	0.47	4.21	0.30	63.7	2.05
Argentina	Camelia	ARZM 03025	NCRPIS	-30.5	-58.3	68	4.48	0.49	4.95	0.47	4.74	0.30	65.7	2.05
Argentina	Canario de Formosa	ARZM 06016	NCRPIS	-1.7	-78.7	3050	3.90	0.49	5.71	0.47	4.97	0.30	66.2	2.05
Argentina	Canario de Ocho	ARG VI	CIMMYT	-32	-58	305	4.10	0.49	3.25	0.47	4.49	0.30	64.8	2.05
Argentina	Capia Blanco	ARG 499 (USDA)	NCRPIS	-23.2	-65.4	2287	4.92	0.49	4.11	0.47	4.73	0.30	65.1	2.05
Argentina	Capia Rosado	ARG 460 (USDA)	NCRPIS	-23.2	-65.4	2287	4.56	0.49	4.88	0.47	4.09	0.30	65.6	2.05
Argentina	Cateto Sulino	ARG I	CIMMYT	-32	-58	305	4.08	0.49	3.91	0.47	4.08	0.30	64.7	2.05
Argentina	Chulpi	ARG 484 (USDA)	NCRPIS	-23.2	-65.4	2287	4.04	0.49	4.19	0.47	4.08	0.30	64.8	2.05
Argentina	Cravo	ARZM 05071	NCRPIS	-33	-71.6	80	4.58	0.49	6.56	0.47	4.91	0.30	66.4	2.05
Argentina	Cristal Sulino	ARG III	CIMMYT	-29	-62	1554	4.07	0.49	4.24	0.47	4.77	0.30	65.0	2.05
Argentina	Cristalino Amarillo	AR 21004	NCRPIS	-38.1	-62.2	295	3.11	0.49	2.01	0.47	3.19	0.30	61.7	2.06
Argentina	Cristalino Amarillo	ARZM 19070	NCRPIS	-39.5	-69.3	381	3.20	0.49	2.36	0.47	3.44	0.30	63.6	2.05
Argentina	Cristalino Blanco	ARZM 19074	NCRPIS	-39.5	-69.3	381	3.00	0.49	2.46	0.47	3.01	0.30	63.6	2.05
Argentina	Cristalino Colorado	ARZM 16021	NCRPIS	-32.6	-69.3	1886	4.18	0.49	5.19	0.47	4.62	0.30	64.5	2.05
Argentina	Cuarentino	ARG 486 (USDA)*	NCRPIS	-34.9	-58	276	4.37	0.49	3.94	0.47	4.18	0.30	64.7	2.05
Argentina	Culli	ARG 471 (USDA)	NCRPIS	-23.2	-65.4	2287	3.54	0.49	4.50	0.47	4.22	0.30	63.5	2.05
Argentina	Dentado Amarillo	ARZM 16062	NCRPIS	-35	-67.7	474	3.83	0.49	3.94	0.47	3.91	0.30	65.7	2.05
Argentina	Dentado Blanco	ARZM 03056	NCRPIS	-39.2	-59.5	58	4.32	0.49	5.34	0.47	4.62	0.30	66.4	2.05
Argentina	Dentado Blanco Rugoso	ARZM 01149	NCRPIS	-38.2	-62.4	285	3.93	0.49	4.56	0.47	4.43	0.30	66.7	2.05

Supplemental Table 2.3 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	GLS	GLS SE	NLB	NLB SE	SLB	SLB SE	DTA	DTA SE
Argentina	Dulce	ARZM 20005B	NCRPIS	-40.8	-63	5	3.27	0.58	3.63	0.55	3.50	0.36	63.6	2.09
Argentina	Marron	ARG 468 (USDA)	NCRPIS	-23.8	-65.5	2359	4.03	0.58	3.77	0.55	4.35	0.36	64.4	2.09
Argentina	Oke	ARG 539 (USDA)	NCRPIS	-23.2	-65.4	2287	4.61	0.49	4.56	0.47	4.51	0.30	65.2	2.05
Argentina	Pisincho	ARG 481 (USDA)*	NCRPIS	-23.2	-65.4	2287	3.56	0.49	2.95	0.47	3.54	0.30	63.9	2.05
Argentina	Pisingallo	ARZM 13095	NCRPIS	-30.3	-66.3	457	3.78	0.49	4.05	0.47	4.06	0.30	64.9	2.05
Barbados	Tuson	BARBGP 2*	NCRPIS	13.1	-59.6	60	5.19	0.49	5.68	0.47	5.65	0.31	67.7	2.05
Bolivia	Altiplano	BOV 903	NRC	-21.8	-64.1	1976	5.15	0.49	4.72	0.47	4.35	0.30	65.0	2.05
Bolivia	Argentino	BOV 920	ICA	-21.8	-64.1	1829	4.87	0.49	6.29	0.47	4.95	0.30	66.2	2.05
Bolivia	Aysuma	BOV 331	ICA	-19	-65.3	2127	5.02	0.49	6.13	0.47	4.70	0.30	65.2	2.05
Bolivia	Camba	BOV 1131	ICA	-16.5	-68.2	1570	5.53	0.49	6.60	0.47	5.25	0.31	69.4	2.05
Bolivia	Cateto	BOV 1083	NRC	-11.3	-67.7	240	4.85	0.49	5.36	0.47	4.86	0.30	67.2	2.05
Bolivia	Cateto	BOV 317	NCRPIS	-17.8	-64.8	2843	4.80	0.49	5.55	0.47	4.32	0.30	66.7	2.05
Bolivia	Chake-Sara	BOV 520	NCRPIS	-17.5	-65.7	2395	3.85	0.49	3.42	0.47	3.71	0.30	65.0	2.05
Bolivia	Checchi	BOV 320	ICA	-17.4	-66.2	2080	4.23	0.49	5.61	0.47	4.48	0.30	66.5	2.05
Bolivia	Checchi	BOV Comp.	NCRPIS	-18.1	-65.8	2542	4.04	0.49	4.11	0.47	4.30	0.30	64.5	2.05
Bolivia	Cholito	BOV 309	NCRPIS	-18.1	-64.4	1581	4.81	0.49	5.92	0.47	4.90	0.30	67.4	2.05
Bolivia	Chuspillu	BOV 883	NCRPIS	-17.5	-65.7	2507	4.78	0.49	5.64	0.47	5.58	0.30	66.3	2.05
Bolivia	Coroico	BOV 1064	NCRPIS	-14	-65	92	5.35	0.49	5.24	0.47	4.70	0.30	66.9	2.05
Bolivia	Coroico Amarillo	BOV 405	NRC	-14.9	-65	160	5.28	0.49	5.65	0.47	5.22	0.31	67.3	2.05
Bolivia	Coroico Blanco	BOV 406	NCRPIS	-14.7	-65	130	5.29	0.49	5.94	0.47	4.78	0.30	67.4	2.05
Bolivia	Cubano Dentado	BOV 440	NRC	-17.8	-63.2	560	4.63	0.49	5.77	0.47	4.99	0.30	66.2	2.05
Bolivia	Cubano Dentado	BOV 585	NRC	-16.4	-61	330	5.38	0.49	5.91	0.47	5.11	0.30	66.6	2.05
Bolivia	Enano	BOV 1032	NCRPIS	-11	-68	180	4.61	0.49	5.12	0.47	5.19	0.30	67.1	2.05
Bolivia	Huilcaparu	BOV 685	ICA	-17.4	-65.9	2721	5.28	0.49	6.32	0.47	4.81	0.31	68.5	2.05
Bolivia	Huilcaparu Moteado	BOV Comp.	NCRPIS	-16.9	-67.1	2760	4.77	0.49	6.19	0.47	5.59	0.30	67.1	2.05
Bolivia	Karapampa	BOV 978	ICA	-21.8	-64.1	1976	4.54	0.49	5.78	0.47	4.46	0.30	65.4	2.05

Supplemental Table 2.3 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	GLS	GLS SE	NLB	NLB SE	SLB	SLB SE	DTA	DTA SE
Bolivia	Kcello	BOV 325	ICA	-17.4	-66.2	1400	5.11	0.49	6.11	0.47	4.54	0.30	65.4	2.05
Bolivia	Kcello	BOV 848	ICA	-19.6	-65.8	1801	4.74	0.49	6.46	0.47	4.75	0.30	66.3	2.05
Bolivia	Kcello	BOV 948	NRC	-19.6	-65.8	3256	3.72	0.49	4.32	0.47	4.07	0.30	64.9	2.05
Bolivia	Morado	BOV 567	ICA	-16.5	-67.5	2270	5.78	0.49	5.86	0.47	4.28	0.31	67.6	2.05
Bolivia	Ninuelo	BOV 1088	ICA	-17.8	-63.2	2201	5.57	0.49	6.25	0.47	4.97	0.31	67.0	2.05
Bolivia	Paru	BOV Comp.	NCRPIS	-15.8	-68.6	2737	4.56	0.49	5.28	0.55	4.03	0.30	67.1	2.07
Bolivia	Patillo Grande	BOV 649	ICA	-17.5	-65.7	2515	4.76	0.49	5.24	0.47	4.73	0.30	65.5	2.05
Bolivia	Perola	BOV 711	NRC	-21.3	-63.5	520	4.85	0.49	6.39	0.47	4.84	0.30	66.9	2.05
Bolivia	Pisankalla	BOV 344	ICA	-21.5	-64.8	1738	4.15	0.49	4.20	0.47	4.66	0.30	63.7	2.05
Bolivia	Pisankalla	BOV 864	ICA	-17.5	-65.7	2175	3.20	0.49	3.04	0.47	4.42	0.30	63.9	2.05
Bolivia	Pisankalla	BOV 965	ICA	-21.8	-64.1	1948	4.80	0.49	4.28	0.47	4.71	0.30	64.2	2.05
Bolivia	Pojoso Chico	BOV 800	NCRPIS	-17.7	-62.8	500	4.48	0.49	5.16	0.47	4.23	0.30	65.0	2.05
Bolivia	Pororo	BOV 583	ICA	-15.7	-67.3	330	5.60	0.49	6.07	0.47	4.95	0.31	67.5	2.05
Bolivia	Pororo	BOV 806	NRC	-18.3	-59.8	1400	4.89	0.49	5.38	0.55	5.11	0.31	68.4	2.07
Bolivia	Uchuquilla	BOV 318	NCRPIS	-17.2	-66.1	1922	5.13	0.49	5.71	0.47	4.75	0.30	66.3	2.05
Bolivia	Uchuquilla	BOV 954	ICA	-21.8	-64.1	1948	4.60	0.49	6.05	0.47	4.41	0.31	67.0	2.05
Bolivia	Yungueno	BOV 362	ICA	-21.8	-64.1	1052	4.45	0.49	6.40	0.47	4.36	0.30	67.0	2.05
Bolivia	Yungueno	BOV 716	ICA	-16.5	-68.2	1400	5.50	0.49	6.63	0.47	5.30	0.31	68.0	2.05
Brazil	Avati Pichinga	BR 2760 (USDA)	NCRPIS	-25	-56	366	4.46	0.49	5.26	0.47	4.19	0.31	68.1	2.05
Brazil	Avati Pichinga	BR 2776 (USDA)	NCRPIS	-25	-56	366	5.24	0.49	5.56	0.47	5.31	0.31	67.7	2.05
Brazil	Avati Pichinga Ihu	BR 2830 (USDA)	NCRPIS	-25	-56	366	4.27	0.49	5.13	0.47	3.50	0.30	66.8	2.05
Brazil	Caingang	PR III	CIMMYT	-23	-51	610	5.35	0.49	6.02	0.47	4.81	0.30	66.7	2.05
Brazil	Caingang	SP XIII	CIMMYT	-22	-51	407	5.21	0.49	5.15	0.47	5.18	0.30	65.7	2.05
Brazil	Caraja	1692 (USDA)	NCRPIS	-27.2	-49.6	433	5.48	0.49	5.92	0.47	5.00	0.31	68.3	2.05
Brazil	Cateto	BA II	CIMMYT	-12.5	-39	610	5.75	0.49	6.20	0.47	5.71	0.30	67.6	2.05
Brazil	Cateto	CE I	CIMMYT	-3.8	-38.8	177	5.25	0.49	6.08	0.47	4.65	0.31	67.3	2.05

Supplemental Table 2.3 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	GLS	GLS SE	NLB	NLB SE	SLB	SLB SE	DTA	DTA SE
Brazil	Cateto Assis Brasil	RGS XIV	NCRPIS	-29	-53	274	5.23	0.49	6.29	0.47	5.44	0.30	66.4	2.06
Brazil	Cateto Grande	MT IV	CIMMYT	-20	-56	366	5.27	0.49	5.91	0.47	5.01	0.31	67.8	2.05
Brazil	Cateto Nortista Precoce	SUR I	CIMMYT	5.8	-55.2	61	4.60	0.49	5.84	0.47	5.27	0.31	67.3	2.05
Brazil	Cravo Paulista	SP I	CIMMYT	-22	-48	579	5.33	0.49	6.78	0.47	4.38	0.30	66.4	2.05
Brazil	Cravo Riograndense	RGS VII	CIMMYT	-30	-53	366	4.95	0.49	5.56	0.47	4.97	0.31	67.1	2.05
Brazil	Cristal	SP X	CIMMYT	-22	-48	803	6.07	0.49	6.06	0.47	5.22	0.31	68.1	2.05
Brazil	Cristal	SP XI	CIMMYT	-22	-48	803	6.06	0.49	6.65	0.47	4.96	0.31	68.3	2.06
Brazil	Cristal Inter. Perola	1115 (USDA)	NCRPIS	-28.4	-54.3	240	4.30	0.49	6.22	0.47	5.65	0.30	67.4	2.05
Brazil	Cristal Paraguay Paulis	2334 (USDA)	NCRPIS	-23.3	-46.1	582	5.13	0.49	5.92	0.47	4.82	0.31	67.9	2.05
Brazil	Dente Branco Paulista	SP V	CIMMYT	-22	-48	579	5.14	0.49	5.44	0.47	5.31	0.31	67.4	2.05
Brazil	Dente Branco R. G.	SC II	CIMMYT	-27	-52	892	4.81	0.49	5.13	0.47	4.91	0.30	66.0	2.05
Brazil	Dente Paulista	SP IV	CIMMYT	-22	-48	518	5.56	0.49	6.30	0.47	4.84	0.31	67.4	2.05
Brazil	Dente R. G. Liso	RGS VI	CIMMYT	-29	-52	366	5.14	0.49	5.98	0.47	4.66	0.31	67.9	2.05
Brazil	Dente R. G. Liso	SC I	CIMMYT	-27	-52	892	4.61	0.49	6.84	0.47	5.14	0.31	67.9	2.05
Brazil	Dente R. G. Rugoso	RGS II	CIMMYT	-30	-53	366	4.98	0.49	5.05	0.47	4.58	0.30	66.9	2.05
Brazil	Dourados Saboro	BR 50 (USDA)	NCRPIS	-22.3	-54.8	340	4.99	0.49	6.03	0.47	5.52	0.31	67.9	2.05
Brazil	Entrelacado	MT VI	CIMMYT	-18	-55	305	5.19	0.49	5.71	0.47	4.89	0.31	68.7	2.05
Brazil	Hickory King	RGS IX*	CIMMYT	-28.5	-51	366	4.98	0.49	5.29	0.47	4.96	0.30	66.1	2.05
Brazil	Moroti	MT I	CIMMYT	-20	-56	366	5.10	0.49	6.01	0.47	4.50	0.31	66.6	2.05
Brazil	Moroti	PE I	NCRPIS	-8	-36	344	5.41	0.49	6.80	0.47	5.14	0.31	68.0	2.05
Brazil	Moroti Precoce	BOL I	CIMMYT	-20	-58	457	3.69	0.49	4.12	0.47	5.21	0.30	64.9	2.05
Brazil	Semi Dente Paulista	SP IX	CIMMYT	-22	-48	305	5.02	0.49	6.19	0.47	4.89	0.30	66.9	2.05
Brazil	Semi Dente R. G.	RGS XV	CIMMYT	-30	-53	366	4.76	0.49	6.03	0.47	5.19	0.31	67.6	2.05
Brazil	Tuson	BAI III	CIMMYT	-12.5	-39	200	5.19	0.49	5.74	0.47	5.21	0.30	66.5	2.05
Brazil	Tuson	BAI IIIB	NCRPIS	-12.5	-39	200	5.04	0.57	5.18	0.55	5.80	0.36	66.6	2.09
Chile	Araucano	CHI 320*	NCGRP	-38.1	-72.3	417	2.67	0.50	2.03	0.47	3.32	0.30	62.1	2.05

Supplemental Table 2.3 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	GLS	GLS SE	NLB	NLB SE	SLB	SLB SE	DTA	DTA SE
Chile	Capia Chico Chileno	CHI 382*	NRC	-23.7	-70.4	40	3.64	0.58	3.11	0.56	3.46	0.36	62.4	2.09
Chile	Cristalino Chico	CHI 324	NCGRP	-38.1	-71.9	66	2.97	0.50	1.68	0.48	3.83	0.30	59.7	2.05
Chile	Cristalino Chileno	CHI 156	NCRPIS	-38.1	-71.9	66	3.21	0.49	4.27	0.47	4.19	0.30	64.6	2.05
Chile	Cristalino Grande	CHI 323*	NCRPIS	-37.5	-72.4	139	3.71	0.58	3.57	0.56	3.50	0.36	62.2	2.09
Chile	Curagua	CHI 301*	NRC	-33	-70.7	732	3.25	0.49	2.71	0.47	3.30	0.30	62.7	2.05
Chile	Curagua	CHI 314*	NCGRP	-33.2	-70.7	457	3.72	0.49	3.30	0.47	3.22	0.30	64.5	2.05
Chile	Curagua Grande	CHI 303	NRC	-33.2	-70.7	457	3.85	0.49	2.66	0.47	3.24	0.30	64.3	2.05
Chile	Dentado Comercial	CHI 326*	NCGRP	-38.1	-71.9	66	3.40	0.49	3.74	0.47	3.77	0.30	65.9	2.05
Chile	Dulce Evergreen	CHI 332*	NCGRP	-38.1	-71.9	66	3.45	0.49	3.14	0.47	3.90	0.30	64.5	2.05
Chile	Dulce Golden Bantam	CHI 335*	NCGRP	-38.1	-71.9	66	3.35	0.49	2.47	0.47	4.30	0.30	63.0	2.05
Chile	Harinoso Tarapaqueno	CHI 421	NRC	-19.9	-69.5	1550	5.19	0.49	4.87	0.47	4.29	0.31	67.9	2.05
Colombia	Amagaceno	ANT 343*	NCRPIS	6.2	-75.8	1800	5.14	0.49	6.11	0.47	4.97	0.31	68.6	2.05
Colombia	Amagaceno	HUI 317*	NCRPIS	2.5	-74.8	1554	5.26	0.49	6.96	0.47	5.36	0.31	68.5	2.05
Colombia	Andaqui	CAQ 307*	NCRPIS	1.2	-75.9	490	5.27	0.49	5.65	0.47	6.24	0.31	67.7	2.05
Colombia	Andaqui	CAQ 333*	NRC	1.8	-75.6	500	5.30	0.49	5.58	0.47	5.14	0.31	67.5	2.06
Colombia	Cabuya	SAN 316*	NRC	7.4	-72.7	2100	4.97	0.49	6.66	0.47	5.07	0.31	67.4	2.05
Colombia	Cacao	SAS 327*	ICA	5.9	-73.7	1600	5.19	0.49	6.34	0.47	5.50	0.31	68.3	2.06
Colombia	Cacao	SAS 335*	NCGRP	6.4	-73.3	1300	4.79	0.49	6.48	0.47	4.67	0.31	68.3	2.06
Colombia	Capio	ANT 348*	ICA	5.9	-75.4	1966	4.95	0.49	7.08	0.47	5.23	0.30	68.5	2.06
Colombia	Capio	ANT 354	ICA	5.7	-75.3	2600	5.21	0.49	6.38	0.47	5.18	0.31	69.3	2.05
Colombia	Capio	NAR 315	ICA	1.2	-77.3	2360	5.71	0.49	6.95	0.47	5.30	0.31	69.7	2.06
Colombia	Caqueteno	CAQ 305*	ICA	1.5	-75.4	300	5.48	0.49	6.17	0.47	5.40	0.31	67.3	2.05
Colombia	Cariaco	COR 338*	NCGRP	8.8	-75.9	200	5.29	0.49	5.71	0.47	5.63	0.31	67.6	2.05
Colombia	Chococeno	CHO 340	NCRPIS	7.5	-77.1	30	5.94	0.49	5.85	0.47	5.64	0.31	69.0	2.05
Colombia	Clavo	NAR 329*	ICA	1.2	-77.3	2360	4.85	0.49	6.22	0.47	4.77	0.31	68.4	2.05
Colombia	Comun	CAU 454*	NCRPIS	7.5	-74.8	600	5.10	0.49	6.48	0.47	5.36	0.31	68.0	2.05

Supplemental Table 2.3 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	GLS	GLS SE	NLB	NLB SE	SLB	SLB SE	DTA	DTA SE
Colombia	Comun	NAR 330*	NCRPIS	1.5	-78.5	118	5.00	0.49	5.87	0.47	5.87	0.30	66.2	2.05
Colombia	Comun	VAL 374*	NCRPIS	3.6	-76.5	980	5.44	0.49	6.55	0.47	5.08	0.30	66.8	2.05
Colombia	Costeno	ANT 394*	NCRPIS	2.2	-76.9	922	5.69	0.49	6.47	0.47	5.49	0.30	67.4	2.05
Colombia	Costeno	ATL 314*	NCRPIS	10.9	-74.8	15	4.75	0.49	5.03	0.47	5.79	0.30	65.9	2.05
Colombia	Costeno	ATL 328*	NRC	10.4	-74.9	7	5.46	0.49	6.06	0.47	5.33	0.30	65.2	2.06
Colombia	Costeno	COR 320*	NCGRP	8.3	-75.2	100	5.43	0.49	6.06	0.47	5.12	0.30	67.3	2.05
Colombia	Guirua	MAG 469*	NCGRP	10.5	-73.3	1870	5.79	0.49	6.40	0.47	5.08	0.31	68.1	2.05
Colombia	Harin. Dent.	NAR 326*	NCRPIS	1.4	-77.6	1400	4.92	0.49	6.23	0.47	5.39	0.31	68.5	2.05
Colombia	Imbricado	NAR 389	ICA	0.8	-77.6	2000	5.05	0.49	6.68	0.47	4.89	0.31	68.5	2.06
Colombia	Montana	NAR 625*	NCRPIS	1.2	-77.3	2542	5.00	0.49	6.76	0.47	5.29	0.31	67.9	2.06
Colombia	Pira	CUN 327*	NRC	4.3	-74.4	1000	4.88	0.49	6.39	0.47	5.13	0.31	67.4	2.05
Colombia	Pira	CUN 480*	NRC	4.8	-74.7	1000	5.30	0.50	6.55	0.47	5.30	0.31	69.0	2.05
Colombia	Pira	TOL 405	NRC	4.2	-74.9	450	5.70	0.49	6.81	0.47	5.20	0.31	69.0	2.05
Colombia	Pollo	CUN 424	NCRPIS	4.8	-73.7	2000	4.48	0.49	5.70	0.47	4.88	0.30	66.3	2.05
Colombia	Pollo	CUN 443*	NRC	4.2	-74.4	1800	4.91	0.49	5.38	0.47	4.72	0.30	64.6	2.05
Colombia	Puya	MAG 355*	NRC	9.4	-75.7	27	5.25	0.49	5.75	0.47	5.70	0.30	67.2	2.05
Colombia	Puya Grande	SAN 347*	NCGRP	8.3	-73.3	1200	5.95	0.49	6.99	0.47	5.33	0.31	67.7	2.05
Colombia	Sabanero	ANT 423*	NCRPIS	7	-75.7	1480	4.66	0.49	5.88	0.47	5.39	0.30	66.5	2.05
Colombia	Sabanero	CUN 342*	NCRPIS	8.5	-75.5	250	4.81	0.49	6.22	0.47	5.43	0.31	68.1	2.05
Colombia	Sabanero	CUN 367	NCRPIS	4.3	-74	2110	5.51	0.49	6.45	0.47	5.07	0.30	67.9	2.05
Colombia	Sabanero	SAN 329	NRC	7.3	-72.5	2626	5.21	0.49	6.54	0.47	4.87	0.30	67.0	2.05
Colombia	Yucatan	TOL 389*	ICA	5	-74.9	450	5.36	0.49	6.38	0.47	4.57	0.31	67.2	2.05
Colombia	Yucatan	TOL 399*	NCGRP	4.6	-74.9	500	5.99	0.49	6.86	0.47	5.43	0.31	68.2	2.06
Costa Rica	Huesillo	CRI 370*	NCRPIS	9.9	-83.9	1500	5.38	0.57	5.64	0.55	5.61	0.36	66.8	2.09
Cuba	Argentino	CUB 113*	NCRPIS	20.3	-76.9	25	4.61	0.49	5.77	0.47	5.52	0.30	66.1	2.05
Cuba	Chandelle	CUB 54*	CIMMYT	20.9	-76.7	305	4.64	0.49	5.50	0.47	4.93	0.31	67.4	2.05

Supplemental Table 2.3 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	GLS	GLS SE	NLB	NLB SE	SLB	SLB SE	DTA	DTA SE
Cuba	Chandelle	CUB 68	NCRPIS	20.7	-76.1	369	5.04	0.49	5.52	0.47	5.14	0.30	66.0	2.05
Cuba	Cuban Flint	CUB 63*	CIMMYT	20.7	-75.7	15	5.27	0.57	5.67	0.55	4.88	0.40	66.1	2.09
Cuba	Maiz Criollo	CUB 136*	NCRPIS	22.9	-82.3	84	4.83	0.49	6.45	0.47	5.70	0.31	67.2	2.05
Cuba	Tuson	CUB 67*	CIMMYT	20.9	-76.5	305	5.23	0.49	7.02	0.47	5.48	0.31	68.4	2.05
Ecuador	Blanco Blandito	ECU 523	NRC	0.4	-78.4	2122	5.66	0.49	6.65	0.47	4.98	0.31	67.9	2.05
Ecuador	Blanco Harinoso Dentado	ECU 640	ICA	-4	-79.2	1921	5.45	0.49	6.29	0.47	5.35	0.31	68.2	2.05
Ecuador	Candela	ECU 344*	ICA	-0.7	-80.1	55	4.14	0.49	5.75	0.47	4.71	0.31	68.5	2.05
Ecuador	Candela	ECU 531	ICA	-1.1	-80.5	27	4.73	0.49	6.23	0.47	4.52	0.30	67.3	2.05
Ecuador	Candela	ECU 699	NCRPIS	-1.1	-80.5	50	4.64	0.49	5.20	0.47	4.70	0.31	67.6	2.05
Ecuador	Canguil	ECU 500	NRC	0.2	-78.4	2213	4.60	0.49	5.02	0.47	3.93	0.30	65.8	2.05
Ecuador	Canguil Gueso	ECU 443	NCRPIS	0	-78.5	2838	5.00	0.49	5.26	0.47	4.73	0.30	66.1	2.05
Ecuador	Canguil Gueso	ECU 447	ICA	0.1	-78.2	2579	4.35	0.49	5.17	0.47	4.87	0.30	65.3	2.05
Ecuador	Chillo	ECU 411	ICA	-0.3	-78.4	2510	5.90	0.49	6.11	0.47	5.27	0.30	68.1	2.05
Ecuador	Chillo	ECU 458	NRC	-2.9	-78.7	2195	5.62	0.49	6.72	0.47	4.66	0.31	68.7	2.05
Ecuador	Chillo	ECU 480B	NCRPIS	0	-78	2241	5.31	0.49	6.68	0.47	4.86	0.31	68.0	2.05
Ecuador	Cholito	ECU 718	ICA	-4.1	-79	1296	5.77	0.49	6.52	0.47	4.85	0.31	68.2	2.05
Ecuador	Chulpi Chico	ECU 424	NRC	0.1	-78.2	2600	4.75	0.49	6.06	0.47	4.90	0.31	67.3	2.05
Ecuador	Clavito	ECU 884	ICA	-1.3	-78.5	1646	4.97	0.49	6.20	0.47	5.01	0.30	66.9	2.05
Ecuador	Conico Dentado	ECU 427	ICA	0.1	-78.4	2058	5.24	0.49	5.90	0.47	4.91	0.31	69.3	2.05
Ecuador	Cubano Amarillo Duro	ECU 326	ICA	-1.1	-80.5	41	4.98	0.49	6.23	0.47	5.29	0.31	67.1	2.05
Ecuador	Cubano Amarillo Duro	ECU 327	NCRPIS	-2.2	-80.1	46	5.06	0.49	6.02	0.47	4.84	0.31	68.5	2.05
Ecuador	Cubano Amarillo Duro	ECU 698	ICA	-1.1	-80.5	50	5.25	0.49	6.08	0.47	5.18	0.30	67.1	2.05
Ecuador	Cubano Amarillo Duro	ECU 957	ICA	-1	-79.4	183	5.22	0.49	5.86	0.47	5.49	0.31	67.8	2.05
Ecuador	Cubano Cateto	ECU 877	ICA	-0.2	-79.3	229	5.58	0.49	6.86	0.47	5.25	0.31	68.3	2.05
Ecuador	Cubano Tuson	ECU 542	ICA	-1.1	-80.5	30	5.37	0.49	5.85	0.47	5.71	0.31	67.7	2.06
Ecuador	Cubano Tuson	ECU 660	ICA	-1.1	-80.5	30	5.56	0.49	5.79	0.47	5.46	0.31	67.5	2.05

Supplemental Table 2.3 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	GLS	GLS SE	NLB	NLB SE	SLB	SLB SE	DTA	DTA SE
Ecuador	Cubano Tuson	ECU 764	ICA	-1.1	-80.5	18	4.68	0.49	6.66	0.47	5.43	0.30	66.3	2.05
Ecuador	Enano Gigante	ECU Comp.	NCRPIS	-1.1	-78	916	5.45	0.49	6.93	0.47	4.67	0.31	68.7	2.05
Ecuador	Gallina	ECU 329	ICA	-1.9	-80	5	5.16	0.49	5.75	0.47	5.13	0.31	67.3	2.05
Ecuador	Huandango	ECU 735	NRC	0.8	-78	2287	5.28	0.50	5.33	0.47	5.07	0.31	68.2	2.05
Ecuador	Mishca	ECU 321	NRC	-1.7	-78.7	2241	4.96	0.49	5.93	0.47	5.29	0.30	65.8	2.05
Ecuador	Morochon	ECU 454B	NCRPIS	0	-78	2195	5.46	0.49	5.96	0.47	5.05	0.30	66.7	2.05
Ecuador	Patillo	ECU 417	ICA	-0.3	-78.6	2287	4.56	0.49	6.36	0.47	5.03	0.30	65.9	2.05
Ecuador	Pojoso Chico Ecuatorian	ECU 522	NCRPIS	-1	-77.8	530	4.32	0.49	4.17	0.47	4.75	0.30	65.8	2.05
Ecuador	Racimo de Uva	ECU 517	NRC	-1.7	-78.7	2287	4.56	0.49	6.10	0.47	4.24	0.30	65.6	2.05
Ecuador	Tusilla	ECU 569	ICA	-4.1	-79	274	5.16	0.49	6.29	0.47	5.13	0.31	67.8	2.05
Ecuador	Tuxpeno	ECU 942	ICA	-1	-79.4	184	5.49	0.49	5.91	0.47	5.34	0.31	67.2	2.05
Ecuador	Uchima	ECU 681	ICA	-4	-79.2	2152	4.96	0.49	6.59	0.47	4.77	0.31	67.6	2.05
Ecuador	Yungueno	ECU 572	ICA	-4.1	-79	1296	4.67	0.49	6.17	0.47	4.70	0.31	68.0	2.05
Ecuador	Yunquillano forma Andaqui	ECU 710	NCRPIS	-4.1	-79	1296	5.42	0.49	5.24	0.47	6.12	0.31	67.1	2.05
Ecuador	Yunquillano forma Andaqui	ECU 853	ICA	-3.5	-78.6	732	4.64	0.49	5.79	0.47	4.92	0.31	67.3	2.05
Ecuador	Yunquillano forma Andaqui	ECU 855	ICA	-3.5	-78.6	1098	5.40	0.49	6.62	0.47	5.51	0.31	67.2	2.05
El Salvad	Amarillo Salvadoreno	Comp.	NCRPIS	13.8	-89.3	721	4.64	0.49	5.76	0.47	4.83	0.30	65.6	2.05
Guatemala	Comiteco	GUA 418	INIFAP	15.4	-91.7	1768	5.05	0.49	6.07	0.47	5.28	0.31	67.9	2.05
Guatemala	Comiteco	GUA 515	NCRPIS	15.7	-91.6	1751	5.10	0.49	5.82	0.47	5.53	0.31	68.1	2.05
Guatemala	Comiteco	GUA 546	NCRPIS	15.7	-91.6	1751	5.49	0.49	6.83	0.47	5.00	0.31	68.7	2.06
Guatemala	Dzit Bacal	GUA 131	CIMMYT	14.3	-89.7	737	4.83	0.49	6.60	0.47	4.18	0.30	66.5	2.05
Guatemala	Imbricado	GUA 493	INIFAP	14.8	-91.6	2317	5.23	0.49	5.92	0.47	5.30	0.30	66.7	2.05
Guatemala	Imbricado	GUA 922	INIFAP	15.6	-91.5	2256	4.79	0.49	6.09	0.47	5.24	0.30	66.9	2.05
Guatemala	N de Chimaltenango	GUA 369	INIFAP	14.6	-90.9	2073	5.57	0.49	6.60	0.47	5.48	0.31	68.4	2.05
Guatemala	N de Chimaltenango	GUA 590	INIFAP	14.7	-90.9	2165	5.24	0.49	6.86	0.47	5.36	0.31	68.4	2.05
Guatemala	N de T Caliente	GUA 159	CIMMYT	14.6	-91.4	1067	5.22	0.49	6.36	0.47	5.30	0.30	66.5	2.05

Supplemental Table 2.3 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	GLS	GLS SE	NLB	NLB SE	SLB	SLB SE	DTA	DTA SE
Guatemala	N de T Fria	GUA 522	INIFAP	15.3	-91.5	1921	4.56	0.49	5.39	0.47	4.66	0.30	66.6	2.05
Guatemala	Nal Tel ATB	GUA 111	CIMMYT	14.6	-90.1	915	5.06	0.49	5.06	0.47	5.27	0.30	64.0	2.05
Guatemala	Nal Tel ATB	GUA 220	CIMMYT	14.6	-89.6	793	3.98	0.49	5.41	0.47	4.94	0.30	64.3	2.05
Guatemala	Nal Tel ATB	GUA 281	CIMMYT	14.3	-90.1	1113	4.47	0.49	6.42	0.47	4.48	0.30	65.6	2.05
Guatemala	Nal Tel BTA	GUA 20	INIFAP	14.6	-91.9	2439	5.76	0.57	5.96	0.56	5.58	0.36	68.5	2.09
Guatemala	Nal Tel BTB	GUA 145*	CIMMYT	15	-90.3	1006	4.78	0.49	4.45	0.47	4.45	0.30	64.5	2.05
Guatemala	Nal Tel BTB	GUA 280	CIMMYT	14.4	-89.9	1021	4.69	0.49	4.80	0.47	4.42	0.30	64.0	2.05
Guatemala	Nal Tel BTB	GUA 765*	CIMMYT	14.4	-89.9	1021	4.28	0.49	5.37	0.47	4.66	0.30	64.5	2.05
Guatemala	Oloton	GUA 383	NCRPIS	14.6	-90.6	1551	5.82	0.49	6.97	0.47	5.48	0.30	67.1	2.05
Guatemala	Quicheno Early	GUA 162	CIMMYT	15.1	-91.1	1860	4.94	0.49	6.73	0.47	5.03	0.31	67.2	2.05
Guatemala	Quicheno Late	GUA 863	INIFAP	15.4	-90.8	1829	5.14	0.49	5.85	0.47	4.92	0.31	68.7	2.06
Guatemala	Quicheno Late	GUA 877	NCRPIS	15.7	-91.5	2365	5.15	0.49	6.30	0.47	5.03	0.31	68.7	2.05
Guatemala	Salpor	GUA 476	INIFAP	14.9	-91.5	2317	5.06	0.49	5.96	0.47	5.05	0.31	68.1	2.05
Guatemala	Salpor Tardio	GUA 485	INIFAP	15	-91.8	2393	5.46	0.49	6.98	0.47	4.93	0.31	67.9	2.05
Guatemala	San Marceno	GUA 506	INIFAP	15.1	-91.7	2134	4.40	0.49	5.21	0.47	5.35	0.31	67.9	2.05
Guatemala	San Marceno	GUA 724	NCRPIS	14.7	-91	2304	5.19	0.49	6.38	0.47	4.86	0.31	68.6	2.05
Guatemala	Serrano	GUA 940	INIFAP	15	-91.8	3049	4.59	0.49	4.44	0.47	5.39	0.30	65.1	2.05
Guatemala	Tepecintle	GUA 597	CIMMYT	14.6	-91.7	427	4.80	0.49	5.83	0.47	5.19	0.30	67.3	2.05
Guatemala	Tepecintle	GUA 65	CIMMYT	14.6	-90.8	152	5.30	0.49	5.86	0.47	5.23	0.31	67.6	2.05
Guatemala	Tepecintle	GUA 651	CIMMYT	14.5	-91.4	290	5.05	0.49	6.48	0.47	5.51	0.31	67.4	2.05
Guatemala	Tepecintle	GUA 79	CIMMYT	15.4	-89.7	122	5.44	0.49	6.50	0.47	5.44	0.31	67.4	2.05
Guatemala	Tuxpeno	GUA 456	CIMMYT	16.5	-90.2	183	5.52	0.49	5.52	0.47	4.94	0.31	68.5	2.05
Guyana	Cateto Nortista	GIN 1	CIMMYT	6.8	-58.2	4	5.37	0.49	6.54	0.47	5.94	0.31	68.0	2.05
Haiti	Chandelle	HTI 14	INIFAP	19.5	-72	20	5.38	0.49	6.43	0.47	4.91	0.31	68.4	2.05
Haiti	Haitian Yellow	HTI 1	INIFAP	18.4	-74.3	580	5.02	0.49	5.97	0.47	4.49	0.31	67.2	2.05
Martinica	Early Carribean	Martinica 9	INIFAP	14.9	-61.1	90	3.82	0.49	4.50	0.47	4.84	0.30	66.4	2.05

Supplemental Table 2.3 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	GLS	GLS SE	NLB	NLB SE	SLB	SLB SE	DTA	DTA SE
Martinica	Unassigned	Martinica 12	NCRPIS	14.9	-61.1	90	4.32	0.49	5.91	0.47	4.50	0.30	66.3	2.05
Mexico	Apachito	CHH 138*	CIMMYT	29.7	-108.3	2210	4.00	0.49	4.44	0.47	4.17	0.30	63.0	2.05
Mexico	Apachito	CHH 166*	INIFAP	28	-107.6	2400	3.60	0.50	3.09	0.47	4.03	0.30	61.9	2.05
Mexico	Apachito	CHH 180*	INIFAP	27.8	-107.6	2180	3.52	0.50	2.71	0.47	4.61	0.30	61.9	2.05
Mexico	Apachito	CHH 207	CIMMYT	26.8	-107.3	2510	4.11	0.49	3.54	0.47	4.59	0.30	63.1	2.05
Mexico	Apachito	CHH 182	NCRPIS	27.8	-107.6	2368	3.95	0.49	3.38	0.47	4.51	0.30	63.1	2.05
Mexico	Arrocillo Amarillo	PUE 91	INIFAP	19.8	-97.6	2317	4.91	0.49	4.70	0.47	4.65	0.30	65.9	2.05
Mexico	Arrocillo Amarillo	VER 311*	INIFAP	19.8	-97.3	2220	5.19	0.49	6.51	0.47	4.96	0.30	66.0	2.05
Mexico	Azul	ACC 70-2	DHT	28.8	-107.7	1970	3.40	0.49	3.08	0.47	4.58	0.30	63.7	2.05
Mexico	Azul	CHH 158*	INIFAP	28.6	-107.5	2040	4.08	0.49	4.45	0.47	3.72	0.30	63.8	2.05
Mexico	Azul	CHH 220	INIFAP	28.7	-107.9	1900	4.27	0.49	3.80	0.47	4.93	0.30	64.1	2.05
Mexico	Azul	CHH 218	NCRPIS	28.9	-107.8	1911	3.60	0.49	3.32	0.47	4.63	0.30	64.3	2.05
Mexico	Bofo	DGO 123	CIMMYT	25	-107	500	4.35	0.49	5.23	0.47	5.27	0.30	64.4	2.05
Mexico	Bofo	NAY 191*	CIMMYT	21.4	-104.1	1000	4.83	0.49	5.48	0.47	4.95	0.30	67.2	2.05
Mexico	Bofo	NAY 203	CIMMYT	21.1	-104.4	1850	5.29	0.49	6.84	0.47	4.79	0.30	66.9	2.05
Mexico	Bolita	OAX 44	INIFAP	17	-96.5	793	4.33	0.49	5.21	0.47	4.01	0.30	65.8	2.05
Mexico	Cacahuacintle	MEX 7	CIMMYT	19.3	-99.7	2652	4.53	0.49	3.82	0.47	4.26	0.30	65.4	2.05
Mexico	Cacahuacintle	PUE 552*	INIFAP	19	-97.4	2600	4.40	0.49	4.47	0.47	4.43	0.30	66.0	2.05
Mexico	Celaya	GTO 36*	INIFAP	20.2	-100.9	1799	5.33	0.49	6.54	0.47	4.97	0.31	67.7	2.05
Mexico	Celaya	GTO 69	INIFAP	20.5	-101	1812	4.28	0.49	6.39	0.47	5.64	0.30	67.8	2.05
Mexico	Celaya	GTO 88	INIFAP	20.2	-101	1768	5.10	0.49	6.15	0.47	4.67	0.31	67.5	2.05
Mexico	Chalqueno	HGO 7	NCRPIS	20.3	-98.9	2100	4.16	0.49	5.87	0.47	4.46	0.30	66.6	2.05
Mexico	Chapalote	SIN 2*	INIFAP	24.8	-107.4	61	4.21	0.49	4.51	0.47	4.69	0.30	65.0	2.05
Mexico	Chapalote	SIN 6	INIFAP	26.4	-108.6	115	4.97	0.49	4.47	0.47	4.99	0.30	64.9	2.05
Mexico	Chapalote	SIN 65	INIFAP	26	-107.4	750	4.18	0.49	4.18	0.47	4.44	0.30	65.8	2.05
Mexico	Conejo	GRO 129	INIFAP	17.7	-101.3	100	5.00	0.49	5.77	0.47	4.99	0.30	66.1	2.05

Supplemental Table 2.3 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	GLS	GLS SE	NLB	NLB SE	SLB	SLB SE	DTA	DTA SE
Mexico	Conejo	GRO 157	INIFAP	17.1	-100.5	30	4.56	0.49	5.10	0.47	5.02	0.30	65.8	2.05
Mexico	Conejo	GRO 17	INIFAP	17	-99.8	100	4.77	0.49	5.29	0.49	4.64	0.30	64.2	2.05
Mexico	Conico	PUE 116	NCRPIS	19.9	-97.7	2243	3.82	0.49	4.06	0.47	4.07	0.30	65.4	2.06
Mexico	Conico	PUE 48	NCRPIS	18.9	-97.9	1720	3.91	0.49	5.29	0.47	4.68	0.30	65.4	2.05
Mexico	Conico Norteno	ZAC 12	INIFAP	21.4	-102.9	1951	4.49	0.49	6.48	0.47	4.47	0.30	66.1	2.05
Mexico	Conico Norteno	ZAC 161*	NCRPIS	22.4	-102.9	1937	4.29	0.49	4.27	0.47	4.37	0.30	64.7	2.05
Mexico	Coscomatepec	VER 110*	INIFAP	19.2	-97	1320	5.53	0.49	6.28	0.47	4.97	0.31	68.2	2.05
Mexico	Coscomatepec	VER 110B*	NCRPIS	19.2	-97	1320	5.25	0.57	6.38	0.55	4.89	0.36	68.3	2.09
Mexico	Cristalino de Chihuahua	CHH 128*	INIFAP	29.2	-108.1	2095	3.60	0.49	3.54	0.47	3.97	0.30	63.6	2.05
Mexico	Cristalino de Chihuahua	CHH 154*	INIFAP	29.4	-107.8	2140	3.70	0.49	3.46	0.47	4.19	0.30	63.5	2.05
Mexico	Cristalino de Chihuahua	CHH 254	INIFAP	28.5	-107.4	1900	3.50	0.49	4.37	0.47	4.59	0.30	65.3	2.05
Mexico	Dulce de Jalisco	JAL304	INIFAP	22.1	-103.3	1700	3.92	0.49	4.94	0.47	3.21	0.30	65.6	2.05
Mexico	Dulce de Jalisco	JAL78	INIFAP	21.2	-102.9	1880	5.08	0.49	4.10	0.47	4.27	0.30	66.2	2.05
Mexico	Dulcillo del Noroeste	SIN 34	INIFAP	25.1	-107.5	500	3.96	0.49	5.22	0.47	5.52	0.30	66.5	2.05
Mexico	Dulcillo del Noroeste	SIN 79	INIFAP	26.4	-108.6	180	4.42	0.49	5.36	0.47	5.15	0.30	65.4	2.05
Mexico	Dulcillo del Noroeste	SON 57*	CIMMYT	26.4	-108.6	180	4.50	0.49	4.84	0.47	4.74	0.30	65.0	2.05
Mexico	Dzit Bacal	VER 96	INIFAP	18.9	-96.9	700	5.26	0.49	6.27	0.47	4.75	0.30	66.6	2.05
Mexico	Elotero de Sinaloa	NAY 32*	INIFAP	22.4	-105.5	100	4.56	0.49	5.77	0.47	5.49	0.30	65.5	2.05
Mexico	Elotero de Sinaloa	NAY 46	INIFAP	22	-105.2	100	4.24	0.49	3.96	0.47	4.81	0.30	65.3	2.05
Mexico	Elotero de Sinaloa	SIN 17	INIFAP	23.5	-106.3	200	4.36	0.49	4.50	0.47	4.77	0.30	65.5	2.05
Mexico	Elotes Occidentales	DGO 236*	NCRPIS	24.5	-104.8	1969	4.13	0.49	4.37	0.47	4.28	0.30	64.6	2.05
Mexico	Elotes Occidentales	GTO 191*	INIFAP	21.1	-101.7	1885	5.19	0.49	5.53	0.47	4.12	0.30	65.8	2.05
Mexico	Elotes Occidentales	NAY 29	INIFAP	22.4	-105.5	46	4.37	0.49	5.26	0.47	4.68	0.30	65.2	2.05
Mexico	Elotes Occidentales	NAY 38	INIFAP	21.9	-105.3	46	3.96	0.49	5.04	0.47	5.14	0.30	65.9	2.05
Mexico	Elotes Occidentales	ZAC 210*	INIFAP	21.6	-103	1500	3.98	0.49	4.80	0.47	4.27	0.30	65.5	2.05
Mexico	Gordo	CHH 131*	CIMMYT	29.2	-108.1	2095	3.66	0.49	3.94	0.47	3.87	0.30	63.8	2.05

Supplemental Table 2.3 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	GLS	GLS SE	NLB	NLB SE	SLB	SLB SE	DTA	DTA SE
Mexico	Gordo	CHH 160*	CIMMYT	28.6	-107.5	2040	3.14	0.49	4.14	0.47	4.48	0.30	64.5	2.05
Mexico	Gordo	CHH 214*	CIMMYT	28.6	-107.5	2040	3.98	0.49	3.58	0.47	4.59	0.30	64.1	2.05
Mexico	Gordo	CHH 256*	CIMMYT	28.5	-107.4	1900	3.31	0.49	4.27	0.47	4.26	0.30	64.3	2.05
Mexico	Harinoso de Ocho	NAY 24	INIFAP	22	-105.3	46	4.86	0.49	4.12	0.47	4.89	0.30	64.6	2.05
Mexico	Jala	JAL44*	CIMMYT	20	-104.3	1300	4.58	0.49	5.34	0.47	4.05	0.30	66.2	2.05
Mexico	Jala	NAY 130	INIFAP	21.1	-104.4	1095	5.25	0.49	6.57	0.47	5.12	0.31	68.4	2.05
Mexico	Mixteco	OAX 569	INIFAP	17.4	-97.4	2500	4.33	0.49	5.56	0.47	4.65	0.31	67.3	2.05
Mexico	Motozinteco	CHS 650	INIFAP	15.4	-92.3	1270	5.63	0.49	6.70	0.47	5.05	0.31	67.5	2.06
Mexico	Motozinteco	CHS 650B	NCRPIS	15.4	-92.3	1270	5.03	0.57	6.53	0.55	4.31	0.36	67.2	2.09
Mexico	Mushito	MIC 371	INIFAP	19.5	-101.6	2100	4.62	0.49	5.16	0.47	4.76	0.30	66.5	2.05
Mexico	Mushito	MIC 317*	NCRPIS	19.3	-101.5	2253	5.20	0.49	6.40	0.47	5.46	0.31	68.2	2.05
Mexico	Nal-Tel	CAM 48	INIFAP	19.8	-90.1	50	5.03	0.49	5.58	0.47	4.52	0.30	65.8	2.05
Mexico	Negrito	OAX 26*	INIFAP	17.2	-96.8	1640	4.28	0.49	4.60	0.47	4.01	0.30	64.3	2.06
Mexico	Olotillo	CHS 53	CIMMYT	16.8	-93.2	579	5.99	0.49	7.29	0.47	4.92	0.31	69.5	2.05
Mexico	Olotillo	CHS 81	INIFAP	16.6	-92.7	686	5.28	0.49	6.29	0.47	5.18	0.30	67.5	2.05
Mexico	Oloton	CHS 684	INIFAP	16.8	-92.5	2100	5.59	0.49	6.43	0.47	5.61	0.30	67.4	2.05
Mexico	Onaveno	SON 114	INIFAP	29	-109.4	410	4.51	0.49	4.79	0.47	4.25	0.30	64.4	2.05
Mexico	Onaveno	SON 24*	NCRPIS	30.8	-110.8	867	4.29	0.49	4.50	0.47	4.45	0.30	65.9	2.05
Mexico	Palomero de Jalisco	JAL154*	INIFAP	20	-103.7	2520	4.83	0.49	4.10	0.47	4.31	0.30	64.7	2.05
Mexico	Palomero Tipo Chihuahua	CHH 148*	INIFAP	29.4	-107.8	2140	3.00	0.49	3.52	0.47	4.25	0.30	64.0	2.05
Mexico	Palomero Tipo Chihuahua	CHH 201*	INIFAP	26.8	-107.1	2130	3.35	0.49	3.51	0.47	3.89	0.30	63.2	2.05
Mexico	Palomero Toluqueno	VER 35*	NCRPIS	19.6	-97.3	2391	3.94	0.49	3.81	0.47	4.56	0.30	64.5	2.05
Mexico	Pepitilla	GRO 3*	INIFAP	18.4	-99.5	747	5.40	0.49	6.60	0.47	4.56	0.31	69.4	2.05
Mexico	Raton	CHH 191*	NCRPIS	28.8	-106.4	1885	3.21	0.49	4.52	0.47	4.40	0.30	64.9	2.05
Mexico	Raton	NLE 9*	INIFAP	25.6	-99.3	250	4.09	0.49	5.35	0.47	3.94	0.30	64.0	2.05
Mexico	Raton	TAM 25*	INIFAP	24.6	-99.6	290	5.04	0.49	5.48	0.47	4.43	0.30	65.8	2.05

Supplemental Table 2.3 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	GLS	GLS SE	NLB	NLB SE	SLB	SLB SE	DTA	DTA SE
Mexico	Reventador	NAY 15*	INIFAP	22.3	-105.4	46	4.66	0.49	4.99	0.47	5.38	0.30	65.7	2.05
Mexico	Reventador	NAY 39	INIFAP	21.9	-105.3	46	4.29	0.49	4.60	0.47	5.34	0.30	66.0	2.05
Mexico	Serrano de Jalisco	JAL133*	INIFAP	20	-103.8	2060	4.44	0.49	4.97	0.47	4.63	0.30	65.7	2.05
Mexico	Serrano de Jalisco	JAL146	INIFAP	20	-103.7	2520	4.57	0.49	4.50	0.47	5.08	0.30	63.8	2.05
Mexico	Serrano Mixe	OAX 565	INIFAP	17.1	-96	2350	5.28	0.49	6.74	0.47	5.63	0.31	68.7	2.05
Mexico	Tablilla de Ocho	JAL301	CIMMYT	22.1	-103.2	1700	4.09	0.49	5.34	0.47	4.66	0.30	65.9	2.05
Mexico	Tablilla de Ocho	NAY 185	CIMMYT	21.7	-104.1	1100	4.51	0.49	5.51	0.47	4.87	0.30	66.7	2.05
Mexico	Tablilla de Ocho	ZAC 187	NCRPIS	22.3	-103.6	2170	4.28	0.49	5.07	0.47	3.71	0.30	64.8	2.05
Mexico	Tabloncillo	JAL102	INIFAP	19.5	-103.3	1280	5.32	0.49	5.89	0.47	4.16	0.30	67.0	2.05
Mexico	Tabloncillo	JAL103*	NCRPIS	19	-103	1290	4.66	0.49	5.64	0.47	4.48	0.30	67.2	2.05
Mexico	Tabloncillo	JAL103B*	NCRPIS	19	-103	1290	5.05	0.57	5.99	0.55	4.27	0.36	65.9	2.09
Mexico	Tabloncillo Perla	NAY 12	INIFAP	22	-105.2	46	4.86	0.49	4.65	0.47	4.82	0.30	64.8	2.05
Mexico	Tabloncillo Perla	NAY 16	CIMMYT	22.1	-105.3	46	4.61	0.49	4.68	0.47	4.89	0.30	65.6	2.05
Mexico	Tehua	CHS 159	CIMMYT	16.5	-92.5	747	5.72	0.49	7.13	0.48	5.38	0.32	70.4	2.06
Mexico	Tehua	CHS 29	CIMMYT	15.8	-92.7	1000	6.11	0.49	6.27	0.47	5.63	0.31	69.1	2.05
Mexico	Tepecintle	CHS 76	INIFAP	16.5	-92.8	579	4.38	0.49	4.21	0.47	5.55	0.30	65.8	2.05
Mexico	Tuxpeno	VER 143*	NCRPIS	19.3	-96.5	141	4.91	0.49	6.72	0.47	5.13	0.30	67.3	2.05
Mexico	Tuxpeno Norteno	CHH 121	INIFAP	30.9	-108.2	1470	3.63	0.49	5.36	0.47	4.54	0.30	65.6	2.05
Mexico	Tuxpeno Norteno	CHH 287*	NCRPIS	30.4	-107.9	1456	4.41	0.49	5.14	0.47	4.84	0.30	63.9	2.06
Mexico	Tuxpeno Norteno	TAM 3*	INIFAP	23.3	-99	300	4.47	0.49	4.74	0.47	4.86	0.30	65.6	2.05
Mexico	Vandeno	GRO 96	NCRPIS	17.5	-101.3	61	5.04	0.49	6.68	0.47	5.51	0.31	68.4	2.06
Mexico	Zamorano Amarillo	GTO 1	INIFAP	21.1	-101.7	1870	4.63	0.49	4.22	0.47	4.33	0.30	65.5	2.05
Mexico	Zamorano Amarillo	MIC 66*	INIFAP	20.1	-102	1645	5.06	0.49	5.53	0.47	4.47	0.30	65.4	2.05
Mexico	Zapalote Chico	CHS 662	INIFAP	16.2	-94	100	4.31	0.49	3.59	0.47	4.54	0.30	63.3	2.05
Mexico	Zapalote Chico	OAX 48	CIMMYT	16.4	-94.2	50	4.34	0.49	4.31	0.47	4.27	0.30	62.8	2.06
Mexico	Zapalote Chico	OAX 50	CIMMYT	16.6	-94.6	107	4.22	0.49	3.99	0.47	4.35	0.30	64.8	2.05

Supplemental Table 2.3 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	GLS	GLS SE	NLB	NLB SE	SLB	SLB SE	DTA	DTA SE
Mexico	Zapalote Chico	OAX 70	CIMMYT	16.3	-95.2	46	3.83	0.49	3.77	0.47	4.65	0.30	63.7	2.05
Mexico	Zapalote Grande	CHS 104	INIFAP	15.3	-92.7	107	5.06	0.49	5.27	0.47	5.60	0.30	66.7	2.06
Mexico	Zapalote Grande	CHS 224	INIFAP	15.3	-92.7	91	5.17	0.49	5.47	0.47	4.99	0.30	66.5	2.05
Mexico	Zapalote Grande	CHS 236	INIFAP	16.7	-93.8	120	4.67	0.49	4.41	0.47	4.48	0.30	64.1	2.05
Mexico	Zapalote Grande	CHS 521	INIFAP	16.7	-93.7	730	4.53	0.49	4.65	0.47	5.13	0.30	65.6	2.05
Paraguay	Avati Moroti Guapi	PAG 139 (USDA)	NCRPIS	-25.5	-56.4	369	4.77	0.49	4.74	0.47	5.08	0.30	66.9	2.05
Paraguay	Avati Moroti Ti	PAG124 (USDA)	NCRPIS	-26.7	-57.2	276	4.84	0.49	4.66	0.47	4.72	0.31	67.6	2.05
Paraguay	Cateto Sabugo Grosso	PAG 422 (USDA)	NCRPIS	-26	-56.5	95	4.99	0.49	5.18	0.47	4.23	0.30	66.4	2.05
Paraguay	Moroti Guapi	PAG VI-A	NCRPIS	-26.1	-56.93	400	4.13	0.49	5.40	0.47	4.50	0.31	67.9	2.06
Paraguay	Semi Dente Paulista	PAG I*	CIMMYT	-26	-56	270	5.01	0.49	6.74	0.47	5.66	0.31	67.2	2.05
Peru	Alazan	LBQ 18	PCIM	-6.7	-79.8	50	4.44	0.49	5.13	0.47	4.35	0.31	67.8	2.05
Peru	Alazan	LIB 34	NCRPIS	-7.8	-79.3	80	4.54	0.49	6.27	0.47	4.29	0.31	67.7	2.05
Peru	Aleman	HCO 38*	NRC	-9.3	-76	700	4.33	0.49	5.79	0.47	5.46	0.30	66.7	2.05
Peru	Amarillo Huancabamba	PIU 17B	NCRPIS	-5	-79	2100	5.73	0.49	5.79	0.47	4.84	0.31	67.6	2.05
Peru	Amarillo Huancabamba	PIU 38B*	NCRPIS	-5.2	-79.5	2000	5.27	0.49	6.24	0.47	4.97	0.31	67.5	2.05
Peru	Ancashino	ANC 102*	NCRPIS	-9.1	-77.8	2600	4.67	0.49	6.35	0.47	4.34	0.30	67.4	2.05
Peru	Arequipeno	ARQ 1*	NCRPIS	-16.2	-71.3	2332	4.63	0.49	4.98	0.47	4.33	0.30	66.5	2.05
Peru	Arizona	LIB 16	NRC	-8.6	-78.8	100	4.31	0.49	4.64	0.47	4.67	0.30	66.1	2.05
Peru	Arizona	LIB 2*	NRC	-8.4	-78.8	80	4.74	0.49	5.63	0.47	5.21	0.30	66.6	2.05
Peru	Blanco Ayabaca	PIU 119	NCRPIS	-4.6	-79.7	2630	4.95	0.49	5.67	0.47	4.75	0.30	67.5	2.05
Peru	Chancayano Blanco	LIM 45*	PCIM	-11.1	-77.6	50	4.78	0.49	6.75	0.47	4.34	0.31	68.0	2.05
Peru	Chancayano Pintado	LIM 46*	NRC	-11.1	-77.6	50	4.40	0.49	5.24	0.47	4.74	0.31	67.7	2.05
Peru	Chaparreno	ARQ34*	PCIM	-17	-72	10	4.40	0.49	5.40	0.47	4.25	0.31	67.9	2.05
Peru	Chulpi	LIM 66*	NCRPIS	-11.4	-77.4	110	5.61	0.49	6.50	0.47	4.68	0.31	67.3	2.06
Peru	Chuncho	CUZ 112*	NCRPIS	-12.8	-72.7	1300	4.84	0.49	6.16	0.47	5.20	0.31	68.5	2.05
Peru	Colorado	LIB 8*	NCRPIS	-7.4	-79.5	51	4.56	0.57	5.91	0.55	4.11	0.36	67.1	2.09

Supplemental Table 2.3 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	GLS	GLS SE	NLB	NLB SE	SLB	SLB SE	DTA	DTA SE
Peru	Confite Morocho	AYA 20	PCIM	-12.9	-74.3	2500	4.69	0.49	3.85	0.47	4.20	0.30	64.3	2.05
Peru	Confite Puneno	APC 56	PCIM	-14.4	-72.9	3600	4.89	0.49	5.25	0.47	4.69	0.30	63.5	2.05
Peru	Confite Puntigudo	CAJ 27	NRC	-7.6	-78	2500	4.19	0.49	4.05	0.47	4.90	0.30	65.1	2.05
Peru	Confite Puntigudo	CUZ 13	NCRPIS	-15.5	-70.1	3832	3.47	0.49	3.34	0.47	3.46	0.30	65.0	2.05
Peru	Coruca	TAC 1*	PCIM	-18	-70.9	500	4.57	0.49	4.51	0.47	4.41	0.30	66.8	2.05
Peru	Cubano Amarillo	UCA 8*	NCRPIS	-5.2	-75.7	129	4.39	0.49	5.98	0.47	5.56	0.31	67.4	2.05
Peru	Cuzco Cristalino Amaril	CUZ 363	NCRPIS	-13.5	-72.1	3375	4.85	0.49	4.53	0.47	4.26	0.30	63.7	2.05
Peru	Cuzco Gigante	CAJ 17	PCIM	-7.2	-78.5	2800	5.32	0.49	5.25	0.47	4.76	0.30	67.1	2.05
Peru	Granada	ANC 57	PCIM	-9.3	-77.6	2600	4.83	0.49	5.28	0.47	5.35	0.30	65.9	2.05
Peru	Huachano	LIM 43*	NRC	-11.1	-77.6	40	4.67	0.49	6.00	0.47	4.42	0.30	67.0	2.05
Peru	Huancavelicano	HVC 179*	NCRPIS	-13	-75.1	4562	5.44	0.50	5.50	0.47	5.24	0.30	65.9	2.05
Peru	Huanuco	HCO 128B*	NCRPIS	-9	-76	2700	6.09	0.49	6.58	0.47	5.32	0.31	69.2	2.05
Peru	Huarmaca	PIU 72*	PCIM	-5.6	-79.5	2300	5.17	0.49	6.71	0.47	5.23	0.31	68.0	2.05
Peru	Huayleno	ANC 180x181	NCRPIS	-9	-77	2600	5.01	0.49	5.93	0.47	5.59	0.31	68.6	2.05
Peru	Huayleno	ANC 291*	NCRPIS	-9.5	-77.5	3059	4.68	0.49	4.69	0.47	4.40	0.30	66.2	2.05
Peru	Jora	ANC 1*	PCIM	-10.1	-78.2	100	4.97	0.49	6.45	0.47	5.40	0.31	68.5	2.05
Peru	Kculli	HVC 137	PCIM	-12.6	-74.9	3100	4.72	0.58	5.34	0.55	5.09	0.36	65.4	2.09
Peru	Maranon	LIB 63B	NCRPIS	-8	-77	2800	5.04	0.49	5.19	0.47	4.32	0.31	69.1	2.05
Peru	Mochero	LBQ 5*	NRC	-6.7	-79.9	25	4.49	0.49	4.54	0.47	4.12	0.30	66.8	2.05
Peru	Morado Canteno	Lima 55*	NCRPIS	-12	-77	60	4.58	0.49	5.90	0.47	4.16	0.30	65.7	2.05
Peru	Morochillo	PIU 96*	PCIM	-4.7	-79.7	2000	5.10	0.49	6.62	0.47	5.75	0.31	67.7	2.05
Peru	Morocho	APC 67*	NCRPIS	-13.6	-72.6	2750	4.78	0.49	4.70	0.47	4.81	0.30	65.6	2.05
Peru	Morocho	APC 77*	NCRPIS	-13.7	-73.1	2977	4.84	0.49	5.47	0.47	5.48	0.30	65.9	2.05
Peru	Morocho Cajabambino	LIB 62*	PCIM	-8.4	-77.3	2800	5.07	0.49	5.75	0.47	5.19	0.31	67.6	2.05
Peru	Pagaladroga	PIU 2	PCIM	-5.1	-80.2	520	4.81	0.49	5.47	0.47	4.81	0.31	67.9	2.05
Peru	Pardo	LIM 19*	NRC	-11.1	-77.6	40	3.94	0.49	5.87	0.47	4.66	0.30	67.5	2.05

Supplemental Table 2.3 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	GLS	GLS SE	NLB	NLB SE	SLB	SLB SE	DTA	DTA SE
Peru	Paro	CUZ 76	PCIM	-13.6	-71.7	3300	5.74	0.49	6.87	0.47	4.52	0.30	67.0	2.05
Peru	Perla	ANC 23*	NCRPIS	-10.1	-78.2	100	4.75	0.49	6.21	0.47	4.55	0.31	67.8	2.05
Peru	Perla	ANC 24*	NRC	-10.1	-78.2	50	5.21	0.49	5.72	0.47	5.14	0.31	67.9	2.05
Peru	Perla	LIM 50*	NRC	-12.1	-77.1	50	5.52	0.49	6.66	0.47	4.84	0.31	68.7	2.05
Peru	Piricincó	SM 8*	NCRPIS	-6.2	-76.6	940	5.35	0.49	6.21	0.47	4.98	0.31	67.5	2.05
Peru	Pisccorunto	APC 13	PCIM	-13.7	-73.4	2900	4.70	0.49	5.12	0.55	4.78	0.30	64.5	2.07
Peru	Pisccorunto	APC 13B	NCRPIS	-13.7	-73.4	2900	4.69	0.57	5.22	0.55	4.50	0.36	66.9	2.09
Peru	Rabo de Zorro	ANC 325*	NCRPIS	-8.5	-78.1	2600	5.42	0.49	6.39	0.47	4.10	0.30	67.2	2.05
Peru	Rienda	CAJ 80	PCIM	-7.6	-78	2000	5.05	0.49	5.60	0.47	4.02	0.30	67.9	2.05
Peru	San Geronimo Huancaveli	JUN 164	NCRPIS	-12	-75.2	3333	4.35	0.49	4.96	0.47	4.35	0.30	64.6	2.05
Peru	Sarco	ANC 184	NRC	-9.4	-77.2	3150	4.86	0.49	6.38	0.47	5.39	0.31	68.2	2.05
Peru	Shajatu	ANC 117	PCIM	-8.5	-77.9	2580	4.63	0.49	6.48	0.47	4.88	0.30	67.1	2.05
Trinidad	Tuson	TRN 1	INIFAP	10.5	-61.1	125	5.47	0.49	5.27	0.47	4.94	0.31	67.8	2.05
Trinidad	Tuson	TRN 10	INIFAP	10.6	-61.1	20	5.63	0.49	6.22	0.47	5.91	0.31	67.9	2.05
U.S. Virgin Islands	St. Croix	IVC 2*	NRC	17.7	-64.7	150	4.87	0.49	5.78	0.47	5.22	0.30	66.9	2.05
Uruguay	Cateto Sulino	URG IV	CIMMYT	-31.7	-56	126	4.06	0.49	3.22	0.47	4.13	0.30	64.8	2.05
Uruguay	Cateto Sulino Escuro	URG V	CIMMYT	-31.7	-56	126	4.53	0.49	3.87	0.47	4.84	0.30	65.8	2.05
Uruguay	Cateto Sulino Grosso	URG III	CIMMYT	-31.7	-56	126	4.14	0.49	4.03	0.47	4.67	0.30	64.6	2.05
Uruguay	Dentado Branco	URZM 13010	NCRPIS	-34	-56	104	4.37	0.49	4.33	0.47	4.35	0.30	65.3	2.05
Uruguay	Semi-Dentado Rugoso	URZM 13052	NCRPIS	-30.8	-66.8	714	4.36	0.49	4.06	0.47	4.20	0.30	65.5	2.05
USA	Apache	PI 213731	NCRPIS	33.4	-110.4	1067	3.09	0.49	3.29	0.47	3.50	0.30	64.8	2.05
USA	Argentine Pop	PI 217404*	NCRPIS	-32	-58	305	5.06	0.49	5.35	0.47	4.73	0.30	66.4	2.05
USA	Bear Isl. Chippewa	PI 213801*	NCRPIS	47	-92.2	457	2.67	0.50	1.77	0.56	3.38	0.30	60.6	2.07
USA	Cherokee	PI 213744*	NCRPIS	36.7	-96	229	4.01	0.49	4.04	0.47	5.17	0.30	65.9	2.05
USA	Cochiti Pueblo	PI 218151*	NCRPIS	35.6	-106.4	1616	3.20	0.49	3.06	0.47	4.13	0.30	63.9	2.05
USA	Domingo Pueblo	PI 218130*	NCRPIS	35.5	-106.4	1585	3.01	0.49	3.40	0.47	4.40	0.30	65.2	2.05

Supplemental Table 2.3 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	GLS	GLS SE	NLB	NLB SE	SLB	SLB SE	DTA	DTA SE
USA	Gaspe Flint	PI 401757*	NCRPIS	48.8	-64.3	173	2.50	0.50	0.84	0.48	2.87	0.31	59.1	2.05
USA	Gourd Seed	PI 217405*	NCRPIS	33	-97.1	229	4.25	0.49	4.71	0.47	4.80	0.30	66.5	2.05
USA	Gourd Seed	PI 414183*	NCRPIS	32	-99	300	4.29	0.49	3.65	0.47	3.87	0.30	66.5	2.05
USA	Havasupai	PI 317675*	NCRPIS	36.3	-112.7	1303	2.74	0.49	3.38	0.47	3.94	0.30	63.9	2.05
USA	Havasupai	PI 317679*	NCRPIS	36.3	-112.7	1303	3.38	0.49	3.76	0.47	4.24	0.30	65.0	2.05
USA	Hopi	PI 213733*	NCRPIS	35.9	-110.7	1941	3.16	0.49	3.17	0.47	3.81	0.30	64.3	2.05
USA	Hualapai	PI 213741*	NCRPIS	35.5	-113.4	1067	3.58	0.49	2.42	0.47	3.70	0.30	64.1	2.05
USA	Isleta-Tiwa	PI 218148*	NCRPIS	34.9	-106.7	1509	3.21	0.49	3.59	0.47	4.44	0.30	66.1	2.06
USA	Jemez Pueblo	PI 218173*	NCRPIS	35.6	-106.7	1829	3.35	0.49	3.65	0.47	4.45	0.30	65.7	2.05
USA	Laguna Pueblo	PI 218169*	NCRPIS	35.1	-107.4	1768	3.19	0.49	3.41	0.47	3.89	0.30	64.6	2.05
USA	Laguna Pueblo	PI 218170*	NCRPIS	35.1	-107.4	1768	2.98	0.49	3.01	0.47	3.90	0.30	65.4	2.05
USA	Longfellow	PI 214195*	NCRPIS	43.6	-80.2	488	3.40	0.49	2.31	0.47	3.92	0.30	62.0	2.05
USA	Longfellow Flint	PI 217408*	NCRPIS	42.3	-71.5	99	2.94	0.50	2.43	0.48	3.63	0.30	60.8	2.05
USA	Mexican June	PI 221889*	NCRPIS	37	-93.2	213	4.50	0.49	5.18	0.47	4.69	0.30	65.9	2.05
USA	Mexican June	PI 311243*	NCRPIS	37	-77	305	4.01	0.49	4.12	0.47	4.16	0.30	65.4	2.05
USA	Moencopi Pueblo	PI 218175*	NCRPIS	36.1	-111.2	1311	3.33	0.49	2.86	0.47	3.75	0.30	64.4	2.05
USA	Moencopi Pueblo	PI 218177*	NCRPIS	36.1	-111.2	1311	3.65	0.49	3.21	0.47	3.86	0.30	65.1	2.05
USA	Mohave	PI 218187*	NCRPIS	34.2	-114.3	91	3.40	0.49	2.62	0.47	3.47	0.30	63.2	2.05
USA	Mohawk Round Nose	PI 483087*	NCRPIS	45	-74.7	59	3.21	0.49	2.79	0.47	3.70	0.30	64.0	2.05
USA	N.W. Dent	PI 217480*	NCRPIS	38.3	-104.7	1444	3.75	0.49	2.66	0.47	3.63	0.30	63.5	2.05
USA	Navajo	PI 218163*	NCRPIS	36.6	-110.6	1616	2.66	0.49	3.27	0.47	4.25	0.30	64.2	2.05
USA	Northeast Flint	WLB	NCRPIS	41.7	-71.7	130	2.98	0.49	3.10	0.47	3.77	0.30	63.6	2.05
USA	Papago-Pimans	PI 217410*	NCRPIS	32.3	-112	1067	3.79	0.49	3.20	0.47	3.33	0.30	65.1	2.05
USA	Pueblo 12-Row Hopi Koko	PI 503564*	NCRPIS	35.9	-110.7	1908	3.15	0.49	4.11	0.47	4.35	0.30	64.3	2.05
USA	Quapaw Red	PI 213757*	NCRPIS	37	-94.8	229	4.49	0.49	3.83	0.47	4.37	0.30	64.9	2.05
USA	Sac And Fox	PI 217411*	NCRPIS	42	-92.6	229	3.66	0.49	2.92	0.47	3.25	0.30	63.9	2.05

Supplemental Table 2.3 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	GLS	GLS SE	NLB	NLB SE	SLB	SLB SE	DTA	DTA SE
USA	San Lorenzo Pueblo	PI 218135	NCRPIS	36.1	-106.3	2104	2.76	0.49	3.20	0.47	3.49	0.30	62.8	2.05
USA	Santo Domingo Pueblo	PI 218143*	NCRPIS	35.5	-106.4	1585	2.98	0.49	3.02	0.47	3.70	0.30	65.1	2.05
USA	Seneca Hominy Corn	PI 401754*	NCRPIS	42.1	-78.9	431	3.07	0.50	2.41	0.47	3.28	0.30	61.1	2.05
USA	Shoshone	PI 213769*	NCRPIS	43	-112.4	229	2.88	0.50	2.69	0.48	2.70	0.30	61.1	2.05
USA	Smut Nose	PI 222490*	NCRPIS	42.7	-84.5	213	3.55	0.49	2.68	0.47	3.43	0.30	63.6	2.05
USA	Supergold Pop	PI 222648*	NCRPIS	38	-96	319	4.51	0.49	4.44	0.47	4.31	0.30	64.8	2.05
USA	Tennessee Red Cob	PI 311235*	NCRPIS	37.2	-80.4	305	4.20	0.49	4.98	0.47	4.26	0.30	65.0	2.05
USA	Tesuque Pueblo	PI 218137*	NCRPIS	35.8	-106	2073	2.70	0.49	3.49	0.47	4.04	0.30	64.7	2.05
USA	White Dent	PI 221885*	NCRPIS	39.1	-93.2	238	4.49	0.49	4.71	0.47	4.42	0.30	65.9	2.05
USA	White Dent	PI 311232*	NCRPIS	37	-77	305	4.42	0.49	5.08	0.47	4.55	0.30	64.9	2.05
USA	Winnebago	PI 213772*	NCRPIS	42.2	-96.5	229	3.30	0.49	2.18	0.47	3.51	0.30	63.3	2.05
USA	Winnebago	PI 213774*	NCRPIS	42.2	-96.5	229	2.75	0.49	2.39	0.47	3.29	0.30	63.4	2.05
USA	Zia Pueblo	PI 218139*	NCRPIS	35.5	-106.7	1829	3.57	0.49	3.74	0.47	4.42	0.30	65.7	2.05
Venezuela	Araguito	VEN 568	NRC	8.9	-64.2	183	3.92	0.49	4.46	0.47	4.92	0.30	64.1	2.05
Venezuela	Araguito	VEN 628	NRC	8.9	-64.2	183	4.26	0.49	4.93	0.47	4.91	0.30	63.0	2.05
Venezuela	Araguito	VEN 678	NCRPIS	8.9	-64.2	73	4.00	0.49	4.00	0.47	4.37	0.30	64.3	2.05
Venezuela	Araguito	VEN 760	NRC	9.6	-63.1	123	4.21	0.49	5.10	0.47	4.97	0.30	66.9	2.05
Venezuela	Cacao	VEN 630	NCRPIS	8.6	-71.2	201	5.57	0.49	6.75	0.47	5.45	0.31	68.6	2.05
Venezuela	Canilla	VEN 693	NRC	8.9	-64.2	91	4.76	0.49	5.67	0.47	5.33	0.31	68.3	2.05
Venezuela	Cariaco	VEN 408	ICA	10.4	-63.8	46	5.37	0.49	6.55	0.47	5.06	0.31	68.9	2.05
Venezuela	Cariaco	VEN 631	NRC	8.1	-63.6	366	4.81	0.49	6.93	0.47	5.44	0.31	68.7	2.05
Venezuela	Cariaco	VEN 639	NCRPIS	8.6	-70.2	194	5.84	0.49	6.96	0.47	5.17	0.31	68.0	2.05
Venezuela	Chandelle	VEN 409	ICA	10.1	-68.4	137	4.85	0.49	6.64	0.47	5.63	0.31	67.5	2.05
Venezuela	Chandelle	VEN 460	ICA	8.1	-63.6	229	5.01	0.49	6.47	0.47	5.56	0.31	67.8	2.05
Venezuela	Chirimito	VEN 703*	ICA	8.1	-63.6	229	5.17	0.49	5.63	0.47	5.47	0.30	67.5	2.05
Venezuela	Comun	VEN 448	ICA	7.6	-72	457	5.30	0.49	6.44	0.47	5.55	0.31	67.3	2.06

Supplemental Table 2.3 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	GLS	GLS SE	NLB	NLB SE	SLB	SLB SE	DTA	DTA SE
Venezuela	Comun	VEN 881	ICA	10	-69.3	607	5.26	0.49	6.68	0.47	5.91	0.31	67.6	2.06
Venezuela	Costeno	VEN 775	NCRPIS	9.2	-68.3	184	4.54	0.49	6.50	0.47	5.73	0.31	67.4	2.05
Venezuela	Cuba Yellow Flint	VEN 331	ICA	10	-68	46	4.87	0.49	6.41	0.47	5.32	0.31	67.6	2.06
Venezuela	Cuba Yellow Flint	VEN 650	ICA	8.9	-64.2	128	4.84	0.49	6.25	0.47	5.35	0.30	67.0	2.05
Venezuela	Guaribero	VEN 653	ICA	8.9	-64.2	73	5.03	0.49	5.41	0.47	5.12	0.30	66.0	2.05
Venezuela	Guaribero	VEN 733	ICA	8.9	-64.2	137	5.08	0.49	5.97	0.47	5.24	0.30	67.5	2.05
Venezuela	Huevito	VEN 396	ICA	8	-71.8	1052	4.93	0.49	6.04	0.47	5.04	0.32	69.7	2.05
Venezuela	Huevito	VEN 445	ICA	7.8	-72.3	823	5.44	0.49	6.19	0.47	5.71	0.30	67.2	2.05
Venezuela	Negrito	VEN 426	ICA	10.3	-67.5	384	5.04	0.49	6.30	0.47	5.31	0.31	68.0	2.05
Venezuela	Negrito	VEN 673	ICA	10.3	-67.5	384	5.35	0.49	6.37	0.47	5.30	0.31	68.3	2.05
Venezuela	Negrito	VEN 870	ICA	10.3	-67.5	384	5.21	0.49	7.13	0.47	5.83	0.31	68.3	2.05
Venezuela	Pira	VEN 457	ICA	8	-72	412	4.68	0.49	6.56	0.47	5.46	0.30	65.6	2.05
Venezuela	Pollo	VEN 310	NRC	8	-72	3088	5.07	0.49	5.08	0.47	5.11	0.30	66.0	2.05
Venezuela	Puya	VEN 946	ICA	9	-72	91	5.20	0.49	5.94	0.47	5.69	0.31	68.2	2.05
Venezuela	Puya Grande	VEN 345	ICA	10	-68	37	5.98	0.49	6.09	0.47	5.72	0.31	68.7	2.06
Venezuela	Puya Grande	VEN 651	NCRPIS	9.6	-63.1	203	5.08	0.49	6.42	0.47	5.16	0.31	67.7	2.05
Venezuela	Tuson	VEN 405	ICA	7.5	-72	389	5.06	0.49	6.38	0.47	5.47	0.31	68.0	2.05
Venezuela	Tuxpeno	VEN 598	ICA	9.5	-69.3	96	5.42	0.49	5.86	0.47	5.48	0.30	67.2	2.05
Venezuela	Tuxpeno	VEN 692	ICA	9.5	-69.3	199	5.44	0.49	6.31	0.47	4.96	0.31	67.6	2.05
Venezuela	Tuxpeno	VEN 891	ICA	10	-69.3	471	6.17	0.49	6.93	0.47	5.22	0.31	67.7	2.05

Notes:

[†]Most accessions were collected during the 1940s and 1950s; additional Mexican accessions were collected during the 1960s and 1970s by E. Hernández X. and R. Ortega P. Data on altitude, latitude and longitude were obtained from Vigouroux et al (2008), from the Original Strains of Corn Vol I and Vol II (NSF-NRC, 1954) and from the studies of the accessions published by the National Academy of Sciences and Harvard (Brieger et al, 1958; Brown, 1960; Grant et al, 1963; Grobman et al, 1961; Hatheway, 1957; Ramírez et al, 1960; Roberts et al, 1957; Timothy et al, 1961; Timothy et al, 1963; Wellhausen et al, 1952; Wellhausen et al, 1957). Vigouroux et al (2008) notes that most accessions were originally acquired from national germplasm banks or CIMMYT in the 1960s and 1970s, but those labeled NRC were acquired directly from the original collections, either from the collections of William L. Brown (Pioneer Hi-Bred, Johnston, IA) or original backup seeds once held in storage at Glenn Dale, MD, by the USDA-ARS. (All those labeled NRC were increased by Major M Goodman and are now deposited with the NCRPIS at Ames, Iowa). Most eastern South American accessions -the collections with Roman numerals- (Brazil, Paraguay, Uruguay, Guianas, some Argentine and a few Bolivian accessions) are actually bulk samples of several accessions, and data shown are means of the accessions (Paterniani and Goodman, 1977). Many accessions sourced from INIFAP are more recent Mexican collections (some from the 1990s or later) made by Sánchez J. and Ortega P. and collaborators, and generally have exact geographic coordinates (Sanchez G. JJ, 2000). Also occasionally seed from a given accession was sampled twice by the Goodman group at different times. These two samples were labeled sample A and B, and these are not different accessions. Accessions labeled with an (USDA) indicate accessions from Brazil which were once held in storage at Glenn Dale, MD, but not from the NRC. They were increased by MMG and are now deposited with the NCRPIS at Ames, Iowa. It is also noted that accessions with an asterisk (*) are those currently available from NCRPIS; unfortunately these number only 170 of the accessions used in this study.

[‡]Source abbreviations are as follows: Intentional Maize and Wheat Improvement Center (CIMMYT), North Central Regional Plant Introduction Station (NCRPIS), National Research Council (NRC), Columbian Agriculture Institute (ICA), National Research Institute for Forestry, Agriculture, and Livestock (INIFAP), National Center for Genetic Resources Preservation (NCGRP), Cooperative Program for Maize Investigations (PCIM), David Timothy personal collection (DHT), and William L. Brown personal collection (WLB).

Supplemental Table 2.4 Disease ratings for check hybrids

Line/Hybrid	Pedigree	Year Released	GLS	GLS SE	NLB	NLB SE	SLB	SLB SE
PHB47	((B37*3) × SD105)	1984	2.29	0.44	2.89	0.38	3.41	0.23
PHB47xDJ7	DJ7 = (B73 x BS16 Synthetic)	1985	4.49	0.44	4.97	0.39	4.51	0.23
DKHBA1xPHB47	DKHBA1 = (Pioneer 3195 x Pioneer 3199)	1985	6.33	0.44	5.89	0.38	7.46	0.23
NC296xPHB47	NC296 = (Pioneer X105A x H5)	1990	7.48	0.44	7.81	0.38	7.69	0.23
Pioneer 3394	unavailable	1991	5.33	0.44	6.05	0.38	5.45	0.23
Pioneer 33M54	unavailable	2003	7.41	0.44	5.74	0.38	6.87	0.23

Note: Disease was scored on a 1 to 9 scale with 9 being resistant.

Supplemental Table 2.5 Details of experimental units at six locations

Location	Row Length (m)	Alley Length (m)	Row Spacing (m)	Number Kernels Planted	Planting density (seeds/ha)
Andrews, NC	3.5	0.8	0.76	15	46000
Cairo, GA	3.9	0.8	0.76	25	70000
Clayton, NC	2.6	0.8	0.97	18	54600
Salisbury, NC	4.9	1	0.76	25	55800
Thomasboro, IL	3.7	1	0.76	20	56000
Windfall, IN	3.5	0.8	0.76	15	45900

Supplemental Table 2.6 Thirty one accessions for which no collection information could be found

Country	Race	Accession	Latitude	Longitude	Altitude (m)
Argentina	Cristalino Amarillo	AR21004	-38.1	-62.2	295
Bolivia	Checchi	BOV Comp.	-18.1	-65.8	2542
Bolivia	Huilcaparu Moteado	BOV Comp.	-16.9	-67.1	2760
Bolivia	Paru	BOV Comp.	-15.8	-68.7	2737
Bolivia	Uchuquilla	BOV318	-17.23	-66.11	1922
Brazil	Avati Pichinga	BR2760	-25.0	-56.0	366
Brazil	Avati Pichinga	BR2776	-25.0	-56.0	366
Brazil	Avati Pichinga Ihu	BR2830	-25.0	-56.0	366
Chile	Cristalino Chileno	CHI156	-38.1	-71.9	66
Colombia	Amagaceño	HUI317	2.5	-74.8	1554
Colombia	Harinoso Dentado	NAR326	1.4	-77.6	1400
Colombia	Montaña	NAR625	1.2	-77.3	2541.8
Colombia	Sabanero	ANT423	7.0	-75.7	1479.8
Colombia	Sabanero	CUN342	8.5	-75.5	250
Colombia	Comun	CAU454	2.2	-76.9	922
Ecuador	Chillo	ECU411	-0.3	-78.4	2510.3
Ecuador	Cubano Amarillo Duro	ECU326	-1.1	-80.5	40.8
Ecuador	Enano Gigante	ECU Comp.	-1.1	-78.0	915.6
El Salvador	Amarillo Salvadoreño	Comp.	13.8	-89.3	721
USA	Northeast Flint	WLB	41.7	-71.7	130
México	Raton	CHH191	28.8	-106.4	1885.3
Paraguay	Cateto Sabugo Grosso	PAG422	-26.0	-56.5	95
Peru	Amarillo Huancabamba	PIU38B	-5.2	-79.5	2000
Peru	Arequipeno	AREQ 1	-16.2	-71.3	2332
Peru	Chulpi	LIM66	-11.4	-77.4	110
Peru	Confite Puntigudo	CUZ13	-15.5	-70.1	3831.9
Peru	Cubano Amarillo	UCA8	-5.2	-75.7	129
Peru	Huancavelicano	HVC179	-13.0	-75.1	4562
Peru	Huayleno	ANC291	-9.53	-77.53	3059
Peru	Piricinco	SM8	-6.2	-76.6	940
Uruguay	Dentado Branco	URZM13010	-34.0	-56.0	104

Note : Coordinates are estimated from the publications of the Committee on Preservation of Indigenous Strains of Maize

Supplemental Table 2.7 Analysis of variance table for GLS

Source	DF	SS	MS	F Value	Pr > F
Model	2291	6343.3	2.77	6.23	<.0001
Error	1700	755.9	0.44		
Total	3991	7099.2			
R-Square	Coeff Var	Root MSE	GLS Mean		
0.89	14.49	0.67	4.6		

Supplemental Table 2.8 GLS analysis of variance by sources of variation

Wald F statistics				
Source	NumDF	DenDF	F Value	P Value
BC₁ F_{1s}	482	1458.9	3.4	<.001
Checks vs. BC₁ F_{1s}	1	340.8	113.02	<.001
Checks vs. Checks	5	334.1	87.8	<.001
DTA (as covariate)	1	1540.4	8.74	<.001
Random Effects				
Source	Component	Comp/SE	DF	
Env	0.58	1.19	3	
block(env)	0.04	2	12	
rep(block(env))	0.009	1.85	16	
col(env)	0.132	8.63	273	
row(env)	0.002	0.82	64	
line*env	0.119	8.16	1434	

Supplemental Table 2.9 Analysis of variance table for NLB

Source	DF	SS	MS	F Value	Pr > F
Model	1655	5252.06	3.17	6.03	<.0001
Error	1347	708.31	0.53		
Total	3002	5960.38			

R-Square	Coeff Var	Root MSE	NLB Mean
0.88	13.76	0.73	5.27

Supplemental Table 2.10 NLB analysis of variance by sources of variation

Wald F statistics				
Source	NumDF	DenDF	F Value	P Value
BC₁ F_{1s}	482	944.8	3.65	<.001
Checks vs. BC₁ F_{1s}	1	310.4	8.38	<.001
Checks vs. Checks	5	307.4	27.43	<.001
DTA (as covariate)	1	2392.1	15.94	<.001

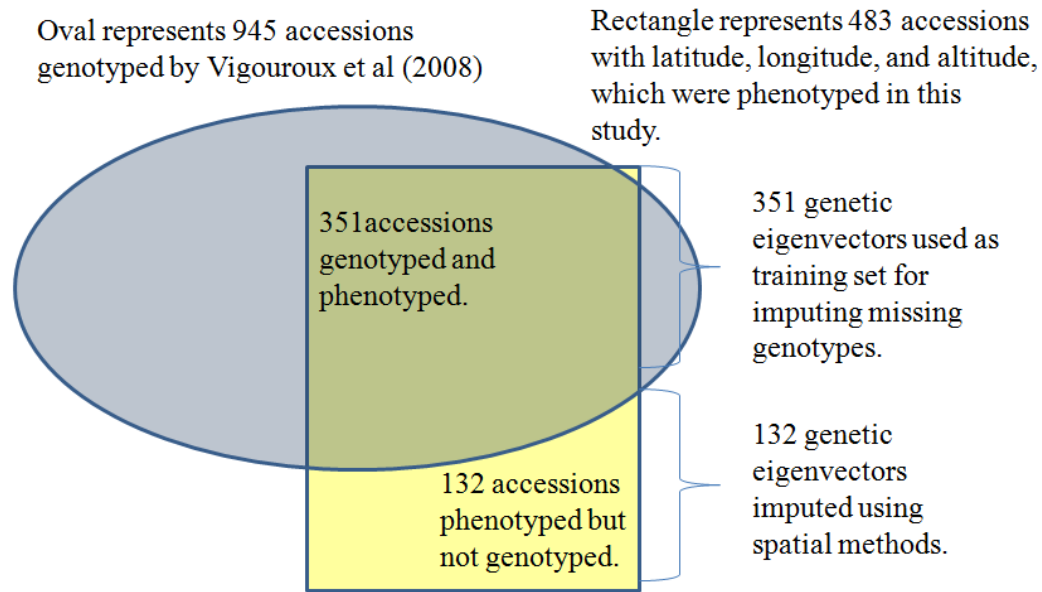
Random Effects			
Source	Component	Comp/SE	DF
Env	0.13	0.91	2
block(env)	0.03	1.3	9
rep(block(env))	0.025	1.35	12
col(env)	0.033	3.91	98
row(env)	0.042	3.81	88
line*env	0.23	9.1	957

Supplemental Table 2.11 Analysis of variance table for SLB

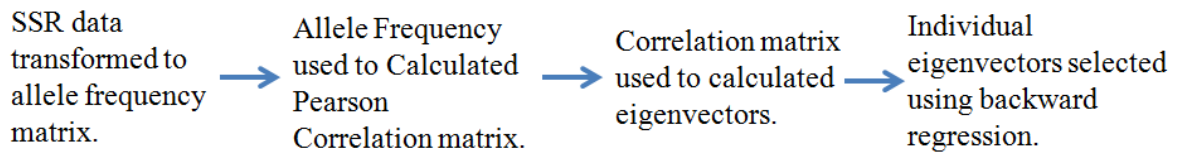
Source	DF	SS	MS	F Value	Pr > F
Model	1719	2796.5	1.62	6.23	<.0001
Error	1291	381.6	0.3		
Total	3010	3178.1			
R-Square	Coeff Var	Root MSE	SLB Mean		
0.88	10.66	0.54	5.1		

Supplemental Table 2.12 SLB analysis of variance by sources of variation

Wald F statistics				
Source	NumDF	DenDF	F Value	P Value
BC₁ F_{1s}	482	998.9	3.29	<.001
Checks vs. BC₁ F_{1s}	1	213	264.73	<.001
Checks vs. Checks	5	207.2	87.3	<.001
DTA (as covariate)	1	1060.9	80.72	<.001
Random Effects				
Source	Component	Comp/SE	DF	
Env	0.046	0.86	2	
block(env)	0.0078	0.63	9	
rep(block(env))	0.022	2.05	12	
col(env)	0.038	5.2	123	
row(env)	0.014	3.01	123	
line*env	0.063	5.97	961	



Process used to develop genetic covariates



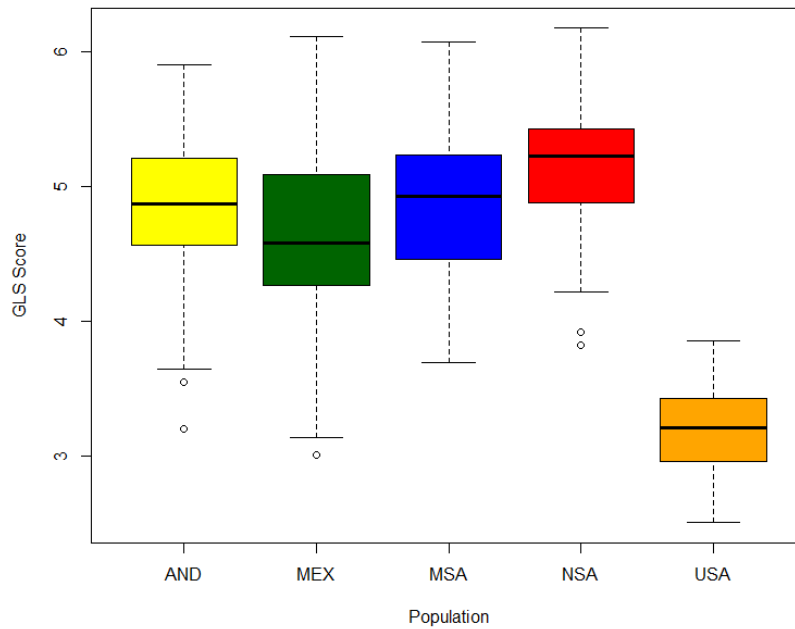
Supplemental Figure 2.1 Development of genotypes used as covariates in analysis.

Supplemental Table 2.13 Tukey test for GLS scores in maize populations

Population	Mean	SE	Set[†]
NSA	5.16	0.07	a
MSA	4.85	0.08	b
AND	4.84	0.05	b
MEX	4.62	0.06	b
USA	3.20	0.06	c

HSD = 0.28

[†]Groupings are based on Tukey HSD, and show which populations are significantly different from one another at $\alpha=0.05$.



Supplemental Figure 2.2 Boxplot of WMD GLS scores by maize population[†]

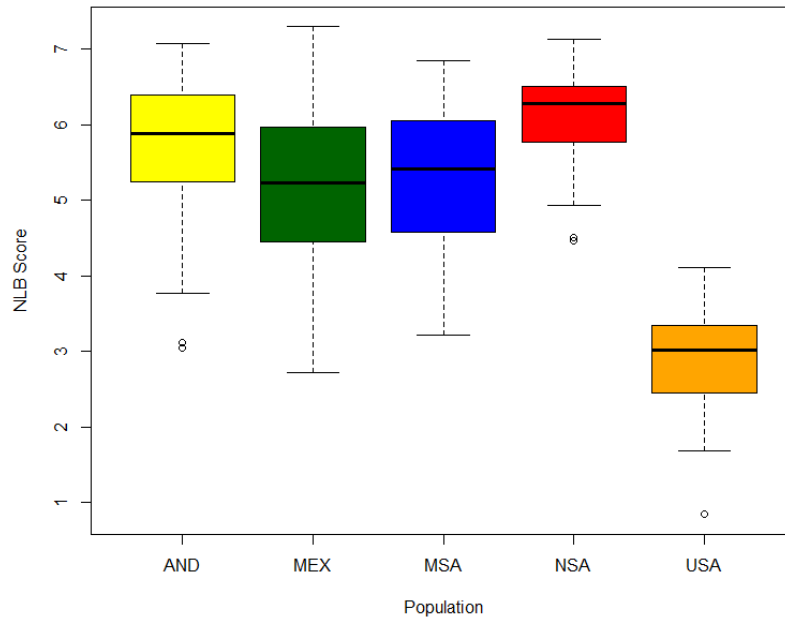
[†]Andean (AND), Mexican (MEX), Middle South America (MSA), Northern South America (NSA), and United States of America (USA). Bold line inside box represents the median, the bottom and top of the box are the first and third quartiles. Whiskers represent 1.5 times the first and third interquartile range. Circles represent scores outside this 1.5 inter quartile range.

Supplemental Table 2.14 Results from Tukey test for NLB scores in maize populations

Population	Mean	SE	Set[†]
NSA	6.13	0.08	a
AND	5.71	0.09	ab
MSA	5.30	0.14	bc
MEX	5.18	0.1	c
USA	2.90	0.10	d

HSD= 0.45

[†]Groupings are based on Tukey HSD, and show which populations are similar or different from one another at $\alpha=0.05$.



Supplemental Figure 2.3. Boxplot of WMD NLB scores by maize population[†]

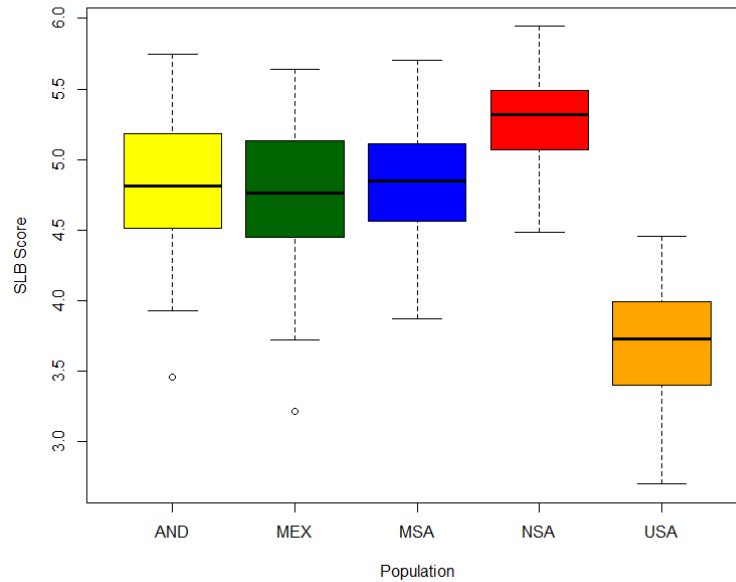
[†] Andean (AND), Mexican (MEX), Middle South America (MSA), Northern South America (NSA), and United States of America (USA). Bold line inside box represents the median, the bottom and top of the box are the first and third quartiles. Whiskers represent 1.5 times the first and third interquartile range. Circles represent scores outside this 1.5 inter quartile range.

Supplemental Table 2.15 Results from Tukey test for SLB scores in maize populations

Population	Mean	SE	Set[†]
NSA	5.29	0.05	a
AND	4.83	0.05	b
MSA	4.82	0.06	b
MEX	4.78	0.05	b
USA	3.73	0.07	c

HSD = 0.22

[†]Groupings are based on Tukey HSD, and show which populations are similar or different from one another at $\alpha=0.05$.



Supplemental Figure 2.4 Boxplot of WMD SLB scores by maize population†

†Andean (AND), Mexican (MEX), Middle South America (MSA), Northern South America (NSA), and United States of America (USA). Bold line inside box represents the median, the bottom and top of the box are the first and third quartiles. Whiskers represent 1.5 times the first and third interquartile range. Circles represent scores outside the 1.5 inter quartile range.

Supplemental Table 2.16 Comparison of percent of variation accounted for by four different types of models.

Trait	OLS	OLS w/ genetic covariates	Spatial	Spatial w/ genetic covariates
GLS	10.6	43.3	50.3	59.1
NLB	7.7	56.6	59.9	63.2
SLB	7	40.1	62.8	62.9

Note: Ordinary Least Squares (OLS), and Spatical methods, using latitude, longitude, and altitude, with and without genetic data used as covariates. Values calculated using the R^2 in the OLS models, and from the five-fold cross validation for the spatical methods.

Supplemental Table 2.17 Parameter estimates for the Matérn Spatial model developed for the three diseases

Model Parameters	GLS	NLB	SLB
Intercept	4.80	3.76	4.26
Latitude [†]	0.01	0.04	0.01
Longitude	-0.01	-0.03	-0.02
Altitude	0.00	0.00	0.00
Eigenvector 1 [‡]	0.05	-0.05	0.05
Eigenvector 2	0.02	0.14	0.03
Eigenvector 3	NA	0.06	0.02
SigmatSq (partial sill) [§]	0.72	56.60	2.56
Phi (range) [¶]	380.80	24.43	8.60
Kappa [#]	0.19	6.63	14.37
Anisotropy angle ^{††}	3.31	0.00	1.94
Anisotropy ratio	1.00	1.06	2.13
Tau sq (nugget) ^{‡‡}	0.11	0.39	0.17

[†]Note: latitude, longitude, and altitude are all important covariates even though estimates are close to zero.

[‡]For each disease a different set of genetic covariates were used in the spatial model. For the GLS the 3rd and 38th Eigenvectors were used, for NLB the 2nd 3rd and 10th Eigenvectors, and for SLB the 3rd, 23rd and 63rd were used.

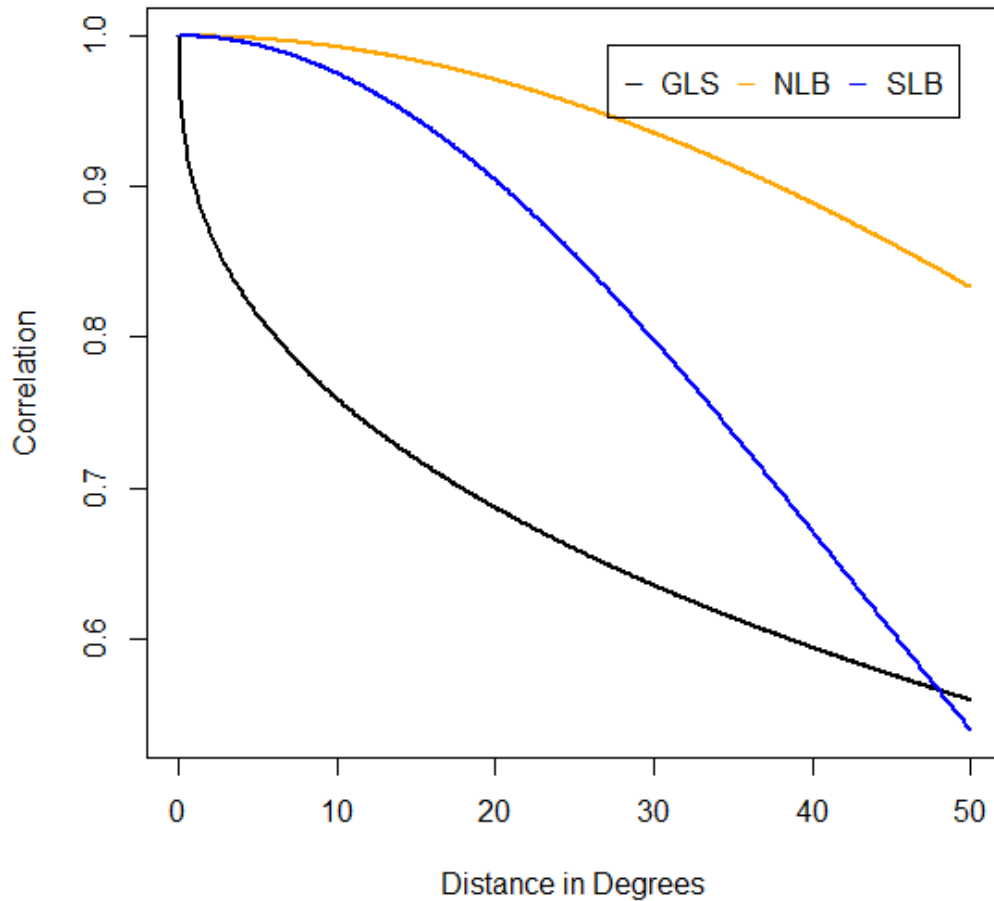
[§]SigmatSq or the partial sill is a parameter of the semivariogram model that represents the variance of a spatially autocorrelated process of disease scores without any nugget effect. In the semivariogram model, the partial sill is the difference between the nugget and the sill.

[¶]Phi (range) is a distance measure in degrees that represents a distance beyond which there is little or no autocorrelation among variables.

[#]Kappa is a smoothness parameter, explains how much the variances fluctuates over distance.

^{††}Anisotropy angle is the direction in which the data is varying. Anisotropy ratio regulates the dependency on anisotropy angle.

^{‡‡}Tau sq (nugget) is measurement error of sampling disease scores of BC₁F₁s at small distances.



Supplemental Figure 2.5 Covariance functions for Matérn models for GLS, NLB, and SLB[†]

[†] This figure gives us an indication of the spatial trends in these diseases, NLB has the furthest range, followed by SLB, and GLS. Note one interpretation may be that NLB resistance does not change much across small distances. One reason for this could be the NLB pathogen is more broadly adapted, thus NLB resistance may have been selected for uniformly across geography. GLS does not have high correlations over the same range, which may indicate that there are more micro-environment effects in the evolution of GLS resistance. All of the diseases show a decrease in correlation as distance increases.

Supplemental References

- Benson J, 2013. Resistance to gray leaf spot of maize: Underlying genetic architecture and associated mechanisms. Cornell University Dissertation. <http://hdl.handle.net/1813/34022> (accessed June 18, 2014)
- Brieger FG, Gurgel JTA, Paterniani E, Blumenschein A, Alleoni MR, 1958. Races of maize in Brazil and other eastern South American countries. National Academy of Science-National Research Council Washington, DC, USA
- Brown WL, 1960. Races of maize in the West Indies. National Academy of Sciences. National Research Council, Washington, DC, USA
- Committee on Preservation of Indigenous Strains of Maize, 1954. Original Strains of Corn, I. National Academy of Sciences, National Research Council, Washington, D.C.
- Committee on Preservation of Indigenous Strains of Maize, 1955. Original strains of corn, II. National Academy of Sciences, National Research Council, Washington, D.C.
- Sanchez G. JJ, Goodman MM, Stuber C. 2000. Isozymatic and morphological diversity in the races of maize of Mexico. *Econ. Bot.* 54:43-59.
- Grant UJ, Hatheway WH, Timothy DH, Cassalet DC, Roberts LM, 1963. Races of maize in Venezuela. National Academy of Sciences. National Research Council, Washington, DC, USA
- Grobman A, Salhuana W, Sevilla R, with Mangelsdorf PC, 1961. Races of maize in Peru. National Academy of Sciences. National Research Council, Washington, DC, USA
- Hatheway WH, 1957. Races of maize in Cuba. National Academy of Sciences. National Research Council, Washington, DC, USA
- Kump KL, Bradbury PJ, Wisser RJ, Buckler ES, Belcher AR, Oropeza-Rosas MA, Zwonitzer JC, Kresovich S, McMullen MD, Ware D, Balint-Kurti PJ, Holland JB, 2011. Genome-wide association study of quantitative resistance to southern leaf blight in the maize nested association mapping population. *Nat Genet* 43:163-168
- McMullen MD, Kresovich S, Villeda HS, Bradbury P, Li H, Sun Q, Flint-Garcia S, Thornsberry J, Acharya C, Bottoms C, Brown P, Browne C, Eller M, Guill K, Harjes C, Kroon D, Lepak N, Mitchell SE, Peterson B, Pressoir G, Romero S, Oropeza M Rosas, Salvo S, Yates H, Hanson M, Jones E, Smith S, Glaubitz JC, Goodman MM, Ware D, Holland JB, Buckler ES, 2009. Genetic properties of the maize nested association mapping population. *Science* 325:737-740

- Paterniani E, Goodman MM, 1977. Races of maize in Brazil and adjacent areas. CIMMYT, Mexico City, Mexico.
- Poland JA, Bradbury PJ, Buckler ES, Nelson RJ, 2011. Genome-wide nested association mapping of quantitative resistance to northern leaf blight in maize. PNAS 108:6893-6898
- R. Ramírez E, Timothy DH, Díaz BE, Grant UJ, with GE Nickerson C, Anderson E, Brown W, 1960. Races of maize in Bolivia. National Academy of Sciences, National Research Council, Washington, DC, USA
- Roberts LM, Grant UJ, R. Ramírez E, Hatheway WH, Smith DL, with Mangelsdorf PC, 1957. Races of maize in Colombia. National Academy of Sciences, National Research Council, Washington, DC, USA
- Timothy DH, Hatheway WH, Grant UJ, Torregroza CM, Sarria VD, Varela AD, 1963. Races of maize in Ecuador. National Academy of Sciences, National Research Council, Washington, DC, USA
- Timothy DH, Peña VB, R. Ramírez E, with Brown WL, Anderson E, 1961. Races of maize in Chile. National Academy of Sciences, National Research Council, Washington, DC, USA
- Wellhausen EJ, Fuentes OA, Hernández-Corzo A, with Mangelsdorf PC, 1957. Races of maize in Central America. National Academy of Sciences, National Research Council, Washington, DC, USA
- Wellhausen EJ, Roberts LM, E. Hernández X., with Mangelsdorf PC, 1952. Races of maize in Mexico: Their origin, characteristic and distribution. Bussey Institution of Harvard University, Cambridge, Massachusetts, USA

-CHAPTER III-

Evaluation of Agronomic Traits in a Set of Semi-Exotic Maize Germplasm Using Population and Spatial Methods

Prepared for submission to *Maydica*

O. O. Ott^{1*}, B. J. Riech², M.M. Goodman¹, J. B. Holland^{1,3}, M. D. Krakowsky^{1,3}

¹Department of Crop Science, NC State University, Raleigh, NC, USA 27695

²Department of Statistics, NC State University, Raleigh, NC, USA 27695

³USDA-ARS. Plant Science Research Unit, Raleigh, NC, USA 27695

*Corresponding author: E-mail:oliver.o.ott@gmail.com

Keywords: maize, flowering time, lodging, accessions, spatial analysis, Kriging

Abstract

The germplasm base of U.S. maize is narrow, with six inbred lines appearing in the pedigrees of 76% of formerly proprietary inbreds that are currently available, based on a recent analysis, through the North Central Plant Introduction Station in Ames, IA. Maize landraces may provide a resource to enhance maize diversity, but their agronomic performance generally hampers their use. In conjunction with the Germplasm Enhancement of Maize Allelic Diversity project, a set of maize landrace accessions has been backcrossed to the Dupont Pioneer formerly proprietary inbred line PHB47. The landrace backcrosses were evaluated for days to anthesis (DTA) and silk (DTS) and lodging, and maize populations were examined for trends in these traits. Accessions from the Northern South America and Middle South America geographic regions tended to be the latest flowering and had lowest lodging rates, followed by accessions from the Andean, Mexican, and USA geographic regions. The spatial geography of these traits was examined using a Matérn spatial model. This model was used in Kriging to predict trait scores of BC₁F_{1s} with theoretical donor parents collected at locations that were not sampled herein. Spatial models accounted for 42, 38, and 47% of the variation across the Americas in DTA, DTS, and lodging respectively. Phenotyping standard errors (SE) and spatial prediction SEs were similar, demonstrating the spatial model's ability to predict trait scores. Anthesis-silk interval was also examined but did not show a subpopulation or spatial pattern. These methodologies form a framework by which researchers can more precisely target accessions of interest to a research program.

Introduction

Maize (*Zea mays L.*) yields in the U.S.A. have increased greatly over the last 80 years. In 1930, the average maize yield was 1.2 MT/ha while in 2013 that value increased to 10 MT/ha (Duvick, 2005; U.S.D.A.–National Agricultural Statistics Service, 2014). This great increase in productivity was due to improvements in both agricultural practices and in hybrid maize varieties (Duvick, 2005). Developments in hybrid maize have focused on improvements in density tolerance, stress resistance, and yield potential. As yield trials are expensive, several maize traits that are important indicators of commercial suitability are assessed in breeding nurseries prior to yield trials, including male and female flowering time and lodging (Troyer, 1996).

Flowering time is important as it integrates environmental signals that control the timing for the transition from the vegetative to the reproductive growth (Colasanti and Muszynski, 2009). Flowering at the correct time can help with the plant avoid drought, prevent kernel abortion, and optimize the light interception period in order to maximize yield potential. Flowering too late delays pollination and the formation of starch, prevents adequate dry down of the grain, and wastes available light energy (Muchow et al, 1990). Elite breeding programs have flowering time highly tailored to the environment that each breeding program is targeting. Consequently flowering time generally does not vary considerably within a breeding program, so as to not waste resources on lines with no commercial prospects (Duvick et al, 2004). The difference between the timing of male and female flowering' or anthesis silk interval (ASI), is also of importance to maize improvement. Extended ASI

indicate that silks emerge well after pollen shed, which may lead to insufficient pollination and loss of yield (Edmeades et al, 1993). A connection between ASI and stress tolerance has also been noted, where by plants under drought stress often have longer ASI than unstressed plants (Fischer et al, 1989). Increased ASI is also undesirable as it makes self-pollination in a breeding nursery very difficult. If a line does not set adequate seed, it is unlikely to be carried forward to subsequent generations.

Lodging and intactness of plants at harvest time only became a real concern with the mechanization of agriculture. Prior to this, maize was tended to by hand and a corn plant that lodged before harvest could still be picked. With mechanization came the need for all plants to be erect in order for harvest machinery to function with minimal yield loss. Several physiological traits have been assessed for their use in selection for lodging resistance, including stalk compressive strength, stem diameter, pith density, and rind penetration resistance (Abedon et al, 1999; Hondroyianni et al, 2000; Thompson, 1969; Zuber and Kang, 1978). Lodging can be influenced by the presence of pathogens which can cause stalk rot (Anderson and White, 1994). Lodging is also connected with flowering time, as plants that flower early and senesce early deteriorate and become un-harvestable more quickly. It is this time between flowering and senescence that is critical to the occurrence of lodging (Borrell et al, 2001). Plants that can “stay green” are more likely to stay erect. Ideally senescence can enable the drying down of the grain in the ear but allow the rest of the plant to remain green so as to help prevent lodging.

In general, non-elite, non-temperate-adapted (or “exotic”) germplasm is later flowering and has higher rates of lodging than improved U.S.A. germplasm. However, there

is variation in maize accessions for flowering time and lodging propensity (Gutiérrez et al, 2003; Kuleshov, 1933). Tropical germplasm has also often been suggested as source of germplasm to increase the productivity of temperate maize (Goodman, 2005; Lonquist, 1974; Melhus, 1948). Tropical and temperate maize landraces provide one such source of genetic variation, but are often difficult to work with, tending to be later flowering, taller, and more prone to lodging than elite, temperate-adapted germplasm, making them unappealing to breeders.

Some of the aversion to working with landraces may be due to the lack of information available to breeders as to which accessions have the most agronomic potential. Breeders continue to use elite inbred lines that have supporting information, and this continual recycling of inbred lines has led to a narrowing of the germplasm base of maize in the U.S.A compared to the amount of genetic variability available in domesticated maize. Troyer (2004) pointed out that five popular, widely adapted, open-pollinated cultivars account for 87% of the background of today's U.S.A. hybrid maize. These cultivars were used to derive the relatively small number of inbred lines that make up a majority of breeding germplasm in the U.S.A., with six lines --B73, A632, Mo17, PH207, Oh43, and B37-- contributing to 76% of pedigrees of inbred lines formerly covered by Plant Variety Protection (ex-PVPs; Nelson et al, 2008). There is concern that this narrowing of the germplasm pool may limit flexibility and ability to respond to maize production challenges (Goodman, 1999).

In order to widen the maize gene pool in the U.S.A., the Germplasm Enhancement of Maize (GEM) project was implemented by the USDA-ARS, involving both public and private research scientists (Pollak, 2003). Currently GEM involves the cooperation of 28

private cooperators (GEM, 2014). Germplasm accessions that have been selected for their potential usefulness as parents, based on agronomics, are crossed by private companies to their proprietary inbreds. To date, a relatively small number of maize landraces (~25) have been used in GEM releases. This fact led to concern that a large amount of genetic diversity may be under-sampled due to the emphasis put on agronomic quality when choosing exotic germplasm for use in GEM. In an effort to represent more racial diversity, GEM initiated the Allelic Diversity (AD) project with a goal of developing adapted sources of germplasm representing a majority of the ~300 races of maize. The accessions used to represent the races of maize are those already in the collections at NCSU, largely the typical accessions of each race as listed by the Committee on Preservation of Indigenous Strains of Maize (Clark, 1956). In order to sample the allelic diversity of maize landraces, accessions are backcrossed, without selection, to the ex-PVP inbred line, PHB47 (PI 601009). The Allelic Diversity project plans to develop inbred or double haploid lines from these BC₁ F₁s, which could be used as a genetic tool for allele mining or QTL mapping (Krakowsky et al, 2008).

The BC₁ F₁s provide a germplasm resource which may, when phenotyped, give an indication as to important patterns of agronomic traits of maize landraces, both within maize populations and across geography. BC₁ F₁s can be informative due to the random dispersal of flowering time genes across the maize genome, as observed in the nested association mapping (NAM) population (Supplemental Table 3.1; Buckler et al, 2009). Genes which control lodging are also assumed to be randomly dispersed. This is important as it would be difficult to generalize from BC₁ F₁s for traits that are controlled by few genes that are not randomly dispersed due to the potential for high plant to plant variability. Thus, screening of

a BC₁ F₁ examines a random sample of the genes from the landrace that control a given trait with the potential to identify landraces that have accumulated multiple alleles at one tail of the trait distribution for male and female flowering time and lodging. This may give an indication as to which landrace accessions are the best targets for incorporation into breeding programs.

Methods and Materials

Germplasm

To develop AD BC₁ F₁s used herein, maize landrace accessions were backcrossed to the Dupont Pioneer ex-PVP inbred line PHB47 (PI 601009; no PHZ51 crosses were used in this study). One to eighteen plants from the landrace were crossed either as male or female to PHB47 to develop the F₁ hybrid. A large proportion of F₁s were produced in off-season nurseries due to photoperiod sensitivity that occurs in tropical germplasm. Supplemental Table 3.2 provides the year, location and the numbers of plants used to produce F₁s and the year and number of plants used to produce BC₁ F₁s. Once F₁s were produced, 3 to 26 plants from the F₁ were used to produce the BC₁ F₁s. This was conducted in summer and winter nurseries in Clayton, NC and Homestead, FL, respectively, from 2005 to 2012. A balanced bulk was then made from the BC₁ F₁s seed for these experiments. Supplemental Table 3.3 presents a full list of landraces included in this study with country of origin, race name, accession name, landrace seed source, collection coordinates, and altitude of collection.

Trait Evaluation

Four hundred and sixty-eight BC₁ F₁s were evaluated in 2012, with 483 BC₁ F₁s evaluated in 2013, primarily as part of a disease study. Male and female flowering time and lodging were taken to assess BC₁ F₁s' agronomic qualities. The BC₁ F₁s were evaluated in

both 2012 and 2013 at the North Carolina State University Central Crops Research Station, Clayton, NC, the North Carolina State University Piedmont Research Station in Salisbury, NC, the Wood Farm in Andrews, NC (in cooperation with DuPont Pioneer (Johnston, IA)), and the DuPont Pioneer Research Station in Windfall, IN. The Monsanto (St. Louis, MO) Research Station in Thomasboro, IL, and the DuPont Pioneer Research Station in Cairo, GA, were added in 2013.

Trials at all locations were arranged using an augmented replication within sets design. BC₁ F₁s were grouped into four sets by flowering time collected on the accessions in crossing nurseries, with two replications of each block planted adjacently. Six checks were included in each block, five of which were F₁ hybrids including, PHB47 x NC 296, DKHBA1 x PHB47, Pioneer 33M54, Pioneer 3394, and PHB47 x DJ7. The sixth check was the recurrent parent PHB47; the available pedigree and release information of checks is presented in supplemental Table 3.4. The experimental units consisted of single row plots with dimensions and seed quantities provided in Supplemental Table 3.5. Plots were maintained using the cultivation practices common to each of the trial locations. Irrigation was used at the DuPont Pioneer Research Station in Cairo, GA, and NCSU Central Crops Research Station, Clayton, NC, while the Piedmont Research Station in Salisbury, NC, Wood Farm in Andrews, NC, DuPont Pioneer Research Station in Windfall, IN, and Monsanto Research Station in Thomasboro, IL were rain fed.

Flowering time was scored in two ways, as days to anthesis (DTA), the number of days from planting to pollen shed of 50% of plants in a row, and as days to silk (DTS), the number of days from planting to emergence of silk on main ear of 50% of plants in a row.

DTA was collected in five environments: Clayton, NC, and Andrews, NC, in 2012 and 2013; and Thomasboro, IL, in 2013. DTS was collected at Clayton NC in 2012 and 2013. Lodging was assessed, typically, six to eight weeks after peak flowering, if the location had notable lodging pressure. Lodging was rated on a one to nine scale with one representing all plants in row lodged, and nine representing all plants in row still erect. Lodging was rated in six environments: at Clayton, NC, Andrews, NC, in 2012 and 2013; at Windfall, IN in 2012; and at Salisbury, NC, in 2013.

Data Analysis

To calculate the least squared mean (LSM) of DTA and DTS, a model was developed using ASReml v. 3.0 software (Gilmour et al, 2009). The model included BC₁ F₁s as a fixed effect, and the random effects included environment, blocks within environment, replications within blocks within environment, and field range (row) and plot (column) as position effects within environment (Brownie et al, 1993), and the interaction of BC₁ F₁s and environment. The model used to estimate lodging LSMs included BC₁ F₁ and DTA (as a covariate) as fixed effects; flowering time is known to affect some agronomic traits. The random effects for lodging were the same as in the above model. In order to separate effects of the six checks from the experimental lines, dummy variables were added to the data set as outlined by Piepho et al (2006), which allowed for comparisons of checks to experimental lines and to one another and of experimental BC₁ F₁s to one another. Once LSMs for DTA and DTS were estimated, ASI was calculated as the difference between the LSMs of DTS and DTA.

Trait values within maize landrace populations were examined once LSMs of BC₁ F₁s had been estimated. Maize landrace population analysis was previously conducted on 945

accessions by Vigouroux et al (2008). Of those accessions, 347 were included in this study, and were able to be assigned to a population. Accessions were divided using individual plant neighbor-joining based upon the log-transformed proportion of shared alleles between individuals, to develop a hierarchical tree of maize relationships. Vigouroux et al (2008) identified nine populations of maize; however, our sampling across populations was not uniform across the nine populations, leaving little power to detect differences in under-sampled populations. Thus, populations with fewer than twenty-five accessions were merged with the populations in which they are nested, based on the hierarchical tree. Caribbean accessions were placed in the Northern South America population (NSA; n=52), to which they are closely related, while Southwest U.S.A., Northern U.S.A., and Chilean accessions (many Chilean materials trace their ancestry to U.S.A. sources) were merged to form a USA population (n=40), and Southeast U.S.A. accessions (many of which were brought to Brazil after the American Civil War (Brieger et al, 1958)) were merged with the Middle South America population (MSA; n=48). The Mexican (MEX; n=114) and Andean (AND; n=92) populations were kept intact, as they were well sampled. Thus for our purposes, five populations were examined for flowering time and lodging. The means of the LSMs of BC₁ F₁s with a donor parent within each of the populations were examined. A Tukey HSD test was conducted to determine if there were significant differences in average trait scores between maize populations using R v. 2.15.2 (R Core Team, 2013).

The spatial process of each of these traits was examined as a way to predict phenotypes of BC₁ F₁s with donor parent accessions collected at locations not represented in this study, but potentially available from germplasm banks. This analysis utilized the spatial

coordinates of the collection locations of the donor parent accessions. The great majority of the landraces had coordinates provided by Vigouroux et al (2008). For those that did not, coordinates were determined in three ways. First, the International Center for Maize and Wheat Improvement (CIMMYT) was contacted for information on collection locations (Kevin Pixley, personal communication). Second, collection data was used which had been compiled by José de Jesús Sánchez-González at the University of Guadalajara (personal communication). If no accession collection data could be found, then the approximate collection location was used, as noted by the publications of the Committee on Preservation of Indigenous Strains of Maize (Brieger et al, 1958; Brown, 1960; Grant et al, 1963; Grobman et al, 1961; Hatheway, 1957; Ramírez et al, 1960; Roberts et al, 1957; Timothy et al, 1961; 1963; Wellhausen et al, 1952; 1957). Accessions with estimated collection locations are noted in Supplemental Table 3.6. In cases where no collection altitude was given by the above sources, altitude was estimated by using GPS Visualizer (www.gpsvisualizer.com/elevation).

To predict the disease scores of BC₁ F₁s across the Americas at locations not sampled in this study, a Matérn spatial model was developed for each disease using latitude, longitude, and altitude using Ordinary Kriging with the geoR package of R v 2.15.2 (Cressie, 1992; Ribeiro Jr and Diggle, 2001). In order to improve model prediction accuracy, genotypic data for 96 simple sequence repeat markers (SSRs), as reported for accessions by Vigouroux et al (2008), were used as covariates. Several steps were involved in developing data which could be used as a covariate in the analysis. First the allele frequency matrix for the 351 landraces with data from Vigouroux et al (2008) that were used herein was generated

using PowerMarker V3.25 (Liu and Muse, 2005). Next this allele frequency matrix was used to calculate a Pearson correlation matrix for the markers from the 351 landraces. From this correlation matrix eigenvectors were calculated using R 2.15.2 (R Core Team, 2013). In total, 91 eigenvectors had eigenvalues over one. As it was computationally difficult to use all 91 eigenvectors in spatial analysis, the number of eigenvectors to be used was reduced. This was done by placing all 91 eigenvectors in a linear model as independent variables, with the phenotypic trait as the dependent variable, and eliminating eigenvectors using backwards stepwise selection, to minimize the Bayesian information criterion (BIC; Schwarz, 1978).

Once a reduced set of eigenvectors for each trait had been selected, the values for the 132 accessions which had phenotypic data, but which lacked genotypic data, were imputed using spatial methods, as the eigenvectors were observed to be following a spatial pattern. This was done by fitting a Matérn spatial model with a maximum likelihood function, using the accession collection-point latitude, longitude, and altitude (Matérn, 1986). This Matérn spatial model was then used to predict the values of the eigenvectors at the 132 locations where genotypic data was not available through Ordinary Kriging with the geoR package of R v 2.15.2 (Cressie, 1992; Ribeiro Jr and Diggle, 2001). These predicted eigenvectors were then merged with the real eigenvectors. This allowed for the use of a full data set with eigenvectors, latitude, longitude, and altitude as predictors in the spatial model. A visual representation of this is given in Supplemental Figure 3.1.

To predict the trait scores of BC₁ F₁s across the Americas at locations outside this study, a Matérn spatial model was developed for each trait using latitude, longitude, and altitude alone and with specific eigenvector covariates. Model parameters were calculated

using maximum likelihood with the geoR package of R v 2.15.2. After maximum likelihood estimation was conducted, each of the eigenvalue covariates was examined to determine if they were still significant when using the spatial model. This was done by calculating the standardized Z-statistic for the eigenvectors, using the beta for each eigenvector and its standard error, and removing covariates which had Z-values inside the range of ± 1.96 . Once a spatial model for each trait was developed, Ordinary Kriging was done to predict the trait scores for BC₁F₁s of accessions outside those used here. Locations which were farther than 5 degrees (~560 km) from the closest sampled data point herein were not predicted.

The predictive ability of both models (with and without genotypic data) were tested using five rounds of five-fold cross validation. This was done by randomly dividing that data into five parts, five different times. A model was estimated using four fifths of the data using the same Matérn spatial model methodology as was used for the entire data set. The resulting model was then used to estimate the trait scores for the remaining one fifth of the data. These estimates were then correlated with the observed phenotypes to test prediction accuracy. This was done five times in total, thus five-fold cross validation, using a different four fifths of the data each time. Total accuracy of prediction was defined as the average square of correlation coefficient between predicted values and observed phenotypes for the traits in the twenty-five validation samples.

Results and Discussion

In this study, a large number of geographically diverse maize landraces have been assessed for three traits that are of agronomic important to maize breeders and growers.

BC₁F₁ effects were significant ($p < .001$) for all traits measured. The ANOVA tables for the

analysis of DTA, DTS, and lodging are given in Supplemental Tables 3.7-3.12 (ASI was not estimated using ANOVA). DTA had an overall range from 59 to 70 days with a mean of 66, and DTS, which occurred 4 days later on average, ranged from 63 to 79 with a mean of 70. There was not a substantial amount of variation in ASI, which ranged from 2 to 9 days with a mean of 4. Only 15 BC₁ F₁s had an ASI value over 6. This may be due to female flowering time only being collected in irrigated locations, which may have not induced long ASIs.

Lodging ranged from 4.6 to 7.0 with a mean of 5.6, with higher numbers indicated lower levels of lodging. A list of the ten best and worst performing BC₁ F₁s for each trait is provided in Table 3.1. A full table of the trait scores and standard errors of the BC₁ F₁s assessed is given in Supplemental Table 3.3.

Many of the BC₁ F₁s showed flowering time and lodging levels similar to the best of the hybrid checks: PHB47x NC296, DK HBA1xPHB47, Pioneer 3394, and Pioneer 33M54. The phenotypic values of checks are provided in Supplemental Table 3.4. This gives the indication that several of the accessions could be used in temperate breeding programs, as only a single backcross was needed to bring lodging and flowering time within range of the lodging and flowering time of commercial hybrids.

Lines that could be considered good candidates for introducing genetic diversity into a temperate breeding program due to their early flowering, short ASI, and high standability include Havasupai (PI 317679), Zia Pueblo (PI 218139), Laguna Pueblo (PI 218169 and PI 218170), and Isleta-Tiwa (PI 218148). Accessions that could be of use in a tropical program include Caingang (SPX III), Cateto Sulino Grosso (URG III), Dente R. G. Rugoso (RGS II), Cateto (BOV 1083), and Chandelle (HTI 14). In Andean environments, some of the

accessions that would be of interest include Chaparreno (ARQ 34), Chancayano Pintado (LIM 46), Cubano Amarillo Duro (ECU 698), Argentino (BOV 920), and Arizona (LIB 16).

Pairwise phenotypic correlations between all traits were significant at ($p < 0.001$), with DTA and DTS having the largest correlation ($r^2 = 0.88$), the lowest correlation was between lodging and ASI ($r^2 = 0.093$). All pairwise comparisons, scatterplots, and histograms of traits can be seen in Figure 3.1. One interesting pattern is the positive correlation between flowering time and lodging. This may be due to many early-flowering families having completely senesced and their stalks and leaves deteriorated when lodging was scored. This is supported by the fact that DTA was significant ($p < 0.001$) covariate in the analysis of lodging as seen in Supplemental Table 3.12.

In examining DTA and DTS scores by donor parent populations, the population with the highest mean DTA score was Northern South America (NSA) at 67.5, followed by Andean (AND) at 66.8, Middle South America (MSA) 66.5, Mexican (MEX) at 66.0 and United States/Canada (USA) with 63.5. For DTA, the Tukey HSD at $\alpha = 0.05$ was 0.8, forming four sets, as can be seen in Supplemental Table 3.13. The NSA population forms part of set A, AND is part of both set A and B, MSA is part of set B and C, MEX in set C, and the USA population makes up set D (Supplemental Figure 3.2).

DTS follows the same grouping pattern as DTA, which is expected given the high correlation between the traits. Silk emergence was three to four days later on average than DTA with NAS at 72.0, AND at 71.5, MSA at 70.5, MEX at 70.0, and USA at 67.5, with a Tukey HSD at $\alpha = 0.05$ of 1.0, shown in Supplemental Table 3.14 and Supplemental Figure 3.3. ASI did not show any notable differences between maize populations. That there was not

more differentiation in flowering time between populations was unexpected, as flowering time is thought of as a trait that contributes greatly to population structure, by reproductively isolating populations (Remington et al, 2001).

In fact, the range between populations was smaller than that within a population. For example the largest difference in mean DTA between populations, that between the USA and NAS populations, is 4 days, while within population DTA ranges were larger with NSA at 7 days, AND at 7.5 days, MSA 4 days, MEX 8.5 days, and USA 7 days. Over the entire experiment there was a relatively small range in flowering time (~12 days) across the BC₁ F₁s.

Population means of lodging scores were 6.0 for NSA, 5.8 for AND, 5.6 for MEX, 5.6 for MSA, and 4.6 for USA. The Tukey HSD at $\alpha=0.05$ for lodging was 0.21, with four sets detected (Supplemental Table 3.15). NSA forms the most resistant set (set A), AND forms set B, MEX is in set C with MSA, and USA forms set D alone. A boxplot of trait scores by population can be seen in Supplemental Figure 3.4. Accessions from NSA are significantly better for lodging than AND, MSA and MEX, with donor parents from the USA population the most prone to lodging. This runs counter popular belief that later tropical material is more prone to lodge. The flowering time range was large enough that when lodging notes were taken, the early flowering families from more temperate regions may have been senescing for much longer than the tropical families, leading to decreased stalk strength and colonization of the stalk by pathogens, which may have increased rates of lodging.

To examine the spatial distribution of these agronomic traits across the Americas, the scores of the BC₁ F₁s at the point of collection of the donor accessions were placed on maps in Figures 3.2-3.4. These show spatial trends in the data for DTA, DTS, and lodging; these trends were further explored with Kriging predictions at unsampled locations. ASI did not show any spatial pattern, and predictions were not made. In these experiments ASI had a small range and did not display any trends among populations or across space. ASI is usually lengthened by drought stress, and the environments where DTS was scored were under irrigation and thus may have not been under enough stress to lengthen ASI.

Two sets of models were developed, one without the use of genotypic data for use as a covariate and one with. Fivefold cross-validation indicated the reduced spatial model accounted for 20% of the variation in DTA in the BC₁ F₁s, while the model with the genotypic data accounted for 42%, and thus the latter was used to produce kriging maps. Moreover, the prediction standard errors are smaller in the case of DTA than the standard errors of the experimental phenotypes themselves. Phenotyping standard errors (SEs) range from 2.05 to 2.09, while prediction SEs for DTA ranged from 0.91 to 1.54, as can be seen in Figure 3.5B. Kriging maps developed as a result of spatial analysis of DTA predict BC₁ F₁s with a donor parent collected in areas in Central America, Northern South American, and the Caribbean tend to be the latest flowering (Figure 3.5A). As the collection location moves further from the equator there is a trend toward earlier flowering of donor landraces. Of interest is the tendency for reduced flowering time in accessions collected in high altitude locations, as can be seen in the flowering times in the high altitude areas of Peru, Bolivia, and mountain ranges of Mexico. This may be due to selective pressure to complete the

reproductive cycle more quickly in cooler, high-altitude environments where growing seasons are shorter.

The prediction map of DTS is similar to that of DTA, with areas around the equator showing donor parents that are the latest flowering as seen in Figure 3.6A. Overall the reduced spatial model accounted for 21% of variation while the model which used eigenvectors accounted for 38% of the variation for DTS across the Americas, with prediction SEs ranging from 1.38 to 1.90 as seen in Figure 3.6B. These are slightly higher than the SE of the phenotypic estimates with a range of 1.36 to 1.60.

Spatial trends in lodging are similar to those found in DTA and DTS. Lodging incidence seems to be lowest around the equator with higher rates of lodging in the extreme North and South, as can be seen in Figure 3.7A. The reduced spatial model accounted for 46% of variation in lodging, this increased to 47% of the variation, with the inclusion of the genetic covariates. SEs of prediction for lodging are similar to those of the actual phenotypes ranging from 0.33 to 0.45, as can be seen in Figure 3.7B. These are somewhat smaller than then phenotyping SE which ranged from 0.65 to 0.74.

For all of these traits, the spatial model with the inclusion of genotypic data accounted for a higher percentage of variation across the Americas than ordinary least squares or a spatial model based solely on latitude, longitude, and altitude. The genotypic data that was useful varied between traits though. For DTA the 2nd, 3rd and 10th eigenvectors were used, while for DTS the 2nd, 3rd, 10th, 49th, and 80th eigenvectors were used. In the analysis of lodging the 2nd, 3rd, 11th, and 28th eigenvectors were used. Eigenvectors two and three were both significant for all of the traits analyzed here, and may be the eigenvectors

playing the biggest role in explaining the population structure of maize landraces. It is difficult to assign any more biological significance as to why any specific eigenvector is useful in developing predictions. Genotypes were compiled from a single plant from each landrace, and that single plant did not contribute to the BC₁ F₁s that were screened here, giving little credence to any conclusions that could be made. Supplemental Table 2.16 gives the amount of variation different types of models account for, Ordinary Least Squares, and Spatial methods, with and without the genetic covariates. Parameter estimates for the spatial models for DTA, DTS, and lodging can be seen in Supplemental Table 3.17. One interesting point of parameter estimates of spatial models is that kriging defines and models the disease scores at a local neighborhood, thus the parameter estimates for latitude, longitude, and altitude are close to zero and do not appear significant in the spatial analysis. The covariance functions for the three Matérn models for DTA, DTS, and lodging are given in Supplemental Figure 3.5, and they provide an indication as to how the correlation of these traits changes as the distance between points increases. The correlation between points for both DTA and DTS falls off rapidly with distance. This may be an indication of divergent selection which enabled flowering time to be tailored to a wide array of specific environmental conditions. Lodging, on the other hand, is very different, showing a large correlation over distance.

In summary, with a relatively small amount of genetic and location data, good predicted accuracy was obtained, given the vast area over which the accessions were collected. Other types of variables could also be used to help make predictions more robust,

including climate data or information about production systems. These would lead to models better able to target accessions which have desired traits of interest.

Using spatial methods to make predictions about accessions may be beneficial for several reasons; spatial methods may provide a method by which previous studies, which have assessed or made crosses with accessions, can be unified into a single predictive platform. This would allow researchers to better target accessions that would be most likely to be useful in their programs. This may reduce the size of screening efforts, and the cost to a researcher, and could be incorporated into a tool which researchers could use to develop core set for screening. Using population and spatial methodologies in conjunction with traditional methods of diversity analysis provides one avenue by which resources that germplasm banks offer can be more comprehensively utilized. This would leverage information that has already been collected, but that has not been fully utilized, and lay out a framework to enable full utilization of the resources that germplasm banks have to offer.

References

- Abedon BG, Darrah LL, Tracy WF, 1999. Developmental changes associated with divergent selection for rind penetrometer resistance in the MoSCSSS maize synthetic. *Crop Sci* 39:108-114
- Anderson B, White D, 1994. Evaluation of methods for identification of corn genotypes with stalk rot and lodging resistance. *Plant Dis* 78:590-593
- Borrell A, Hammer G, Oosterom E, 2001. Stay-green: A consequence of the balance between supply and demand for nitrogen during grain filling. *Ann Appl Biol* 138:91-95
- Brieger FG, Gurgel JTA, Paterniani E, Blumenschein A, Alleoni MR, 1958. Races of maize in Brazil and other eastern South American countries. National Academy of Science-National Research Council Washington, DC, USA
- Brown WL, 1960. Races of maize in the West Indies. National Academy of Sciences, National Research Council, Washington, DC, USA
- Brownie C, Bowman DT, Burton JW, 1993. Estimating spatial variation in analysis of data from yield trials: a comparison of methods. *Agron J* 85:1244-1253
- Buckler ES, Holland JB, Bradbury PJ, Acharya CB, Brown PJ, Browne C, Ersoz E, Flint-Garcia S, Garcia A, Glaubitz JC, Goodman MM, Harjes C, Guill K, Kroon DE, Larsson S, Lepak NK, Li H, Mitchell SE, Pressoir G, Peiffer JA, Rosas MO, Rocheford TR, Romay MC, Romero S, Salvo S, Sanchez Villeda H, da Silva HS, Sun Q, Tian F, Upadyayula N, Ware D, Yates H, Yu J, Zhang Z, Kresovich S, McMullen MD, 2009. The genetic architecture of maize flowering time. *Science* 325:714-718
- Colasanti J, Muszynski M, 2009. The maize floral transition, pp41-55. In: *Handbook of maize: its biology*. Bennetzen J, Hake S, eds. Springer, NY
- Clark, J. 1956. Collection, preservation and utilization of indigenous strains of maize. *J. Econ. Bot.* 10:194–200.
- Cressie N, 1992. Statistics for spatial data. *Terra Nova* 4:613-617
- Duvick D, 2005. Genetic progress in yield of United States maize (*Zea mays L.*). *Maydica* 50:193
- Duvick D, Smith J, Cooper M, 2004. Long-term selection in a commercial hybrid maize breeding program. *Plant Breed Rev* 24:109-152

- Edmeades G, Bolaños J, Hernandez M, Bello S, 1993. Causes for silk delay in a lowland tropical maize population. *Crop Sci* 33:1029-1035
- Fischer K, Edmeades G, Johnson E, 1989. Selection for the improvement of maize yield under moisture-deficits. *Field Crops Res* 22:227-243
- Germplasm Enhancement of Maize Website, 2014. www.publiciastate.edu/~usda-gem. (accessed 17 June 2014)
- Gilmour AR, Gogel B, Cullis B, Thompson R, 2009. ASReml user guide release 3.0. VSN International Ltd. Hemel Hempstead, UK
- Goodman MM, 1999. Broadening the genetic diversity in maize breeding by use of exotic germplasm, pp139-148. In: *The Genetics and Exploitation of Heterosis in Crops*. Coors JG, Pandey S, Gerdes JT eds. ASA-CSSA-SSSA, Madison, WI
- Goodman MM, 2005. Broadening the US maize germplasm base. *Maydica* 50:203
- Grant UJ, Hatheway WH, Timothy DH, Cassalet DC, Roberts LM, 1963. Races of maize in Venezuela. National Academy of Sciences. National Research Council, Washington, DC, USA
- Grobman A, Salhuana W, Sevilla R, with Mangelsdorf PC, 1961. Races of maize in Peru. National Academy of Sciences. National Research Council, Washington, DC, USA
- Gutiérrez L, Franco J, Crossa J, Abadie T, 2003. Comparing a preliminary racial classification with a numerical classification of the maize landraces of Uruguay. *Crop Sci* 43:718-727
- Hatheway WH, 1957. Races of maize in Cuba. National Academy of Sciences-National Research Council, Washington, DC, USA
- Hondroyianni E, Papakosta D, Gagianas A, Tsatsarelis K, 2000. Corn stalk traits related to lodging resistance in two soils of differing salinity. *Maydica* 45:125-133
- Krakowsky MD, Holley R, Deutsch J, Rice J, Blanco MH, Goodman MM, 2008. Maize allelic diversity project. Maize Genetics Conference Abstracts. 50th Maize Genetics Conference. Washington D.C. Feb 27 - Mar 2, 2008.
- Kuleshov N, 1933. World's diversity of phenotypes of maize. *J Am Soc Agron* Vol 25 10:688-700

- Liu K, Muse SV, 2005. PowerMarker: An integrated analysis environment for genetic marker analysis. *Bioinformatics* 21:2128-2129
- Lonnquist J, 1974. Consideration and experiences with recombinations of exotic and corn belt maize germplasm. *Corn and Sorghum Res. Conf. Proc.* 29:102-117
- Matérn B, 1986. *Spatial Variation: Meddelanden fran Statens Skogsforskningsinstitut*, Vol. 49, pp. 1–144, Ed. 2. Springer, Berlin.
- Melhus, L.E. 1948. Exploring the maize germ plasm of the tropics. p. 7-19 *In Proc. 3rd Annu. Hybrid Corn Ind. Res. Conf.*, Chicago, IL. 1-2 Dec. 1948. Am. Seed Trade Assoc., Washington, DC.
- Muchow R, Sinclair T, Bennett J, 1990. Temperature and solar radiation effects on potential maize yield across locations. *Agron J* 82:338-343
- National Agricultural Statistics Service, 2014. Crop production 2013 summary. US Dept Agr, Washington, DC.
<http://usda01.library.cornell.edu/usda/current/CropProdSu/CropProdSu-01-10-2014.pdf>
- Nelson PT, Coles ND, Holland JB, Bubeck DM, Smith OSC, Goodman MM, 2008. Molecular characterization of maize inbreds with expired US plant variety protection. *Crop Sci* 48:1673-1685
- Piepho H, Williams E, Fleck M, 2006. A note on the analysis of designed experiments with complex treatment structure. *Hort Sci* 41:446-452
- Pollak LM, 2003. The history and success of the public–private project on germplasm enhancement of maize (GEM). *Adv Agron* 78:45-87
- R Core Team, 2013. R: A Language and environment for statistical computing. R Foundation for Statistical Computing. Vienna, Austria, www.r-project.org
- R. Ramírez E., Timothy DH, Díaz BE, Grant UJ, with GE Nickerson C, Anderson E, Brown W, 1960. Races of maize in Bolivia. National Academy of Sciences, National Research Council, Washington, DC, USA
- Remington DL, Thornsberry JM, Matsuoka Y, Wilson LM, Whitt SR, Doebley J, Kresovich S, Goodman MM, Buckler IV ES, 2001. Structure of linkage disequilibrium and phenotypic associations in the maize genome. *PNAS* 98:11479-11484
- Ribeiro Jr PJ, Diggle PJ, 2001. geor: A package for geostatistical analysis. *R News* 1:14-18

- Roberts LM, Grant UJ, R. Ramírez E, Hatheway WH, Smith DL, with Mangelsdorf PC, 1957. Races of maize in Colombia. National Academy of Sciences, National Research Council, Washington, DC, USA
- Schwarz G, 1978. Estimating the dimension of a model. *Annals of Statistics* 6:461-464
- Thompson D, 1969. Selection for stalk quality in corn. *Annual Corn Sorghum Research Conference Proc.* 24:7-14
- Timothy DH, Hatheway WH, Grant UJ, Torregroza CM, Sarria VD, Varela AD, 1963. Races of maize in Ecuador. National Academy of Sciences, National Research Council, Washington, DC, USA
- Timothy DH, Peña VB, R. Ramírez E, with Brown WL, Anderson E, 1961. Races of maize in Chile. National Academy of Sciences, National Research Council, Washington, DC, USA
- Troyer AF, 1996. Breeding widely adapted, popular maize hybrids. *Euphytica* 92:163-174
- Troyer AF, 2004. Background of US hybrid corn II. *Crop Sci* 44:370-380
- Vigouroux Y, Glaubitz JC, Matsuoka Y, Goodman MM, Sánchez J, Doebley J, 2008. Population structure and genetic diversity of New World maize races assessed by DNA microsatellites. *Am J Bot* 95:1240-1253
- Wellhausen EJ, Fuentes OA, Hernández-Corzo A, with Mangelsdorf PC, 1957. Races of maize in Central America. National Academy of Sciences, National Research Council, Washington, DC, USA
- Wellhausen EJ, Roberts LM, E. Hernández X, with Mangelsdorf PC, 1952. Races of maize in Mexico: Their origin, characteristic and distribution. Bussey Institution of Harvard University, Cambridge, Massachusetts, USA
- Zuber M, Kang M, 1978. Corn lodging slowed by sturdier stalks. *Crops and Soils* 30:13-15

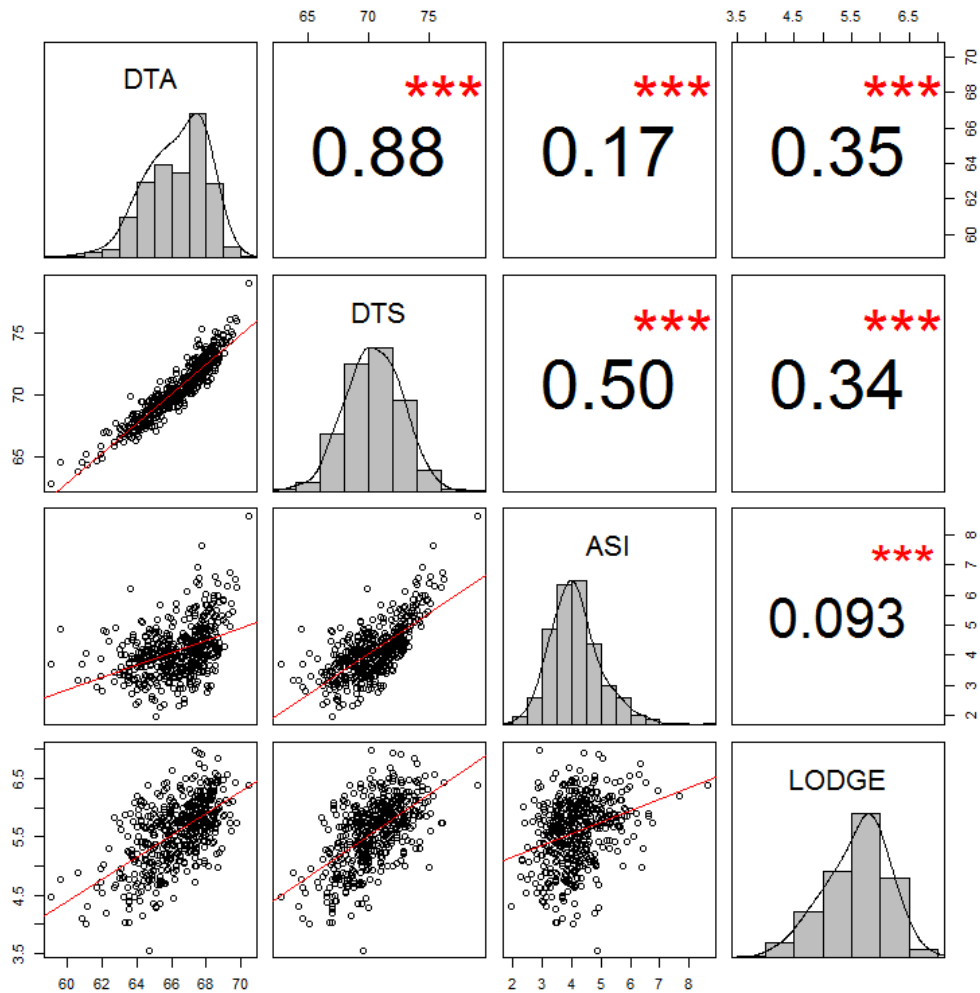


Figure 3.1 Pairwise correlations between observed traits

Upper diagonal indicates significance (***) level of pairwise linear regression and pairwise r^2 . Diagonal shows distribution of scores for each trait. Below diagonal shows the pairwise linear regressions and scatter of points.

Table 3.1 Range of performance values of BC₁F₁s for observed traits

Rank	Race	Accession	DTA	Race	Accession	DTS	Race	Accession	ASI	Race	Accession	Lodging [†]
483	Gaspe Flint	PI 401757	59.1	Gaspe Flint	PI 401757	62.8	Papago-Pimans	PI 217410	1.9	Tesuque Pueblo	PI 218137	3.56
482	Cristalino Chico	CHI 324	59.7	Bear Isl. Chippewa	P I213801	63.8	Argentine Pop	PI 217404	2.3	Shoshone	PI 213769	4
481	Bear Isl. Chippewa	PI 213801	60.6	Seneca Hominy Corn	PI 401754	64.3	Tabloncillo Perla	NAY 16	2.3	Winnebago	PI 213774	4.03
480	Longfellow Flint	PI 217408	60.8	Cristalino Chico	CHI 324	64.5	Pisankalla	BOV 864	2.3	Cristalino Amarillo	ARZM 19070	4.03
479	Shoshone	PI 213769	61.1	Longfellow Flint	PI 217408	64.5	Dentado Branco	URZM 13010	2.3	Longfellow Flint	PI 217408	4.1
478	Seneca Hominy Corn	PI 401754	61.1	Cristalino Amarillo	AR 21004	64.6	Morochon	ECU 454B	2.4	Hopi	PI 213733	4.14
477	Cristalino Amarillo	AR 21004	61.7	Longfellow	PI 214195	64.8	Mochero	LBQ 5	2.5	Cristalino Grande	CHI 323	4.19
476	Apachito	CHH 180	61.9	Shoshone	PI 213769	65.2	Chapalote	SIN 2	2.5	Smut Nose	PI 222490	4.26
475	Apachito	CHH 166	61.9	Apachito	CHH 180	65.2	Raton	CHH 191	2.5	Santo Domingo Pueblo	PI 218143	4.29
474	Longfellow	PI 214195	62	Apachito	CHH 166	65.8	Hualapai	PI 213741	2.5	Seneca Hominy Corn	PI 401754	4.3
	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮
10	Maranon	LIB 63B	69.1	Olotillo	CHS 53	74.9	Quicheno Late	GUA 863	6.3	Yunquillano F Ven Bl	ECU 853	6.54
9	Huanuco	HCO 128B	69.2	Quicheno Late	GUA 863	75	Amarillo Huancabamba	PIU 17B	6.4	Huanuco	HCO 128B	6.57
8	Conico Dentado	ECU 427	69.3	Capio	ANT 348	75.1	Motozinteco	CHS 650	6.4	Naltel BTA	GUA 20	6.59
7	Capio	ANT 354	69.3	Camba	BOV 1131	75.1	Capio	NAR 315	6.5	Canguil Grueso	ECU 443	6.63
6	Pepitilla	GRO 3	69.4	Alazan	LIB 34	75.4	Celaya	GTO 88	6.5	Montana	NAR 625	6.69
5	Camba	BOV 1131	69.4	Huanuqueno	HCO 128B	75.5	Capio	ANT 348	6.6	Amarillo Huancabamba	PIU 17B	6.75
4	Olotillo	CHS 53	69.5	Huevito	VEN 396	76	Capio	ANT 354	6.8	Chillo	ECU 458	6.84
3	Capio	NAR 315	69.7	Capio	ANT 354	76.1	Amarillo Huancabamba	PIU 38B	6.9	Tuxpeno	VEN 891	6.91
2	Huevito	VEN 396	69.7	Capio	NAR 315	76.2	Alazan	LIB 34	7.7	Uchima	ECU 681	6.93
1	Tehua	CHS 159	70.4	Tehua	CHS 159	79	Tehua	CHS 159	8.6	Costeno	ANT 394	6.99

[†]Lodging was rated on a one to nine scale with one representing all plants in row lodged, and nine representing all plants in row still erect.

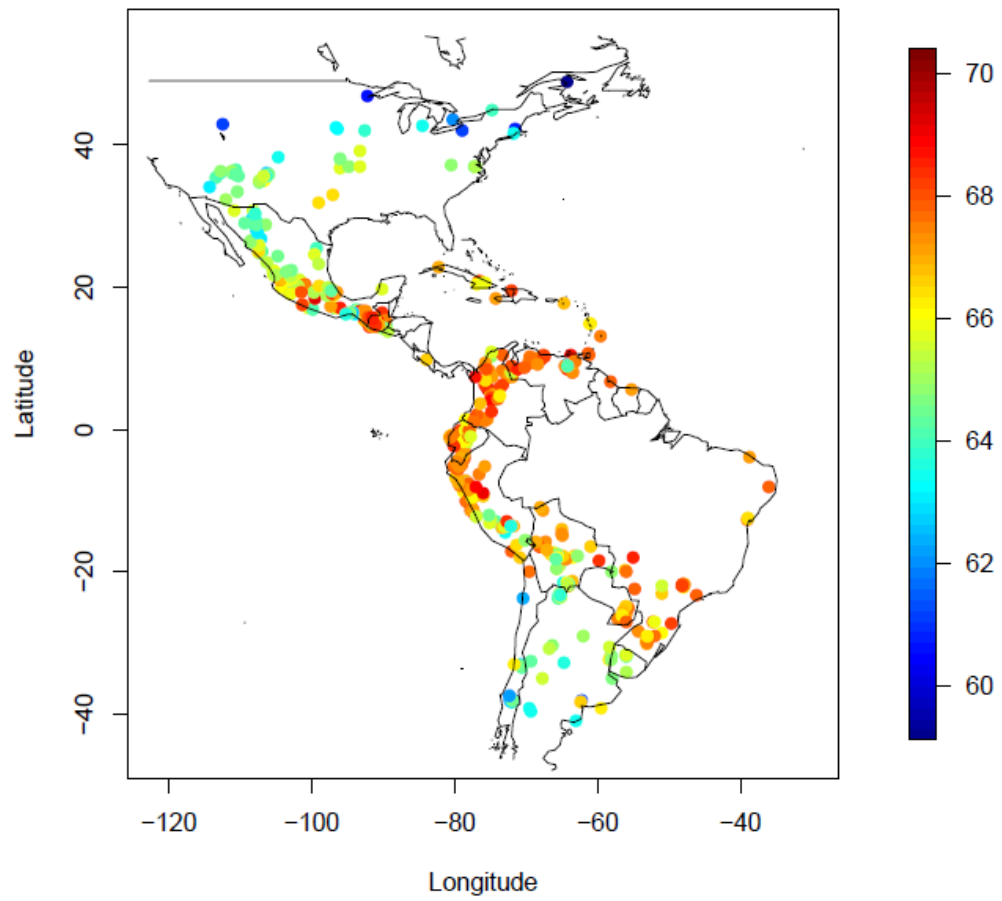


Figure 3.2 Raw point pattern data of DTA scores of BC₁ F₁s at point of collection of donor landraces

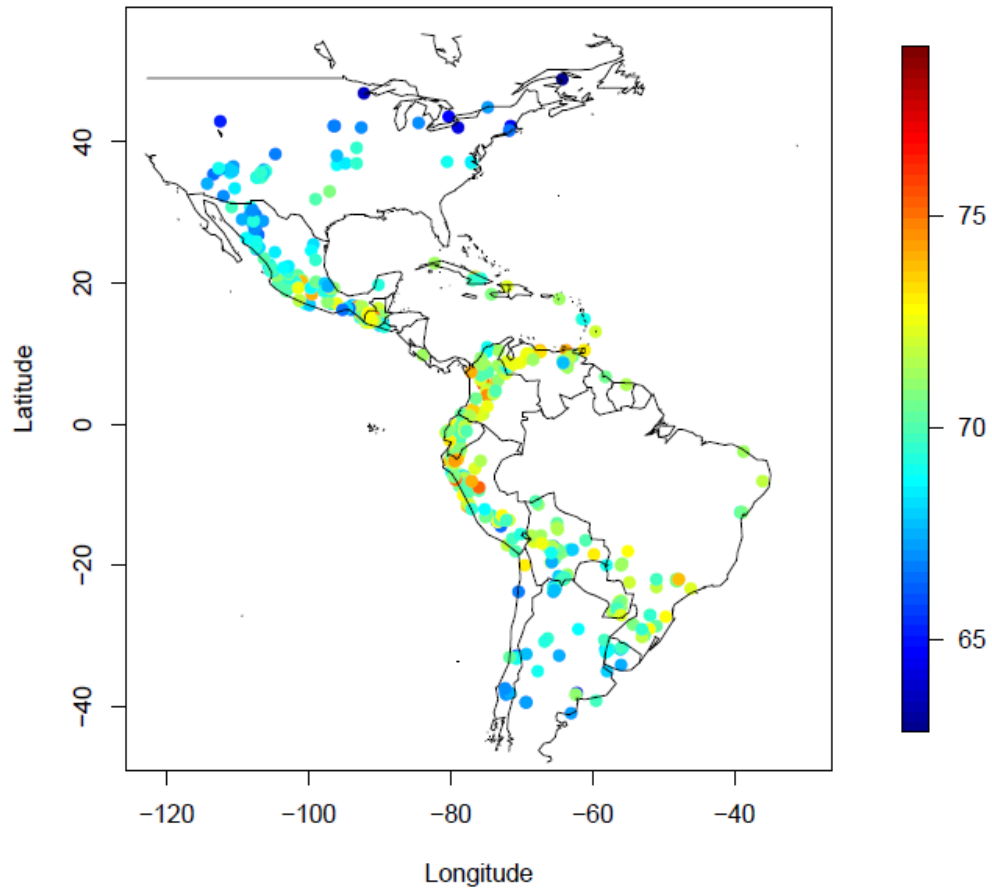


Figure 3.3 Raw point pattern data of DTS Scores of $BC_1 F_1$ s at point of collection of donor landraces

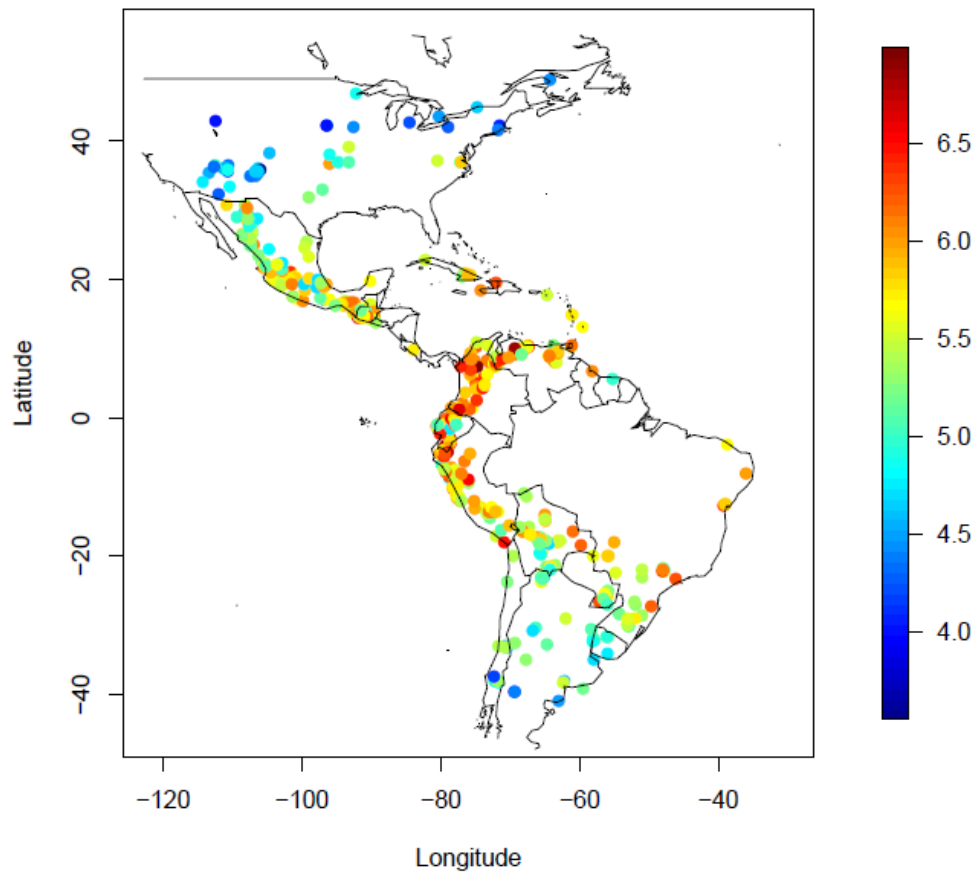


Figure 3.4 Raw point pattern data of lodging scores of BC₁ F₁s at point of collection of donor landraces

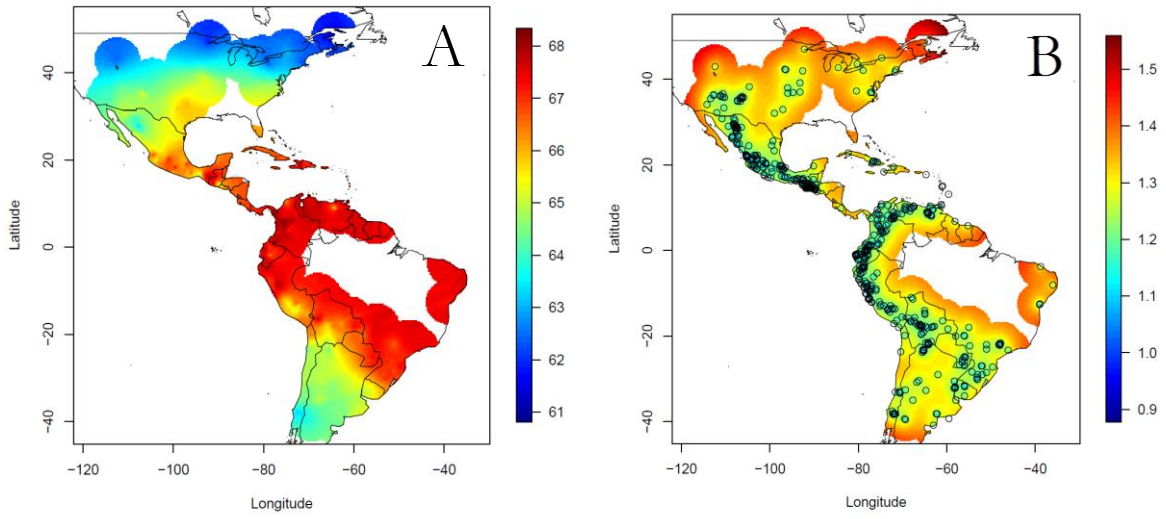


Figure 3.5A-B 3.5A shows predicted DTA scores of $BC_1 F_1$ s with possible donor parents from locations across the Americas; 3.5B shows the standard errors of the estimates

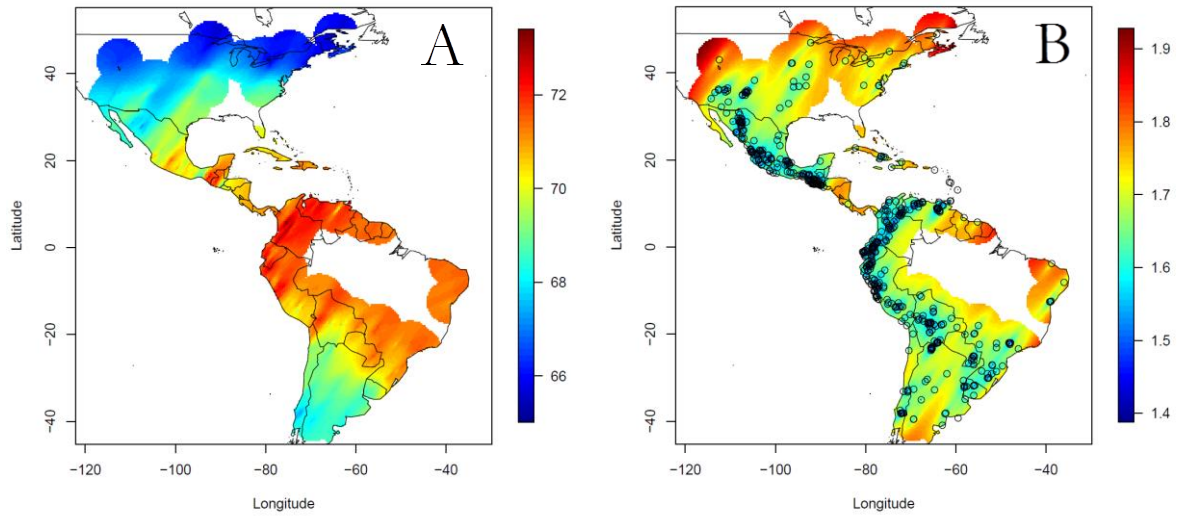


Figure 3.6A-B 3.6A shows predictions DTS scores of $BC_1 F_1$ s with possible donor parents from locations across the Americas; 3.6B shows the standard errors of the estimates

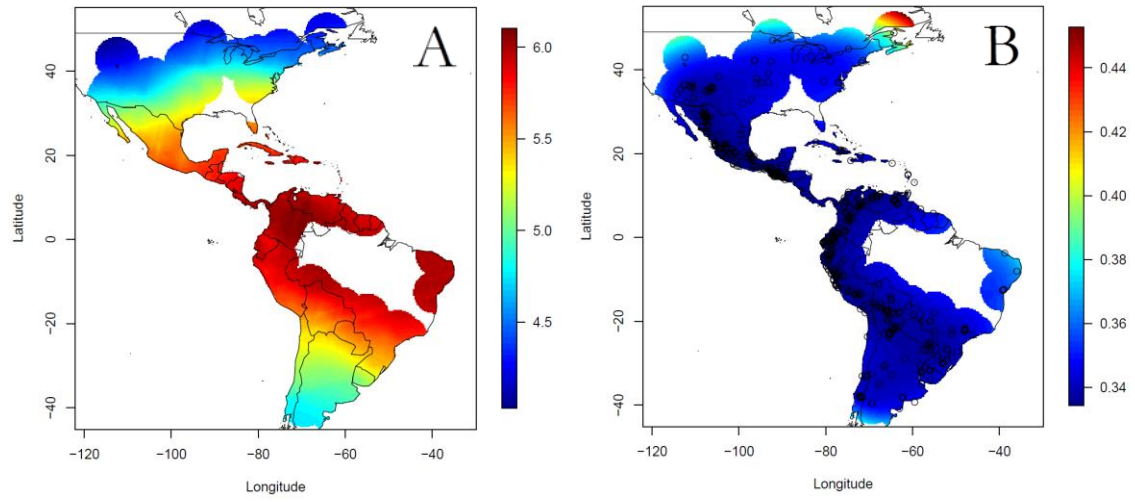


Figure 3.7A-B 3.7A shows predictions Lodging scores of $BC_1 F_1$ s with possible donor parents from locations across the Americas; 3.7B shows the standard errors of the estimates

Supplemental Table 3.1 Yates corrected Chi-square tests for random distribution of QTL discovered in Nested Association Mapping Population studies for Days to Anthesis (DTA) and for Days to Silk (DTS)

Chromosome	Proportion of Genome	Observed # of QTL DTA	Expected # of QTL DTA	DTA Chi square [†]
1	0.14	7	5.04	0.42
2	0.11	4	3.96	0.05
3	0.11	6	3.96	0.60
4	0.1	2	3.6	0.34
5	0.11	3	3.96	0.05
6	0.08	3	2.88	0.05
7	0.1	3	3.6	0.00
8	0.09	3	3.24	0.02
9	0.08	3	2.88	0.05
10	0.07	2	2.52	0.00
Total	1	36	36	1.59
w/9 df crit = 16.91				
Chromosome	Proportion of Genome	Observed # of QTL DTS	Expected # of QTL DTS	DTS Chi square [†]
1	0.14	6	5.46	0.00
2	0.11	5	4.29	0.01
3	0.11	5	4.29	0.01
4	0.1	3	3.9	0.04
5	0.11	5	4.29	0.01
6	0.08	4	3.12	0.05
7	0.1	4	3.9	0.04
8	0.09	3	3.51	0.00
9	0.08	2	3.12	0.12
10	0.07	2	2.73	0.02
Total	1	39	39	0.30
w/9 df crit = 16.91				

[†]Note: First, using the NAM map, the proportion of the genome for each chromosome was calculated (McMullen et al, 2009). Next, the numbers of QTL observed from the NAM mapping studies were counted on each chromosome (Buckler et al, 2009). The expected number of QTL on each chromosome was calculated proportional to each chromosome's proportion of the genome. The observed QTL counts per chromosome were compared to expected counts with a Chi square test, with 9 df.

Supplemental Table 3.2 BC₁ F₁ Development

Country	Race	Accession [†]	Plant Number and (Year) F ₁	Plant Number and (Year) BC ₁	Location and (Year) of F ₁ Production
Argentina	Amargo	ARZM 03014	5 (10) + 9 (11)	12 (12)	CLY (10) + CLY (11)
Argentina	Bola Blanca	ARG 532 (USDA)	4 (07)	8 (08)	Pioneer (07)
Argentina	Calchaqui Small White	ARG 2420 (USDA)	8 (07)	12 (08)	Pioneer (07)
Argentina	Camelia	ARZM 03025	8 (10)	12 (11)	CLY (10)
Argentina	Canario de Formosa	ARZM 06016	12 (10)	12 (11)	CLY (10)
Argentina	Canario de Ocho	ARG VI	8 (08)	12 (09)	Pioneer (08)
Argentina	Capia Blanco	ARG 499 (USDA)	7 (08)	12 (09)	Pioneer (08)
Argentina	Capia Rosado	ARG 460 (USDA)	5 (07)	10 (08)	Pioneer (07)
Argentina	Cateto Sulino	ARG I	8 (10)	12 (11)	CLY (10)
Argentina	Chulpi	ARG 484 (USDA)	7 (08)	12 (09)	Syngenta (08)
Argentina	Cravo	ARZM 05071	12 (10)	12 (11)	CLY (10)
Argentina	Cristal Sulino	ARG III	12 (10)	12 (11)	CLY (10)
Argentina	Cristalino Amarillo	AR 21004	1 (06)	9 (07)	Pioneer (06)
Argentina	Cristalino Amarillo	ARZM 19070	7 (08)	12 (09)	Syngenta (08)
Argentina	Cristalino Blanco	ARZM 19074	7 (08)	12 (09)	Syngenta (08)
Argentina	Cristalino Colorado	ARZM 16021	12 (10)	12 (11)	CLY (10)
Argentina	Cuarentino	ARG 486 (USDA)*	9 (10)	12 (11)	CLY (10)
Argentina	Culli	ARG 471 (USDA)	12 (07)	12 (08)	Pioneer (07)
Argentina	Dentado Amarillo	ARZM 16062	12 (10)	12 (11)	CLY (10)
Argentina	Dentado Blanco	ARZM 03056	12 (10)	12 (11)	CLY (10)
Argentina	Dentado Blanco Rugoso	ARZM 01149	12 (10)	12 (11)	CLY (10)
Argentina	Dulce	ARZM 20005B	12 (11)	12 (12)	CLY (11)
Argentina	Marron	ARG 468 (USDA)	10 (11)	16 (12)	FL (11)
Argentina	Oke	ARG 539 (USDA)	6 (07)	12 (08)	Pioneer (07)

Supplemental Table 3.2 Continued

Country	Race	Accession [†]	Plant Number and (Year) F ₁	Plant Number and (Year) BC ₁	Location and (Year) of F ₁ Production
Argentina	Pisincho	ARG 481 (USDA)*	12 (10)	12 (11)	CLY (10)
Argentina	Pisingallo	ARZM 13095	7 (08)	11 (09)	Syngenta (08)
Barbados	Tuson	BARBGP 2*	8 (10)	10 (11)	FL (10)
Bolivia	Altiplano	BOV 903	2 (06)	6 (07)	Pioneer (06)
Bolivia	Argentino	BOV 920	8 (07)	12 (08)	Pioneer (07)
Bolivia	Aysuma	BOV 331	4 (06)	5 (07)	Pioneer (06)
Bolivia	Camba	BOV 1131	7 (06)	9 (07)	Pioneer (06)
Bolivia	Cateto	BOV 1083	9 (09)	12 (10)	FL (09)
Bolivia	Cateto	BOV 317	7 (08)	12 (09)	Pioneer (08)
Bolivia	Chake-Sara	BOV 520	3 (07) + 3 (08)	6 (09)	Pioneer (07) + Pioneer (08)
Bolivia	Checchi	BOV 320	7 (08)	12 (09)	Syngenta (08)
Bolivia	Checchi	BOV Comp.	8 (09)	12 (10)	FL (09)
Bolivia	Cholito	BOV 309	3 (06)	5 (07)	Pioneer (06)
Bolivia	Chuspillu	BOV 883	4 (09) + 7 (10)	4 (10) + 5 (11) + 4 (11)	Syngenta (09) + FL (10)
Bolivia	Coroico	BOV 1064	8 (06)	15 (07)	Pioneer (06)
Bolivia	Coroico Amarillo	BOV 405	9 (07)	12 (08)	Pioneer (07)
Bolivia	Coroico Blanco	BOV 406	6 (07)	10 (08)	Pioneer (07)
Bolivia	Cubano Dentado	BOV 440	14 (09)	12 (10)	FL (09)
Bolivia	Cubano Dentado	BOV 585	10 (07)	10 (08)	Pioneer (07)
Bolivia	Enano	BOV 1032	2 (06)	5 (07)	Pioneer (06)
Bolivia	Huilcaparu	BOV 685	5 (10)	8 (11)	FL (10)
Bolivia	Huilcaparu Moteado	BOV Comp.	5 (07)	5 (08)	Pioneer (07)
Bolivia	Karapampa	BOV 978	5 (06)	7 (07)	Pioneer (06)
Bolivia	Kcello	BOV 325	9 (09)	5 + 8 (10)	FL (09)
Bolivia	Kcello	BOV 848	9 (09)	12 (10)	FL (09)
Bolivia	Kcello	BOV 948	6 (06)	5 (07)	Pioneer (06)

Supplemental Table 3.2 Continued

Country	Race	Accession [†]	Plant Number and (Year) F ₁	Plant Number and (Year) BC ₁	Location and (Year) of F ₁ Production
Bolivia	Morado	BOV 567	1 (06)	7 (07)	Pioneer (06)
Bolivia	Ninuelo	BOV 1088	13 (07)	7 (08)	Pioneer (07)
Bolivia	Paru	BOV Comp.	6 (09)	3 (10)	FL (10)
Bolivia	Patillo Grande	BOV 649	2 (06)	6 (07)	Pioneer (06)
Bolivia	Perola	BOV 711	3 (06)	4 (07)+ 8 (08)	Pioneer (06)
Bolivia	Pisankalla	BOV 344	6 (06)	4 (07)	Pioneer (06)
Bolivia	Pisankalla	BOV 864	6 (10)	12 (11)	CLY (10)
Bolivia	Pisankalla	BOV 965	5 (10)	17 (11)	CLY (10)
Bolivia	Pojoso Chico	BOV 800	8 (06)	6 (07)	Pioneer (06)
Bolivia	Pororo	BOV 583	14 (09)	11 (10)	FL (09)
Bolivia	Pororo	BOV 806	7 (10)	13 (11)	CLY (10)
Bolivia	Uchuquilla	BOV 318	1 (06)	5 (07)	Pioneer (06)
Bolivia	Uchuquilla	BOV 954	13 (09)	12 (10)	FL (09)
Bolivia	Yungueno	BOV 362	3 (06)	4 (07)	Pioneer (06)
Bolivia	Yungueno	BOV 716	7 (07)	7 (08)	Syngenta (07)
Brazil	Avati Pichinga	BR 2760 (USDA)	16 (09)	15 (11)	FL (09)
Brazil	Avati Pichinga	BR 2776 (USDA)	5 (10)	15 (11)	CLY (10)
Brazil	Avati Pichinga Ihu	BR 2830 (USDA)	10 (07)	3 (08)	Pioneer (07)
Brazil	Caingang	PR III	18 (09)	12 (10)	FL (09)
Brazil	Caingang	SP XIII	4 (09)	15 (10)	FL (09)
Brazil	Caraja	1692 (USDA)	7 (07)	10 (08)	Pioneer (07)
Brazil	Cateto	BA II	8 (09)	12 (10)	FL (09)
Brazil	Cateto	CE I	6 (10)	22 (11)	FL (10)
Brazil	Cateto Assis Brasil	RGS XIV	12 (08)	12 (09)	Pioneer (08)
Brazil	Cateto Grande	MT IV	12 (09)	12 (11)	FL (09)
Brazil	Cateto Nortista Precoce	SUR I	9 (08)	12 (09)	Pioneer (08)

Supplemental Table 3.2 Continued

Country	Race	Accession [†]	Plant Number and (Year) F ₁	Plant Number and (Year) BC ₁	Location and (Year) of F ₁ Production
Brazil	Cravo Paulista	SP I	1 (08) + 2 (09)	7 (10)	Pioneer (08) +Pioneer (09)
Brazil	Cravo Riograndense	RGS VII	6 (07)	12 (08)	Pioneer (07)
Brazil	Cristal	SP X	7 (07)	11 (08)	Pioneer (07)
Brazil	Cristal	SP XI	7 (09)	12 (10)	FL (09)
Brazil	Cristal Inter. Perola	1115 (USDA)	6 (08)	12 (09)	Syngenta (08)
Brazil	Cristal Paraguay Paulista	2334 (USDA)	2 (08) + 4 (09)	12 (10)	Syngenta (08) +FL (09)
Brazil	Dente Branco Paulista	SP V	6 (07)	11 (08)	Syngenta (07)
Brazil	Dente Branco R. G.	SC II	10 (09)	12 (10)	FL (09)
Brazil	Dente Paulista	SP IV	7 (07)	11 (08)	Syngenta (07)
Brazil	Dente R. G. Liso	RGS VI	11 (09)	12 (10)	FL (09)
Brazil	Dente R. G. Liso	SC I	6 (07)	10 (08)	Syngenta (07)
Brazil	Dente R. G. Rugoso	RGS II	11 (09)	12 (10)	FL (09)
Brazil	Dourados Saboro	BR 50 (USDA)	9 (09)	12 (10)	Pioneer (09)
Brazil	Entrelacado	MT VI	6 blk (09)	12 (10)	Pioneer (09)
Brazil	Hickory King	RGS IX*	6 (10)	15 (11)	CLY (10)
Brazil	Moroti	MT I	7 (09)	13 (10)	FL (09)
Brazil	Moroti	PE I	4 (06)	5 (07)	Pioneer (06)
Brazil	Moroti Precoce	BOL I	5 (09)	12 (10)	Pioneer (09)
Brazil	Semi Dente Paulista	SP IX	15 (09)	12 (10)	FL (09)
Brazil	Semi Dente R. G.	RGS XV	9 (09)	12 (10)	Pioneer (09)
Brazil	Tuson	BAI III	5 (10)	21 (11)	FL (10)
Brazil	Tuson	BAI IIIB	2 (10) + 8 (11)	12 (12)	FL (10) + CLY (11)
Chile	Araucano	CHI 320*	6 (06)	4 (07)+ 8 (08)	Pioneer (06)
Chile	Capia Chico Chileno	CHI 382*	7 (06)	4 (07)+ 8 (08)	Pioneer (06)
Chile	Cristalino Chico	CHI 324	7 (10)	15 (11)	CLY (10)
Chile	Cristalino Chileno	CHI 156	7 (07)	12 (08)	Pioneer (07)

Supplemental Table 3.2 Continued

Country	Race	Accession [†]	Plant Number and (Year) F ₁	Plant Number and (Year) BC ₁	Location and (Year) of F ₁ Production
Chile	Cristalino Grande	CHI 323*	12 (11)	12 (12)	CLY (11)
Chile	Curagua	CHI 301*	4 (10)	10 (11)	CLY (10)
Chile	Curagua	CHI 314*	7 (06)	4 (07)+ 8 (08)	Pioneer (06)
Chile	Curagua Grande	CHI 303	4 (06)	5 (07)	Pioneer (06)
Chile	Dentado Comercial	CHI 326*	7 (10)	12 (11)	CLY (10)
Chile	Dulce Evergreen	CHI 332*	5 (10)	16 (11)	CLY (10)
Chile	Dulce Golden Bantam	CHI 335*	6 (10)	26 (11)	CLY (10)
Chile	Harinoso Tarapaqueno	CHI 421	4 (11)	11 (12)	CLY (11)
Colombia	Amagaceno	ANT 343*	5 (07)	11 (08)	Syngenta (07)
Colombia	Amagaceno	HUI 317*	5 (07)	10 (08)	Pioneer (07)
Colombia	Andaqui	CAQ 307*	2 (06)	7 (07)	Pioneer (06)
Colombia	Andaqui	CAQ 333*	10 (09)	12 (10)	Pioneer (09)
Colombia	Cabuya	SAN 316*	2 (06)	7 (07)	Pioneer (06)
Colombia	Cacao	SAS 327*	4 (07)	10 (08)	Pioneer (07)
Colombia	Cacao	SAS 335*	4 (10)	7 (11)	FL (10)
Colombia	Capio	ANT 348*	2 (07)	5 (08)	Pioneer (07)
Colombia	Capio	ANT 354	2 (10)	7 (11)	FL (10)
Colombia	Capio	NAR 315	3 (06)	6 (07)	Pioneer (06)
Colombia	Caqueteno	CAQ 305*	5 (08)	12 (09)	Pioneer (08)
Colombia	Cariaco	COR 338*	8 (10)	7 (11)	FL (10)
Colombia	Chococeno	CHO 340	2 (07) + 1 (08)	5 (09)	Pioneer (07) + Pioneer (08)
Colombia	Clavo	NAR 329*	2 (07) + 3 (10)	7 (11)	Pioneer (07) + FL (10)
Colombia	Comun	NAR 330*	8 (08)	8 (10)	Ames (08)
Colombia	Comun	VAL 374*	7 (06)	4 (07)+ 8 (08)	Pioneer (06)
Colombia	Comun	CAU 454*	4 (06)	5 (07)	Pioneer (06)
Colombia	Costeno	ANT 394*	7 (07)	12 (08)	Pioneer (07)

Supplemental Table 3.2 Continued

Country	Race	Accession [†]	Plant Number and (Year) F ₁	Plant Number and (Year) BC ₁	Location and (Year) of F ₁ Production
Colombia	Costeno	ATL 314*	7 (07)	6 (08)	Syngenta (07)
Colombia	Costeno	ATL 328*	5 (10)	13 (11)	FL (10)
Colombia	Costeno	COR 320*	9 (10)	15 (11)	FL (10)
Colombia	Guirua	MAG 469*	4 (07)	4 (08)	Pioneer (07)
Colombia	Harin. Dent.	NAR 326*	5 (10)	12 (11)	FL (10)
Colombia	Imbricado	NAR 389	8 (10)	6 (11)	FL (10)
Colombia	Montana	NAR 625*	5 (06)	8 (07)	Pioneer (06)
Colombia	Pira	CUN 327*	8 (10)	9 (11)	FL (10)
Colombia	Pira	CUN 480*	8 (10)	8 (11)	FL (10)
Colombia	Pira	TOL 405	4 (07)	10 (08)	Pioneer (07)
Colombia	Pollo	CUN 424	10 (05)	4 (08)	Syngenta (05)
Colombia	Pollo	CUN 443*	12 (10)	14 (11)	FL (10)
Colombia	Puya	MAG 355*	7 (07)	12 (08)	Pioneer (07)
Colombia	Puya Grande	SAN 347*	10 (09)	20 (10)	FL (09)
Colombia	Sabanero	ANT 423*	8 (08)	12 (10)	Ames (08)
Colombia	Sabanero	CUN 342*	5 (06)	7 (07)	Pioneer (06)
Colombia	Sabanero	CUN 367	7 (06)	4 (07)	Pioneer (06)
Colombia	Sabanero	SAN 329	4 (07)	10 (08)	Pioneer (07)
Colombia	Yucatan	TOL 389*	3 (06)	7 (07)	Pioneer (06)
Colombia	Yucatan	TOL 399*	8 (09)	12 (10)	FL (09)
Costa Rica	Huesillo	CRI 370*	8 (11)	11 (12)	FL (11)
Cuba	Argentino	CUB 113*	11 (09)	12 (10)	Pioneer (09)
Cuba	Chandelle	CUB 54*	6 (09)	12 (10)	FL (09)
Cuba	Chandelle	CUB 68	9 (05)	12 (09)	Syngenta (05)
Cuba	Cuban Flint	CUB 63*	11 (11)	11 (12)	FL (11)
Cuba	Maiz Criollo	CUB 136*	9 (09)	12 (10)	Pioneer (09)

Supplemental Table 3.2 Continued

Country	Race	Accession [†]	Plant Number and (Year) F ₁	Plant Number and (Year) BC ₁	Location and (Year) of F ₁ Production
Cuba	Tuson	CUB 67*	4 (10)	9 (11)	CLY (10)
Ecuador	Blanco Blandito	ECU 523	4 (07)	7 (08)	Pioneer (07)
Ecuador	Blanco Harinoso Dentado	ECU 640	2 (07) + 4 (10)	11 (11)	Pioneer (07) + FL (10)
Ecuador	Candela	ECU 344*	7 (09)	11 (10)	FL (09)
Ecuador	Candela	ECU 531	4 (06)	4 (07)	Pioneer (06)
Ecuador	Candela	ECU 699	1 (06)	3 (07)	Pioneer (06)
Ecuador	Canguil	ECU 500	6 (08)	13 (09)	Syngenta (08)
Ecuador	Canguil Grueso	ECU 443	7 (10)	9 (11)	FL (10)
Ecuador	Canguil Grueso	ECU 447	12 (07)	12 (08)	Pioneer (07)
Ecuador	Chillo	ECU 411	4 (07)	7 (08)	Pioneer (07)
Ecuador	Chillo	ECU 458	5 (07)	10 (08)	Pioneer (07)
Ecuador	Chillo	ECU 480B	11 (10)	9 (11)	FL (10)
Ecuador	Cholito	ECU 718	2 (06)	7 (07)	Pioneer (06)
Ecuador	Chulpi Chico	ECU 424	9 (09)	10 (11)	Syngenta (09)
Ecuador	Clavito	ECU 884	7 (06)	7 (07)	Pioneer (06)
Ecuador	Conico Dentado	ECU 427	2 (07) + 4 (09)	2 (10) + 7 (11)	Pioneer (07) + Syngenta (09)
Ecuador	Cubano Amarillo Duro	ECU 326	10 (09)	12 (10)	FL (09)
Ecuador	Cubano Amarillo Duro	ECU 327	3 (06)	3 (07)+ 7 (08)	Pioneer (06)
Ecuador	Cubano Amarillo Duro	ECU 698	12 (09)	12 (10)	FL (09)
Ecuador	Cubano Amarillo Duro	ECU 957	13 (09)	12 (10)	FL (09)
Ecuador	Cubano Cateto	ECU 877	11 (09)	12 (10)	FL (09)
Ecuador	Cubano Tuson	ECU 542	7 (08)	12 (09)	Syngenta (08)
Ecuador	Cubano Tuson	ECU 660	6 (10)	16 (11)	FL (10)
Ecuador	Cubano Tuson	ECU 764	10 (10)	14 (11)	FL (10)
Ecuador	Enano Gigante	ECU Comp.	2 (06)	6 (07)	Pioneer (06)

Supplemental Table 3.2 Continued

Country	Race	Accession [†]	Plant Number and (Year) F ₁	Plant Number and (Year) BC ₁	Location and (Year) of F ₁ Production
Ecuador	Gallina	ECU 329	2 (09) + 7 (10)	8 (11)	Pioneer (09) + FL (10)
Ecuador	Huandango	ECU 735	2 (07)	3 (09)	Pioneer (07)
Ecuador	Mishca	ECU 321	6 (06)	10 (07)	Pioneer (06)
Ecuador	Morochon	ECU 454B	7 (06)	5 (07)	Pioneer (06)
Ecuador	Patillo	ECU 417	8 (07)	11 (08)	Pioneer (07)
Ecuador	Pojoso Chico Ecuatorian	ECU 522	14 (07)	12 (08)	Pioneer (07)
Ecuador	Racimo de Uva	ECU 517	9 (07)	5 (08)	Pioneer (07)
Ecuador	Tusilla	ECU 569	5 (07)	10 (08)	Pioneer (07)
Ecuador	Tuxpeno	ECU 942	8 (10)	12 (11)	FL (10)
Ecuador	Uchima	ECU 681	1 (06)	7 (07)	Pioneer (06)
Ecuador	Yungueno	ECU 572	7 (08)	12 (09)	Syngenta (08)
Ecuador	Yunquillano forma Andaqui	ECU 710	1 (06)	8 (07)	Pioneer (06)
Ecuador	Yunquillano forma Andaqui	ECU 853	6 (08)	12 (09)	Syngenta (08)
Ecuador	Yunquillano forma Andaqui	ECU 855	3 (08)	8 (10)	Pioneer (08)
El Salvador	Amarillo Salvadoreno	Comp.	6 (09) + 5 (09)	12 (10)	FL (09)+PR09
Guatemala	Comiteco	GUA 418	7 (09)	8 (10)	FL (09)
Guatemala	Comiteco	GUA 515	12 (07)	12 (08)	Pioneer (07)
Guatemala	Comiteco	GUA 546	2 (05)	5 (08)	Syngenta (05)
Guatemala	Dzit Bacal	GUA 131	5 (06)	8 (07)	Pioneer (06)
Guatemala	Imbricado	GUA 493	3 (10)	18 (11)	FL (10)
Guatemala	Imbricado	GUA 922	3 (10)	16 (11)	FL (10)
Guatemala	N de Chimaltenango	GUA 369	5 (10)	12 (11)	FL (10)
Guatemala	N de Chimaltenango	GUA 590	9 (09)	6 (10)	Syngenta (09)
Guatemala	N de T Caliente	GUA 159	12 (05)	8 (08)	Syngenta (05)
Guatemala	N de T Fria	GUA 522	2 (08)	7 (09)	Pioneer (08)
Guatemala	Nal Tel ATB	GUA 111	11 (09)	12 (10)	FL (09)

Supplemental Table 3.2 Continued

Country	Race	Accession [†]	Plant Number and (Year) F ₁	Plant Number and (Year) BC ₁	Location and (Year) of F ₁ Production
Guatemala	Nal Tel ATB	GUA 220	12 (05)	12 (08)	Syngenta (05)
Guatemala	Nal Tel ATB	GUA 281	4 (10)	19 (11)	CLY (10)
Guatemala	Nal Tel BTA	GUA 20	5 (11)	12 (12)	FL (11)
Guatemala	Nal Tel BTB	GUA 145*	14 (09)	12 (10)	FL (09)
Guatemala	Nal Tel BTB	GUA 280	9 (09)	12 (10)	FL (09)
Guatemala	Nal Tel BTB	GUA 765*	7 (10) + 10 (10)	23 (11)	CLY (10) + FL (10)
Guatemala	Oloton	GUA 383	12 (05)	12 (08)	Syngenta (05)
Guatemala	Quicheno Early	GUA 162	11 (09) + 6 (09)	12 (10)	FL (09) + Syngenta (09)
Guatemala	Quicheno Late	GUA 863	1 (08) + 4 (10)	12 (11)	Syngenta (08) + FL (10)
Guatemala	Quicheno Late	GUA 877	4 (10)	9 (11)	FL (10)
Guatemala	Salpor	GUA 476	6 (08)	11 (09)	Syngenta (08)
Guatemala	Salpor Tardio	GUA 485	6 (07)	8 (08)	Syngenta (07)
Guatemala	San Marceno	GUA 506	7 (07)	2 (08)	Syngenta (07)
Guatemala	San Marceno	GUA 724	11 (05)	12 (08)	Syngenta (05)
Guatemala	Serrano	GUA 940	2 (09)	7 (11)	FL (10)
Guatemala	Tepecintle	GUA 597	13 (09)	18 (10)	FL (09)
Guatemala	Tepecintle	GUA 65	8 (07)	12 (08)	Pioneer (07)
Guatemala	Tepecintle	GUA 651	13 (09)	12 (10)	FL (09)
Guatemala	Tepecintle	GUA 79	7 (09)	12 (10)	FL (09)
Guatemala	Tuxpeno	GUA 456	6 (07)	12 (08)	Pioneer (07)
Guyana	Cateto Nortista	GIN I	8 (07)	12 (08)	Pioneer (07)
Haiti	Chandelle	HTI 14	7 (09)	12 (10)	FL (09)
Haiti	Haitian Yellow	HTI 1	11 (09)	12 (10)	FL (09)
Martinica	Early Carribean	Martinica 9	5 (09)	7 (07)	Pioneer (06)
Martinica	Unassigned	Martinica 12	2 (06)	12 (10)	FL (09)
Mexico	Apachito	CHH 138*	5 (10)	16 (11)	CLY (10)

Supplemental Table 3.2 Continued

Country	Race	Accession [†]	Plant Number and (Year) F ₁	Plant Number and (Year) BC ₁	Location and (Year) of F ₁ Production
Mexico	Apachito	CHH 166*	9 (10)	17 (11)	FL (10)
Mexico	Apachito	CHH 180*	8 (10)	25 (11)	FL (10)
Mexico	Apachito	CHH 182	6 (10)	12 (11)	Syngenta (09)
Mexico	Apachito	CHH 207	13 (10)	14 (11)	CLY (10)
Mexico	Arrocillo Amarillo	PUE 91	6 (10)	14 (11)	FL (10)
Mexico	Arrocillo Amarillo	VER 311*	7 (10)	12 (11)	FL (10)
Mexico	Azul	ACC 70-2	12 (09)	12 (10)	FL (09)
Mexico	Azul	CHH 158*	9 (10)	15 (11)	FL (10)
Mexico	Azul	CHH 220	8 (10)	22 (11)	FL (10)
Mexico	Azul	CHH 218	7 (07)	12 (09)	Pioneer (07)
Mexico	Bofo	DGO 123	2 (06)	4 (07)+ 6 (08)	Pioneer (06)
Mexico	Bofo	NAY 191*	11 (09)	18 (10)	FL (09)
Mexico	Bofo	NAY 203	8 (09)	20 (10)	FL (09)
Mexico	Bolita	OAX 44	7 (09)	11 (10)	FL (09)
Mexico	Cacahuacintle	MEX 7	6 (07)	4 (08)	Syngenta (07)
Mexico	Cacahuacintle	PUE 552*	8 (10)	13 (11)	FL (10)
Mexico	Celaya	GTO 36*	5 (07)	7 (08)	Syngenta (07)
Mexico	Celaya	GTO 69	8 (10)	15 (11)	FL (10)
Mexico	Celaya	GTO 88	9 (10)	15 (11)	CLY (10)
Mexico	Chalqueno	HGO 7	3 (08) + 4 (09)	7 (10)	Syngenta (08) + Syngenta (09)
Mexico	Chapalote	SIN 2*	11 (09)	12 (10)	Pioneer (09)
Mexico	Chapalote	SIN 6	8 (10)	15 (11)	FL (10)
Mexico	Chapalote	SIN 65	5 (10)	11 (11)	FL (10)
Mexico	Conejo	GRO 17	6 (10)	16 (11)	FL (10)
Mexico	Conejo	GRO 129	6 (10)	14 (11)	FL (10)

Supplemental Table 3.2 Continued

Country	Race	Accession [†]	Plant Number and (Year) F ₁	Plant Number and (Year) BC ₁	Location and (Year) of F ₁ Production
Mexico	Conejo	GRO 157	12 (10)	16 (11)	FL (10)
Mexico	Conico	PUE 48	12 (08)	10 (09)	Syngenta (08)
Mexico	Conico	PUE 116	15 (05)	12 (08)	Syngenta (05)
Mexico	Conico Norteno	ZAC 12	4 (09)	11 (10)	FL (09)
Mexico	Conico Norteno	ZAC 161*	1 (06)	6 (07)	Pioneer (06)
Mexico	Coscomatepec	VER 110*	5 (10)	10 (11)	FL (10)
Mexico	Coscomatepec	VER 110B*	5 (10)+4 (11)	12 (12)	FL (10) + FL (11)
Mexico	Cristalino de Chihuahua	CHH 128*	10 (10)	7 (11)	FL (10)
Mexico	Cristalino de Chihuahua	CHH 154*	9 (10)	19 (11)	FL (10)
Mexico	Cristalino de Chihuahua	CHH 254	6 (10)	16 (11)	CLY (10)
Mexico	Dulce de Jalisco	JAL78	4 +7 (10)	2 (11)	CLY (10) + FL (10)
Mexico	Dulce de Jalisco	JAL304	1 (10)	3 (11)	CLY (11)
Mexico	Dulcillo del Noroeste	SIN 34	5 (10)	8 (11)	FL (10)
Mexico	Dulcillo del Noroeste	SIN 79	6 (10)	16 (11)	FL (10)
Mexico	Dulcillo del Noroeste	SON 57*	4 (06)	7 (07)	Pioneer (06)
Mexico	Dzit Bacal	VER 96	3 (10)	10 (11)	FL (10)
Mexico	Elotero de Sinaloa	NAY 32*	5 (10)	9 (11)	FL (10)
Mexico	Elotero de Sinaloa	NAY 46	10 (10)	19 (11)	FL (10)
Mexico	Elotero de Sinaloa	SIN 17	8 (10)	16 (11)	FL (10)
Mexico	Elotes Occidentales	DGO 236*	7 (07)	12 (08)	Pioneer (07)
Mexico	Elotes Occidentales	GTO 191*	4 (10)	12 (11)	FL (10)
Mexico	Elotes Occidentales	NAY 29	7 (09)	10 (10)	Syngenta (09)
Mexico	Elotes Occidentales	NAY 38	4 (10)	11 (11)	CLY (10)
Mexico	Elotes Occidentales	ZAC 210*	2 (10)	5 (11)	FL (10)
Mexico	Gordo	CHH 131*	10 (05)	10 (08)	Syngenta (05)
Mexico	Gordo	CHH 160*	9 (10)	24 (11)	FL (10)

Supplemental Table 3.2 Continued

Country	Race	Accession [†]	Plant Number and (Year) F ₁	Plant Number and (Year) BC ₁	Location and (Year) of F ₁ Production
Mexico	Gordo	CHH 214*	5 (10)	12 (11)	CLY (10)
Mexico	Gordo	CHH 256*	5 (10)	14 (11)	CLY (10)
Mexico	Harinoso de Ocho	NAY 24	7 (07)	4 (08)	Syngenta (07)
Mexico	Jala	JAL44*	6 (07)	8 (08)	Syngenta (07)
Mexico	Jala	NAY 130	6 (10)	8 (11)	FL (10)
Mexico	Mixteco	OAX 569	6 (10)	12 (11)	FL (10)
Mexico	Motozinteco	CHS 650	2 (10)	10 (11)	FL (10)
Mexico	Motozinteco	CHS 650B	10 (10+11)	12 (12)	FL (10) + FL (11)
Mexico	Mushito	MIC 317*	8 (09)	12 (10)	FL (09)
Mexico	Mushito	MIC 371	10 (10)	9 (11)	FL (10)
Mexico	Nal-Tel	CAM 48	8 (10)	11 (11)	FL (10)
Mexico	Negrito	OAX 26*	8 (11)	4 (11)	CLY (11)
Mexico	Olotillo	CHS 53	2 (10)	9 (11)	CLY (11)
Mexico	Olotillo	CHS 81	14 (09)	18 (10)	FL (09)
Mexico	Oloton	CHS 684	3 (10)	7 (11)	FL (10)
Mexico	Onaveno	SON 24*	6 (06)	6 (07)	Pioneer (06)
Mexico	Onaveno	SON 114	8 (10)	26 (11)	FL (10)
Mexico	Palomero de Jalisco	JAL154*	12 (09)	12 (10)	FL (09)
Mexico	Palomero Tipo Chihuahua	CHH 148*	10 (10)	13 (11)	FL (10)
Mexico	Palomero Tipo Chihuahua	CHH 201*	5 (10)	26 (11)	CLY (10)
Mexico	Palomero Toluqueno	VER 35*	7 (08)	12 (09)	Syngenta (08)
Mexico	Pepitilla	GRO 3*	10 (07)	10 (08)	Pioneer (07)
Mexico	Raton	CHH 191*	1 (06) + 3 (07)	12 (08)	Pioneer (06) + Pioneer (07)
Mexico	Raton	NLE 9*	7 (10)	14 (11)	CLY (10)
Mexico	Raton	TAM 25*	11 (10)	16 (11)	CLY (10)
Mexico	Reventador	NAY 15*	10 (09)	12 (10)	FL (09)

Supplemental Table 3.2 Continued

Country	Race	Accession [†]	Plant Number and (Year) F ₁	Plant Number and (Year) BC ₁	Location and (Year) of F ₁ Production
Mexico	Reventador	NAY 39	10 (07)	7 (08)	Pioneer (07)
Mexico	Serrano de Jalisco	JAL133*	3 (10)	11 (11)	CLY (10)
Mexico	Serrano de Jalisco	JAL146	12 (10)	10 (11)	FL (10)
Mexico	Serrano Mixe	OAX 565	2 (10)	12 (11)	FL (10)
Mexico	Tablilla de Ocho	JAL301	4 (09)	12 (10)	FL (09)
Mexico	Tablilla de Ocho	NAY 185	10 (07)	9 (08)	Pioneer (07)
Mexico	Tablilla de Ocho	ZAC 187	13 (05)	10 (08)	Syngenta (05)
Mexico	Tabloncillo	JAL102	4 (10)	13 (11)	CLY (10)
Mexico	Tabloncillo	JAL103*	5 (09)	3 (10)	Pioneer (09)
Mexico	Tabloncillo	JAL103B*	9 (11)	7 (12)	FL (11)
Mexico	Tabloncillo Perla	NAY 12	13 (09)	10 (10)	FL (09)
Mexico	Tabloncillo Perla	NAY 16	3 (10) + 3 (10)	15 (11)	CLY (10) + FL (10)
Mexico	Tehua	CHS 29	5 (07)	12 (08)	Pioneer (07)
Mexico	Tehua	CHS 159	2 (09) + 2 (10)	14 (11)	FL (09) + FL (10)
Mexico	Tepecintle	CHS 76	9 (09)	19 (10)	FL (09)
Mexico	Tuxpeno	VER 143*	7 (08)	12 (09)	Syngenta (08)
Mexico	Tuxpeno Norteno	CHH 121	5 (10)	16 (11)	FL (10)
Mexico	Tuxpeno Norteno	CHH 287*	3 (06)	9 (08)	Syngenta (07)
Mexico	Tuxpeno Norteno	TAM 3*	2 (10)	14 (11)	FL (10)
Mexico	Vandeno	GRO 96	5 (07)	12 (08)	Pioneer (07)
Mexico	Zamorano Amarillo	GTO 1	3 (10)	23 (11)	CLY (10)
Mexico	Zamorano Amarillo	MIC 66*	12 (10)	8 (11)	FL (10)
Mexico	Zapalote Chico	CHS 662	3 (10)	13 (11)	FL (10)
Mexico	Zapalote Chico	OAX 48	8 (10) + 2 (10)	22 (11)	CLY (10) + FL (10)
Mexico	Zapalote Chico	OAX 50	12 (10)	12 (11)	CLY (10)
Mexico	Zapalote Chico	OAX 70	10 (10)	15 (11)	CLY (10)

Supplemental Table 3.2 Continued

Country	Race	Accession [†]	Plant Number and (Year) F ₁	Plant Number and (Year) BC ₁	Location and (Year) of F ₁ Production
Mexico	Zapalote Grande	CHS 104	9 (10)	16 (11)	CLY (10)
Mexico	Zapalote Grande	CHS 224	5 (08)	12 (09)	Pioneer (08)
Mexico	Zapalote Grande	CHS 236	9 (10)	14 (11)	FL (10)
Mexico	Zapalote Grande	CHS 521	9 (10)	21 (11)	FL (10)
Paraguay	Avati Moroti Guapi	PAG 139 (USDA)	7 (07)	12 (08)	Pioneer (07)
Paraguay	Avati Moroti Ti	PAG124 (USDA)	8 (07)	12 (08)	Pioneer (07)
Paraguay	Cateto Sabugo Grosso	PAG 422 (USDA)	6 (08)	12 (09)	Syngenta (08)
Paraguay	Semi Dente Paulista	PAG I*	8 (07)	12 (08)	Pioneer (07)
Paraguay	Moroti Guapi	PAG VI-A	7 (08)	12 (09)	Syngenta (08)
Peru	Alazan	LBQ 18	13 (09)	10 (10)	FL (09)
Peru	Alazan	LIB 34	6 (07)	12 (08)	Pioneer (07)
Peru	Aleman	HCO 38*	10 (10)	12 (11)	FL (10)
Peru	Amarillo Huancabamba	PIU 17B	2 (07)	3 (08)	Pioneer (07)
Peru	Amarillo Huancabamba	PIU 38B*	5 (07)	7 (08)	Pioneer (07)
Peru	Ancashino	ANC 102*	1 (06)	4 (07)	Pioneer (06)
Peru	Arequipeno	ARQ 1*	8 (07)	12 (08)	Pioneer (07)
Peru	Arizona	LIB 2*	8 (07)	12 (08)	Pioneer (07)
Peru	Arizona	LIB 16	11 (09)	19 (10)	FL (09)
Peru	Blanco Ayabaca	PIU 119	7 (06)	4 (07)+ 8 (08)	Pioneer (06)
Peru	Chancayano Blanco	LIM 45*	3 (08) + 1 (09)	3 (11) + 8 (11)	Pioneer (08) + FL (09)
Peru	Chancayano Pintado	LIM 46*	8 (10)	9 (11)	FL (10)
Peru	Chaparreno	ARQ34*	5 (08)	10 (09)	Pioneer (08)
Peru	Chulpi	LIM 66*	1 (06)	6 (07)	Pioneer (06)
Peru	Chuncho	CUZ 112*	3 (10)	10 (11)	FL (10)
Peru	Colorado	LIB 8*	11 (11)	12 (12)	FL (11)
Peru	Confite Morocho	AYA 20	7 (09)	12 (10)	Syngenta (09)

Supplemental Table 3.2 Continued

Country	Race	Accession [†]	Plant Number and (Year) F ₁	Plant Number and (Year) BC ₁	Location and (Year) of F ₁ Production
Peru	Confite Puneno	APC 56	7 (09)	9 (10)	Syngenta (09)
Peru	Confite Puntigudo	CAJ 27	7 (10)	9 (11)	FL (10)
Peru	Confite Puntigudo	CUZ 13	7 (06)	5 (07)	Pioneer (06)
Peru	Coruca	TAC 1*	6 (07)	12 (08)	Pioneer (07)
Peru	Cubano Amarillo	UCA 8*	11 (09)	12 (10)	Pioneer (09)
Peru	Cuzco Cristalino Amaril	CUZ 363	7 (07)	7 (08)	Syngenta (07)
Peru	Cuzco Gigante	CAJ 17	7 (09)	12 (11)	Syngenta (09)
Peru	Granada	ANC 57	6 (09)	12 (11)	Syngenta (09)
Peru	Huachano	LIM 43*	7 (07)	10 (08)	Pioneer (07)
Peru	Huancavelicano	HVC 179*	7 (08)	6 (09)+ 8 (09)	Syngenta (08)
Peru	Huanuco	HCO 128B*	1 (08) + 5 (10)	12 (11)	Pioneer (08) + FL (10)
Peru	Huarmaca	PIU 72*	8 (07)	10 (09)	Pioneer (07)
Peru	Huayleno	ANC 180x181	5 (07)	3 (08)	Pioneer (07)
Peru	Huayleno	ANC 291*	1 (06)	5 (07)	Pioneer (06)
Peru	Jora	ANC 1*	6 (07)	10 (08)	Pioneer (07)
Peru	Kculli	HVC 137	8 (11)	12 (12)	FL (11)
Peru	Maranon	LIB 63B	5 (06)	8(07)	Pioneer (06)
Peru	Mochero	LBQ 5*	9 (06)	6 (07)	Pioneer (06)
Peru	Morado Canteno	Lima 55*	1 (06)	4 (07)	Pioneer (06)
Peru	Morochillo	PIU 96*	6 (09)	7 (10)	FL (09)
Peru	Morocho	APC 67*	7 (06)	9 (07)	Pioneer (06)
Peru	Morocho	APC 77*	1 (06)	7 (07)	Pioneer (06)
Peru	Morocho Cajabambino	LIB 62*	4 (07)	4 (09)	Syngenta (07)
Peru	Pagaladroga	PIU 2	3 (08) + 8 (09)	12 (10)	Pioneer (08) + Syngenta (09)
Peru	Pardo	LIM 19*	3 (10)	11 (11)	FL (10)

Supplemental Table 3.2 Continued

Country	Race	Accession [†]	Plant Number and (Year) F ₁	Plant Number and (Year) BC ₁	Location and (Year) of F ₁ Production
Peru	Paro	CUZ 76	7 (06)	12 (07)	Pioneer (06)
Peru	Perla	ANC 23*	6 (06)	6 (07)	Pioneer (06)
Peru	Perla	ANC 24*	11 (09)	12 (10)	FL (09)
Peru	Perla	LIM 50*	10 (09)	21 (10)	FL (09)
Peru	Piricincó	SM 8*	6 (07)	10 (08)	Pioneer (07)
Peru	Pisccorunto	APC 13	7 (09)	2 (10)	Syngenta (09)
Peru	Pisccorunto	APC 13B	6 (11)	16 (12)	FL (11)
Peru	Rabo de Zorro	ANC 325*	9 (07)	12 (08)	Pioneer (07)
Peru	Rienda	CAJ 80	2 (06)	6 (07)	Pioneer (06)
Peru	San Geronimo Huancaveli	JUN 164	4 (07)	12 (08)	Pioneer (07)
Peru	Sarco	ANC 184	1 (06)	5 (07)	Pioneer (06)
Peru	Shajatu	ANC 117	2 (07) + 4 (08)	12 (09)+ 10 (09)	Pioneer (07) + Pioneer (08)
Trinidad	Tuson	TRN 1	9 (10)	22 (11)	FL (10)
Trinidad	Tuson	TRN 10	7 (07)	9 (08)	Syngenta (07)
Uruguay	Cateto Sulino	URG IV	7 (10)	12 (11)	CLY (10)
Uruguay	Cateto Sulino Escuro	URG V	9 (10)	15 (11)	CLY (10)
Uruguay	Cateto Sulino Grosso	URG III	7 (10)	12 (11)	CLY (10)
Uruguay	Dentado Branco	URZM 13010	12 (10)	12 (11)	CLY (10)
Uruguay	Semi-Dentado Rugoso	URZM 13052	12 (10)	12 (11)	CLY (10)
USA	Apache	PI 213731	7 (11)	7 (11)	CLY (11)
USA	Argentine Pop	PI 217404*	5 (10)	16 (11)	CLY (10)
USA	Bear Isl. Chippewa	PI 213801*	1 (10)	7 (11)	CLY (11)
USA	Cherokee	PI 213744*	8 (10)	12 (11)	CLY (10)
USA	Cochiti Pueblo	PI 218151*	10 (10)	17 (11)	CLY (10)
USA	Domingo Pueblo	PI 218130*	6 (10)	15 (11)	CLY (10)
USA	Gaspé Flint	PI 401757*	6 (10)	4 (11)	CLY (10)

Supplemental Table 3.2 Continued

Country	Race	Accession [†]	Plant Number and (Year) F ₁	Plant Number and (Year) BC ₁	Location and (Year) of F ₁ Production
USA	Gourd Seed	PI 217405*	7 (10)	14 (11)	CLY (10)
USA	Gourd Seed	PI 414183*	10 (10)	12 (11)	CLY (10)
USA	Havasupai	PI 317675*	7 (10)	15 (11)	CLY (10)
USA	Havasupai	PI 317679*	6 (10)	14 (11)	CLY (10)
USA	Hopi	PI 213733*	8 (10)	23 (11)	CLY (10)
USA	Hualapai	PI 213741*	11 (11)	9 (11)	CLY (11)
USA	Isleta-Tiwa	PI 218148*	7 (10)	16 (11)	CLY (10)
USA	Jemez Pueblo	PI 218173*	6 (10)	13 (11)	CLY (10)
USA	Laguna Pueblo	PI 218169*	6 (10)	13 (11)	CLY (10)
USA	Laguna Pueblo	PI 218170*	6 (10)	13 (11)	CLY (10)
USA	Longfellow Flint	PI 217408*	6 (10)	25 (11)	CLY (10)
USA	Longfellow	PI 214195*	12 (10)	15 (11)	CLY (10)
USA	Mexican June	PI 221889*	4 (10)	14 (11)	CLY (10)
USA	Mexican June	PI 311243*	10 (10)	16 (11)	CLY (10)
USA	Moencopi Pueblo	PI 218175*	6 (10)	18 (11)	CLY (10)
USA	Moencopi Pueblo	PI 218177*	4 (10)	15 (11)	CLY (10)
USA	Mohave	PI 218187*	6 (10)	12 (11)	CLY (10)
USA	Mohawk Round Nose	PI 483087*	5 (10)	24 (11)	CLY (10)
USA	N.W. Dent	PI 217480*	7 (10)	26 (11)	CLY (10)
USA	Navajo	PI 218163*	11 (11)	8 (11)	CLY (11)
USA	Northeast Flint	WLB	6 (10)	16 (11)	CLY (10)
USA	Papago-Pimans	PI 217410*	7 (10)	21 (11)	CLY (10)
USA	Pueblo 12-Row Hopi Koko	PI 503564*	7 (10)	20 (11)	CLY (10)
USA	Quapaw Red	PI 213757*	10 (10)	12 (11)	CLY (10)
USA	Sac And Fox	PI 217411*	4 (10)	23 (11)	CLY (10)
USA	San Lorenzo Pueblo	PI 218135	4 (10)	21 (11)	CLY (10)

Supplemental Table 3.2 Continued

Country	Race	Accession [†]	Plant Number and (Year) F ₁	Plant Number and (Year) BC ₁	Location and (Year) of F ₁ Production
USA	Santo Domingo Pueblo	PI 218143*	5 (10)	13 (11)	CLY (10)
USA	Seneca Hominy Corn	PI 401754*	1 (10)	7 (11)	CLY (11)
USA	Shoshone	PI 213769*	2 (10)	9 (11)	CLY (11)
USA	Smut Nose	PI 222490*	4 (10)	16 (11)	CLY (10)
USA	Supergold Pop	PI 222648*	9 (10)	12 (11)	CLY (10)
USA	Tennessee Red Cob	PI 311235*	11 (10)	12 (11)	CLY (10)
USA	Tesuque Pueblo	PI 218137*	6 (10)	15 (11)	CLY (10)
USA	White Dent	PI 221885*	11 (10)	12 (11)	CLY (10)
USA	White Dent	PI 311232*	7 (10)	16 (11)	CLY (10)
USA	Winnebago	PI 213772*	3 (10)	17 (11)	CLY (10)
USA	Winnebago	PI 213774*	3 (10)	8 (11)	CLY (11)
USA	Zia Pueblo	PI 218139*	4 (10)	15 (11)	CLY (10)
U.S. Virgin Islands	St. Croix	IVC 2*	9 (09)	19 (10)	FL (09)
Venezuela	Araguito	VEN 568	1 (09) + 8 (10)	23 (11)	Pioneer (09) + FL (10)
Venezuela	Araguito	VEN 628	12 (10)	13 (11)	FL (10)
Venezuela	Araguito	VEN 678	1 (06)	6 (07)	Pioneer (06)
Venezuela	Araguito	VEN 760	3 (10)	12 (11)	FL (10)
Venezuela	Cacao	VEN 630	3 (06)	9 (07)	Pioneer (06)
Venezuela	Canilla	VEN 693	4 (07)	10 (08)	Pioneer (07)
Venezuela	Cariaco	VEN 408	13 (09)	9 (10)	FL (09)
Venezuela	Cariaco	VEN 631	5 (10)	9 (11)	FL (10)
Venezuela	Cariaco	VEN 639	9 (05)	6 (08)	Syngenta (05)
Venezuela	Chandelle	VEN 409	9 (07)	12 (08)	Pioneer (07)
Venezuela	Chandelle	VEN 460	15 (09)	20 (10)	FL (09)
Venezuela	Chirimito	VEN 703*	8 (07)	10 (08)	Pioneer (07)
Venezuela	Comun	VEN 448	12 (09)	11 (10)	FL (09)

Supplemental Table 3.2 Continued

Country	Race	Accession [†]	Plant Number and (Year) F ₁	Plant Number and (Year) BC ₁	Location and (Year) of F ₁ Production
Venezuela	Comun	VEN 881	13 (09)	7 + 5 (10)	FL (09)
Venezuela	Costeno	VEN 775	8 (05)	8 (08)	Syngenta (05)
Venezuela	Cuba Yellow Flint	VEN 331	4 (07)	12 (08)	Syngenta (07)
Venezuela	Cuba Yellow Flint	VEN 650	6 (10)	11 (11)	FL (10)
Venezuela	Guaribero	VEN 653	11 (07)	12 (08)	Pioneer (07)
Venezuela	Guaribero	VEN 733	14 (09)	13 (10)	FL (09)
Venezuela	Huevito	VEN 396	4 (07)	5 (08)	Pioneer (07)
Venezuela	Huevito	VEN 445	14 (09)	21 (10)	FL (09)
Venezuela	Negrito	VEN 426	12 (09)	10 (10)	FL (09)
Venezuela	Negrito	VEN 673	15 (09)	19 (10)	FL (09)
Venezuela	Negrito	VEN 870	12 (05)	10 (08)	Syngenta (05)
Venezuela	Pira	VEN 457	12 (09)	11 (10)	FL (09)
Venezuela	Pollo	VEN 310	1 (09) + 5 (10)	12 (11)	CLY (09) + FL (10)
Venezuela	Puya	VEN 946	7 (08)	12 (09)	Pioneer (08)
Venezuela	Puya Grande	VEN 345	10 (09)	21 (10)	FL (09)
Venezuela	Puya Grande	VEN 651	5 (08)	12 (09)	Pioneer (08)
Venezuela	Tuson	VEN 405	4 (07)	9 (08)	Syngenta (07)
Venezuela	Tuxpeno	VEN 598	6 (09)	14 (10)	FL (09)
Venezuela	Tuxpeno	VEN 692	7 (07)	11 (08)	Syngenta (07)
Venezuela	Tuxpeno	VEN 891	10 (09)	16 (10)	FL (09)

Notes: Country, Race, and Accession of each landrace used are given. Plant Number and Year F_1 is the number of plants that were used to make the F_1 , inside parentheses the year that cross was made. Plant Number and Year BC_1 is the number of plants that were used to make the BC_1 , and inside parentheses the year that cross was made. Location of F_1 Production gives the location and year where F_1 s were made. F_1 s were made by GEM project personnel in both Clayton, NC (CLY) and Homestead, FL (FL) or in locations donated with in kind support from Dupont Pioneer in Hawaii, and Syngenta in Puerto Rico.

Most accessions were collected during the 1940s and 1950s; additional Mexican accessions were collected during the 1960s and 1970s by E. Hernández X. and R. Ortega P. Data on Altitude, Latitude and Longitude were obtained from Vigouroux et al (2008), from the Original Strains of Corn Vol I and Vol II (NSF-NRC, 1954) and from the studies of the accessions published by the National Academy of Sciences and Harvard (Brieger et al, 1958; Brown 1960; Grant et al, 1963; Grobman et al, 1961; Hatheway, 1957; Ramírez et al, 1960; Roberts et al, 1957; Timothy et al, 196,1963; Wellhausen et al, 1952, 1957). Also occasionally seed from a given accession was sampled twice by the Goodman group at different times. These two samples were labeled sample A and B, these are not different accessions. Accessions labeled with (USDA) indicate accessions from Brazil which were once held in storage at Glenn Dale, MD, but not from the NRC. They were increased by MMG and are now deposited with the NCRPIS at Ames, Iowa. It is also noted that accessions noted with an asterisk (*) are those currently available from NCRPIS, unfortunately these number only 170 of the accessions used in this study.

Supplemental Table 3.3 List of accessions used, country of origin, race name, accession name, source, and latitude, longitude, and altitude at point of collection with least square means and standard errors of DTA, DTS, ASI, and Lodging.

DTA was scored as number of days after planting till 50% of plants in row showed pollen shed, DTS scored as number of days after planting till 50% of plants in row showed silk. ASI was the difference between DTS and DTA. Lodging was scored on a 1 to 9 scale with 9 being resistant.

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	DTA	DTA SE	DTS	DTS SE	ASI	ASI SE	LODGE	LODGE SE
Argentina	Amargo	ARZM 03014	NCRPIS	-32.2	-58.1	20	65.0	2.09	68.8	1.59	3.86	0.13	4.9	0.74
Argentina	Bola Blanca	ARG 532 (USDA)	NCRPIS	-23.2	-65.4	2287	63.9	2.05	67.6	1.36	3.74	0.13	4.8	0.65
Argentina	Calchaqui Small White	ARG 2420 (USDA)	NCRPIS	-32.7	-64.7	895	63.7	2.05	67.6	1.37	3.90	0.13	5.2	0.65
Argentina	Camelia	ARZM 03025	NCRPIS	-30.5	-58.3	68	65.7	2.05	69.8	1.36	4.05	0.13	5.1	0.65
Argentina	Canario de Formosa	ARZM 06016	NCRPIS	-1.7	-78.7	3050	66.2	2.05	70.1	1.37	3.92	0.13	4.8	0.65
Argentina	Canario de Ocho	ARG VI	CIMMYT	-32	-58	305	64.8	2.05	68.1	1.36	3.24	0.13	5.3	0.65
Argentina	Capia Blanco	ARG 499 (USDA)	NCRPIS	-23.2	-65.4	2287	65.1	2.05	69.7	1.36	4.53	0.13	5.7	0.65
Argentina	Capia Rosado	ARG 460 (USDA)	NCRPIS	-23.2	-65.4	2287	65.6	2.05	69.6	1.36	3.99	0.13	5.2	0.65
Argentina	Cateto Sulino	ARG I	CIMMYT	-32	-58	305	64.7	2.05	69.4	1.37	4.73	0.13	5.1	0.65
Argentina	Chulpi	ARG 484 (USDA)	NCRPIS	-23.2	-65.4	2287	64.8	2.05	68.5	1.36	3.70	0.13	5.0	0.65
Argentina	Cravo	ARZM 05071	NCRPIS	-33	-71.6	80	66.4	2.05	70.4	1.37	3.98	0.13	5.4	0.65
Argentina	Cristal Sulino	ARG III	CIMMYT	-29	-62	1554	65.0	2.05	68.9	1.36	3.90	0.13	5.5	0.65
Argentina	Cristalino Amarillo	AR 21004	NCRPIS	-38.1	-62.2	295	61.7	2.06	64.6	1.36	2.92	0.13	4.6	0.65
Argentina	Cristalino Amarillo	ARZM 19070	NCRPIS	-39.5	-69.3	381	63.6	2.05	67.1	1.37	3.50	0.13	4.0	0.65
Argentina	Cristalino Blanco	ARZM 19074	NCRPIS	-39.5	-69.3	381	63.6	2.05	67.3	1.36	3.75	0.13	4.4	0.65
Argentina	Cristalino Colorado	ARZM 16021	NCRPIS	-32.6	-69.3	1886	64.5	2.05	67.8	1.36	3.31	0.13	5.4	0.65
Argentina	Cuarentino	ARG 486 (USDA)*	NCRPIS	-34.9	-58	276	64.7	2.05	68.0	1.36	3.30	0.13	4.7	0.65
Argentina	Culli	ARG 471 (USDA)	NCRPIS	-23.2	-65.4	2287	63.5	2.05	67.9	1.37	4.46	0.13	5.5	0.65
Argentina	Dentado Amarillo	ARZM 16062	NCRPIS	-35	-67.7	474	65.7	2.05	69.2	1.36	3.42	0.13	5.3	0.65
Argentina	Dentado Blanco	ARZM 03056	NCRPIS	-39.2	-59.5	58	66.4	2.05	69.8	1.37	3.42	0.13	5.2	0.65

Supplemental Table 3.3 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	DTA	DTA SE	DTS	DTS SE	ASI	ASI SE	LODGE	LODGE SE
Argentina	Dentado Blanco Rugoso	ARZM 01149	NCRPIS	-38.2	-62.4	285	66.7	2.05	71.3	1.37	4.55	0.13	5.6	0.65
Argentina	Dulce	ARZM 20005B	NCRPIS	-40.8	-63	5	63.6	2.09	67.3	1.59	3.69	0.13	4.5	0.74
Argentina	Marron	ARG 468 (USDA)	NCRPIS	-23.8	-65.5	2359	64.4	2.09	67.5	1.59	3.14	0.13	5.7	0.74
Argentina	Oke	ARG 539 (USDA)	NCRPIS	-23.2	-65.4	2287	65.2	2.05	69.5	1.36	4.36	0.13	5.0	0.65
Argentina	Pisincho	ARG 481 (USDA)*	NCRPIS	-23.2	-65.4	2287	63.9	2.05	67.8	1.36	3.87	0.13	5.1	0.65
Argentina	Pisingallo	ARZM 13095	NCRPIS	-30.3	-66.3	457	64.9	2.05	69.5	1.36	4.63	0.13	5.1	0.65
Barbados	Tuson	BARBGP 2*	NCRPIS	13.1	-59.6	60	67.7	2.05	72.2	1.37	4.52	0.13	5.7	0.65
Bolivia	Altiplano	BOV 903	NRC	-21.8	-64.1	1976	65.0	2.05	69.8	1.36	4.72	0.13	6.0	0.65
Bolivia	Argentino	BOV 920	ICA	-21.8	-64.1	1829	66.2	2.05	69.6	1.36	3.40	0.13	5.5	0.65
Bolivia	Aysuma	BOV 331	ICA	-19	-65.3	2127	65.2	2.05	70.4	1.36	5.19	0.13	5.8	0.65
Bolivia	Camba	BOV 1131	ICA	-16.5	-68.2	1570	69.4	2.05	75.1	1.37	5.72	0.13	5.6	0.65
Bolivia	Cateto	BOV 1083	NRC	-11.3	-67.7	240	67.2	2.05	71.2	1.36	4.06	0.13	5.4	0.65
Bolivia	Cateto	BOV 317	NCRPIS	-17.8	-64.8	2843	66.7	2.05	70.8	1.36	4.06	0.13	5.4	0.65
Bolivia	Chake-Sara	BOV 520	NCRPIS	-17.5	-65.7	2395	65.0	2.05	68.9	1.36	3.89	0.13	5.4	0.65
Bolivia	Checchi	BOV 320	ICA	-17.4	-66.2	2080	66.5	2.05	70.4	1.36	3.92	0.13	5.8	0.65
Bolivia	Checchi	BOV Comp.	NCRPIS	-18.1	-65.8	2542	64.5	2.05	69.1	1.36	4.66	0.13	5.2	0.65
Bolivia	Cholito	BOV 309	NCRPIS	-18.1	-64.4	1581	67.4	2.05	70.8	1.37	3.48	0.13	4.7	0.65
Bolivia	Chuspillu	BOV 883	NCRPIS	-17.5	-65.7	2507	66.3	2.05	71.7	1.36	5.49	0.13	5.9	0.65
Bolivia	Coroico	BOV 1064	NCRPIS	-14	-65	92	66.9	2.05	70.4	1.36	3.48	0.13	6.0	0.65
Bolivia	Coroico Amarillo	BOV 405	NRC	-14.9	-65	160	67.3	2.05	71.8	1.37	4.51	0.13	5.9	0.65
Bolivia	Coroico Blanco	BOV 406	NCRPIS	-14.7	-65	130	67.4	2.05	71.7	1.37	4.27	0.13	5.5	0.65
Bolivia	Cubano Dentado	BOV 440	NRC	-17.8	-63.2	560	66.2	2.05	69.5	1.37	3.29	0.13	5.7	0.65
Bolivia	Cubano Dentado	BOV 585	NRC	-16.4	-61	330	66.6	2.05	70.2	1.37	3.58	0.13	6.2	0.65
Bolivia	Enano	BOV 1032	NCRPIS	-11	-68	180	67.1	2.05	70.1	1.36	3.05	0.13	5.4	0.65
Bolivia	Huilcaparu	BOV 685	ICA	-17.4	-65.9	2721	68.5	2.05	73.0	1.37	4.43	0.13	5.7	0.65
Bolivia	Huilcaparu Moteado	BOV Comp.	NCRPIS	-16.9	-67.1	2760	67.1	2.05	72.6	1.36	5.54	0.13	5.8	0.65

Supplemental Table 3.3 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	DTA	DTA SE	DTS	DTS SE	ASI	ASI SE	LODGE	LODGE SE
Bolivia	Karapampa	BOV 978	ICA	-21.8	-64.1	1976	65.4	2.05	69.9	1.36	4.55	0.13	4.9	0.65
Bolivia	Kcello	BOV 325	ICA	-17.4	-66.2	1400	65.4	2.05	69.6	1.37	4.22	0.13	6.2	0.65
Bolivia	Kcello	BOV 848	ICA	-19.6	-65.8	1801	66.3	2.05	72.0	1.36	5.73	0.13	5.0	0.65
Bolivia	Kcello	BOV 948	NRC	-19.6	-65.8	3256	64.9	2.05	67.5	1.36	2.62	0.13	4.9	0.65
Bolivia	Morado	BOV 567	ICA	-16.5	-67.5	2270	67.6	2.05	72.5	1.36	4.88	0.13	5.7	0.65
Bolivia	Ninuelo	BOV 1088	ICA	-17.8	-63.2	2201	67.0	2.05	72.2	1.37	5.20	0.13	5.8	0.65
Bolivia	Paru	BOV Comp.	NCRPIS	-15.8	-68.6	2737	67.1	2.07	71.6	1.37	4.45	0.13	5.4	0.65
Bolivia	Patillo Grande	BOV 649	ICA	-17.5	-65.7	2515	65.5	2.05	69.2	1.36	3.64	0.13	5.8	0.65
Bolivia	Perola	BOV 711	NRC	-21.3	-63.5	520	66.9	2.05	71.5	1.37	4.58	0.13	5.4	0.65
Bolivia	Pisankalla	BOV 344	ICA	-21.5	-64.8	1738	63.7	2.05	68.2	1.37	4.49	0.13	5.3	0.65
Bolivia	Pisankalla	BOV 864	ICA	-17.5	-65.7	2175	63.9	2.05	66.2	1.37	2.33	0.13	5.1	0.65
Bolivia	Pisankalla	BOV 965	ICA	-21.8	-64.1	1948	64.2	2.05	68.1	1.37	3.88	0.13	5.8	0.65
Bolivia	Pojoso Chico	BOV 800	NCRPIS	-17.7	-62.8	500	65.0	2.05	68.1	1.37	3.18	0.13	5.5	0.65
Bolivia	Pororo	BOV 583	ICA	-15.7	-67.3	330	67.5	2.05	71.3	1.37	3.86	0.13	5.4	0.65
Bolivia	Pororo	BOV 806	NRC	-18.3	-59.8	1400	68.4	2.07	73.3	1.37	4.87	0.13	6.3	0.65
Bolivia	Uchuquilla	BOV 318	NCRPIS	-17.2	-66.1	1922	66.3	2.05	70.5	1.37	4.18	0.13	6.0	0.65
Bolivia	Uchuquilla	BOV 954	ICA	-21.8	-64.1	1948	67.0	2.05	70.3	1.37	3.23	0.13	5.3	0.65
Bolivia	Yungueno	BOV 362	ICA	-21.8	-64.1	1052	67.0	2.05	72.2	1.36	5.22	0.13	5.9	0.65
Bolivia	Yungueno	BOV 716	ICA	-16.5	-68.2	1400	68.0	2.05	72.5	1.37	4.54	0.13	6.1	0.65
Brazil	Avati Pichinga	BR 2760 (USDA)	NCRPIS	-25	-56	366	68.1	2.05	73.0	1.37	4.85	0.13	5.0	0.65
Brazil	Avati Pichinga	BR 2776 (USDA)	NCRPIS	-25	-56	366	67.7	2.05	72.9	1.37	5.16	0.13	5.9	0.65
Brazil	Avati Pichinga Ihu	BR 2830 (USDA)	NCRPIS	-25	-56	366	66.8	2.05	70.9	1.36	4.13	0.13	5.3	0.65
Brazil	Caingang	PR III	CIMMYT	-23	-51	610	66.7	2.05	71.9	1.37	5.18	0.13	5.4	0.65
Brazil	Caingang	SP XIII	CIMMYT	-22	-51	407	65.7	2.05	69.8	1.36	4.09	0.13	5.5	0.65
Brazil	Caraja	1692 (USDA)	NCRPIS	-27.2	-49.6	433	68.3	2.05	73.1	1.37	4.82	0.13	6.3	0.65
Brazil	Cateto	BA II	CIMMYT	-12.5	-39	610	67.6	2.05	71.7	1.36	4.04	0.13	5.8	0.65

Supplemental Table 3.3 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	DTA	DTA SE	DTS	DTS SE	ASI	ASI SE	LODGE	LODGE SE
Brazil	Cateto	CE I	CIMMYT	-3.8	-38.8	177	67.3	2.05	71.4	1.37	4.03	0.13	5.7	0.65
Brazil	Cateto Assis Brasil	RGS XIV	NCRPIS	-29	-53	274	66.4	2.06	69.7	1.36	3.25	0.13	5.6	0.66
Brazil	Cateto Grande	MT IV	CIMMYT	-20	-56	366	67.8	2.05	71.4	1.37	3.63	0.13	5.9	0.65
Brazil	Cateto Nortista Precoce	SUR I	CIMMYT	5.8	-55.2	61	67.3	2.05	71.6	1.36	4.27	0.13	5.0	0.65
Brazil	Cravo Paulista	SP I	CIMMYT	-22	-48	579	66.4	2.05	70.7	1.36	4.26	0.13	5.3	0.65
Brazil	Cravo Riograndense	RGS VII	CIMMYT	-30	-53	366	67.1	2.05	70.4	1.37	3.30	0.13	5.3	0.65
Brazil	Cristal	SP X	CIMMYT	-22	-48	803	68.1	2.05	71.0	1.36	2.97	0.13	6.4	0.65
Brazil	Cristal	SP XI	CIMMYT	-22	-48	803	68.3	2.06	73.9	1.37	5.65	0.13	6.1	0.65
Brazil	Cristal Inter. Perola	1115 (USDA)	NCRPIS	-28.4	-54.3	240	67.4	2.05	71.0	1.37	3.66	0.13	5.2	0.65
Brazil	Cristal Paraguay Paulis	2334 (USDA)	NCRPIS	-23.3	-46.1	582	67.9	2.05	72.4	1.37	4.49	0.13	6.3	0.65
Brazil	Dente Branco Paulista	SP V	CIMMYT	-22	-48	579	67.4	2.05	71.1	1.37	3.71	0.13	5.0	0.65
Brazil	Dente Branco R. G.	SC II	CIMMYT	-27	-52	892	66.0	2.05	69.7	1.37	3.75	0.13	5.4	0.65
Brazil	Dente Paulista	SP IV	CIMMYT	-22	-48	518	67.4	2.05	71.0	1.37	3.65	0.13	5.8	0.65
Brazil	Dente R. G. Liso	RGS VI	CIMMYT	-29	-52	366	67.9	2.05	72.9	1.37	5.00	0.13	5.7	0.65
Brazil	Dente R. G. Liso	SC I	CIMMYT	-27	-52	892	67.9	2.05	71.7	1.36	3.83	0.13	5.3	0.65
Brazil	Dente R. G. Rugoso	RGS II	CIMMYT	-30	-53	366	66.9	2.05	71.0	1.36	4.12	0.13	4.9	0.65
Brazil	Dourados Saboro	BR 50 (USDA)	NCRPIS	-22.3	-54.8	340	67.9	2.05	72.3	1.37	4.42	0.13	5.6	0.65
Brazil	Entrelacado	MT VI	CIMMYT	-18	-55	305	68.7	2.05	72.9	1.37	4.22	0.13	6.0	0.65
Brazil	Hickory King	RGS IX*	CIMMYT	-28.5	-51	366	66.1	2.05	70.3	1.36	4.20	0.13	5.4	0.65
Brazil	Moroti	MT I	CIMMYT	-20	-56	366	66.6	2.05	71.2	1.37	4.60	0.13	5.9	0.65
Brazil	Moroti	PE I	NCRPIS	-8	-36	344	68.0	2.05	72.0	1.37	3.96	0.13	6.1	0.65
Brazil	Moroti Precoce	BOL I	CIMMYT	-20	-58	457	64.9	2.05	69.1	1.37	4.22	0.13	5.7	0.65
Brazil	Semi Dente Paulista	SP IX	CIMMYT	-22	-48	305	66.9	2.05	71.2	1.37	4.28	0.13	5.6	0.65
Brazil	Semi Dente R. G.	RGS XV	CIMMYT	-30	-53	366	67.6	2.05	71.8	1.37	4.27	0.13	5.5	0.65
Brazil	Tuson	BAI III	CIMMYT	-12.5	-39	200	66.5	2.05	69.4	1.37	2.87	0.13	6.3	0.65
Brazil	Tuson	BAI IIIB	NCRPIS	-12.5	-39	200	66.6	2.09	70.5	1.59	3.97	0.13	5.9	0.74

Supplemental Table 3.3 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	DTA	DTA SE	DTS	DTS SE	ASI	ASI SE	LODGE	LODGE SE
Chile	Araucano	CHI 320*	NCGRP	-38.1	-72.3	417	62.1	2.05	67.0	1.36	4.84	0.13	5.0	0.65
Chile	Capia Chico Chileno	CHI 382*	NRC	-23.7	-70.4	40	62.4	2.09	66.9	1.59	4.45	0.13	5.3	0.74
Chile	Cristalino Chico	CHI 324	NCGRP	-38.1	-71.9	66	59.7	2.05	64.5	1.36	4.85	0.13	4.8	0.66
Chile	Cristalino Chileno	CHI 156	NCRPIS	-38.1	-71.9	66	64.6	2.05	67.6	1.36	2.93	0.13	5.4	0.65
Chile	Cristalino Grande	CHI 323*	NCRPIS	-37.5	-72.4	139	62.2	2.09	67.0	1.59	4.79	0.13	4.2	0.74
Chile	Curagua	CHI 301*	NRC	-33	-70.7	732	62.7	2.05	65.9	1.37	3.12	0.13	4.6	0.65
Chile	Curagua	CHI 314*	NCGRP	-33.2	-70.7	457	64.5	2.05	69.1	1.36	4.59	0.13	5.4	0.65
Chile	Curagua Grande	CHI 303	NRC	-33.2	-70.7	457	64.3	2.05	68.3	1.36	4.07	0.13	4.7	0.65
Chile	Dentado Comercial	CHI 326*	NCGRP	-38.1	-71.9	66	65.9	2.05	69.9	1.36	4.05	0.13	5.1	0.65
Chile	Dulce Evergreen	CHI 332*	NCGRP	-38.1	-71.9	66	64.5	2.05	67.3	1.36	2.83	0.13	5.1	0.65
Chile	Dulce Golden Bantam	CHI 335*	NCGRP	-38.1	-71.9	66	63.0	2.05	66.5	1.36	3.44	0.13	4.9	0.65
Chile	Harinoso Tarapaqueno	CHI 421	NRC	-19.9	-69.5	1550	67.9	2.05	73.2	1.37	5.30	0.13	5.4	0.65
Colombia	Amagaceno	ANT 343*	NCRPIS	6.2	-75.8	1800	68.6	2.05	72.6	1.37	3.96	0.13	6.0	0.65
Colombia	Amagaceno	HUI 317*	NCRPIS	2.5	-74.8	1554	68.5	2.05	72.7	1.37	4.20	0.13	6.4	0.65
Colombia	Andaqui	CAQ 307*	NCRPIS	1.2	-75.9	490	67.7	2.05	72.3	1.37	4.66	0.13	6.3	0.65
Colombia	Andaqui	CAQ 333*	NRC	1.8	-75.6	500	67.5	2.06	72.1	1.37	4.58	0.13	5.7	0.65
Colombia	Cabuya	SAN 316*	NRC	7.4	-72.7	2100	67.4	2.05	72.7	1.36	5.31	0.13	6.2	0.65
Colombia	Cacao	SAS 327*	ICA	5.9	-73.7	1600	68.3	2.06	73.9	1.37	5.66	0.13	6.4	0.65
Colombia	Cacao	SAS 335*	NCGRP	6.4	-73.3	1300	68.3	2.06	71.3	1.37	2.98	0.13	5.7	0.65
Colombia	Capio	ANT 348*	ICA	5.9	-75.4	1966	68.5	2.06	75.1	1.37	6.63	0.13	5.9	0.65
Colombia	Capio	ANT 354	ICA	5.7	-75.3	2600	69.3	2.05	76.1	1.37	6.74	0.13	5.7	0.65
Colombia	Capio	NAR 315	ICA	1.2	-77.3	2360	69.7	2.06	76.2	1.37	6.52	0.13	6.4	0.65
Colombia	Caqueteno	CAQ 305*	ICA	1.5	-75.4	300	67.3	2.05	72.0	1.37	4.65	0.13	5.7	0.65
Colombia	Cariaco	COR 338*	NCGRP	8.8	-75.9	200	67.6	2.05	71.6	1.37	3.97	0.13	6.4	0.65
Colombia	Chococeno	CHO 340	NCRPIS	7.5	-77.1	30	69.0	2.05	74.2	1.37	5.19	0.13	6.5	0.65
Colombia	Clavo	NAR 329*	ICA	1.2	-77.3	2360	68.4	2.05	74.3	1.37	5.88	0.13	5.4	0.65

Supplemental Table 3.3 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	DTA	DTA SE	DTS	DTS SE	ASI	ASI SE	LODGE	LODGE SE
Colombia	Comun	CAU 454*	NCRPIS	7.5	-74.8	600	68.0	2.05	73.7	1.36	5.69	0.13	6.1	0.65
Colombia	Comun	NAR 330*	NCRPIS	1.5	-78.5	118	66.2	2.05	70.3	1.36	4.11	0.13	6.0	0.65
Colombia	Comun	VAL 374*	NCRPIS	3.6	-76.5	980	66.8	2.05	70.6	1.37	3.79	0.13	5.9	0.65
Colombia	Costeno	ANT 394*	NCRPIS	2.2	-76.9	922	67.4	2.05	70.3	1.37	2.91	0.13	7.0	0.65
Colombia	Costeno	ATL 314*	NCRPIS	10.9	-74.8	15	65.9	2.05	69.0	1.36	3.13	0.13	5.6	0.65
Colombia	Costeno	ATL 328*	NRC	10.4	-74.9	7	65.2	2.06	68.8	1.36	3.61	0.13	6.2	0.65
Colombia	Costeno	COR 320*	NCGRP	8.3	-75.2	100	67.3	2.05	71.5	1.36	4.12	0.13	6.1	0.65
Colombia	Guirua	MAG 469*	NCGRP	10.5	-73.3	1870	68.1	2.05	71.4	1.37	3.38	0.13	5.6	0.65
Colombia	Harin. Dent.	NAR 326*	NCRPIS	1.4	-77.6	1400	68.5	2.05	73.5	1.37	4.96	0.13	5.6	0.65
Colombia	Imbricado	NAR 389	ICA	0.8	-77.6	2000	68.5	2.06	74.0	1.37	5.48	0.13	6.4	0.65
Colombia	Montana	NAR 625*	NCRPIS	1.2	-77.3	2542	67.9	2.06	71.8	1.36	3.92	0.13	6.7	0.66
Colombia	Pira	CUN 327*	NRC	4.3	-74.4	1000	67.4	2.05	73.1	1.37	5.61	0.13	5.7	0.65
Colombia	Pira	CUN 480*	NRC	4.8	-74.7	1000	69.0	2.05	74.9	1.37	5.88	0.13	6.3	0.65
Colombia	Pira	TOL 405	NRC	4.2	-74.9	450	69.0	2.05	74.8	1.37	5.80	0.13	5.9	0.65
Colombia	Pollo	CUN 424	NCRPIS	4.8	-73.7	2000	66.3	2.05	70.3	1.37	3.98	0.13	5.8	0.65
Colombia	Pollo	CUN 443*	NRC	4.2	-74.4	1800	64.6	2.05	69.1	1.36	4.47	0.13	5.9	0.65
Colombia	Puya	MAG 355*	NRC	9.4	-75.7	27	67.2	2.05	71.1	1.36	3.92	0.13	6.0	0.65
Colombia	Puya Grande	SAN 347*	NCGRP	8.3	-73.3	1200	67.7	2.05	71.5	1.37	3.76	0.13	6.1	0.65
Colombia	Sabanero	ANT 423*	NCRPIS	7	-75.7	1480	66.5	2.05	70.2	1.36	3.69	0.13	6.4	0.65
Colombia	Sabanero	CUN 342*	NCRPIS	8.5	-75.5	250	68.1	2.05	71.5	1.37	3.46	0.13	6.1	0.65
Colombia	Sabanero	CUN 367	NCRPIS	4.3	-74	2110	67.9	2.05	72.0	1.37	4.16	0.13	6.5	0.65
Colombia	Sabanero	SAN 329	NRC	7.3	-72.5	2626	67.0	2.05	71.3	1.36	4.29	0.13	6.3	0.65
Colombia	Yucatan	TOL 389*	ICA	5	-74.9	450	67.2	2.05	71.7	1.37	4.46	0.13	6.5	0.65
Colombia	Yucatan	TOL 399*	NCGRP	4.6	-74.9	500	68.2	2.06	72.5	1.37	4.31	0.13	6.1	0.65
Costa Rica	Huesillo	CRI 370*	NCRPIS	9.9	-83.9	1500	66.8	2.09	71.4	1.59	4.63	0.13	5.8	0.74
Cuba	Argentino	CUB 113*	NCRPIS	20.3	-76.9	25	66.1	2.05	69.8	1.36	3.66	0.13	5.3	0.65

Supplemental Table 3.3 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	DTA	DTA SE	DTS	DTS SE	ASI	ASI SE	LODGE	LODGE SE
Cuba	Chandelle	CUB 54*	CIMMYT	20.9	-76.7	305	67.4	2.05	71.2	1.37	3.72	0.13	5.4	0.65
Cuba	Chandelle	CUB 68	NCRPIS	20.7	-76.1	369	66.0	2.05	69.6	1.37	3.66	0.13	5.9	0.65
Cuba	Cuban Flint	CUB 63*	CIMMYT	20.7	-75.7	15	66.1	2.09	69.0	1.60	2.91	0.13	5.8	0.74
Cuba	Maiz Criollo	CUB 136*	NCRPIS	22.9	-82.3	84	67.2	2.05	71.5	1.36	4.29	0.13	5.6	0.65
Cuba	Tuson	CUB 67*	CIMMYT	20.9	-76.5	305	68.4	2.05	73.7	1.37	5.27	0.13	5.9	0.65
Ecuador	Blanco Blandito	ECU 523	NRC	0.4	-78.4	2122	67.9	2.05	72.3	1.37	4.37	0.13	6.0	0.65
Ecuador	Blanco Harinoso Dentado	ECU 640	ICA	-4	-79.2	1921	68.2	2.05	73.7	1.37	5.55	0.13	5.7	0.65
Ecuador	Candela	ECU 344*	ICA	-0.7	-80.1	55	68.5	2.05	73.8	1.37	5.29	0.13	5.9	0.65
Ecuador	Candela	ECU 531	ICA	-1.1	-80.5	27	67.3	2.05	71.5	1.37	4.23	0.13	6.0	0.65
Ecuador	Candela	ECU 699	NCRPIS	-1.1	-80.5	50	67.6	2.05	71.0	1.37	3.43	0.13	5.1	0.65
Ecuador	Canguil	ECU 500	NRC	0.2	-78.4	2213	65.8	2.05	71.1	1.37	5.28	0.13	5.7	0.65
Ecuador	Canguil Grueso	ECU 443	NCRPIS	0	-78.5	2838	66.1	2.05	70.3	1.36	4.27	0.13	6.6	0.65
Ecuador	Canguil Grueso	ECU 447	ICA	0.1	-78.2	2579	65.3	2.05	69.5	1.36	4.16	0.13	4.7	0.65
Ecuador	Chillo	ECU 411	ICA	-0.3	-78.4	2510	68.1	2.05	71.0	1.36	2.88	0.13	6.4	0.65
Ecuador	Chillo	ECU 458	NRC	-2.9	-78.7	2195	68.7	2.05	73.7	1.37	5.06	0.13	6.8	0.65
Ecuador	Chillo	ECU 480B	NCRPIS	0	-78	2241	68.0	2.05	72.0	1.36	3.94	0.13	5.7	0.65
Ecuador	Cholito	ECU 718	ICA	-4.1	-79	1296	68.2	2.05	72.1	1.37	3.95	0.13	6.1	0.65
Ecuador	Chulpi Chico	ECU 424	NRC	0.1	-78.2	2600	67.3	2.05	71.8	1.37	4.48	0.13	5.6	0.65
Ecuador	Clavito	ECU 884	ICA	-1.3	-78.5	1646	66.9	2.05	71.2	1.37	4.30	0.13	5.7	0.65
Ecuador	Conico Dentado	ECU 427	ICA	0.1	-78.4	2058	69.3	2.05	74.6	1.36	5.35	0.13	6.1	0.65
Ecuador	Cubano Amarillo Duro	ECU 326	ICA	-1.1	-80.5	41	67.1	2.05	72.0	1.37	4.94	0.13	5.8	0.65
Ecuador	Cubano Amarillo Duro	ECU 327	NCRPIS	-2.2	-80.1	46	68.5	2.05	73.3	1.37	4.78	0.13	6.5	0.65
Ecuador	Cubano Amarillo Duro	ECU 698	ICA	-1.1	-80.5	50	67.1	2.05	71.2	1.37	4.13	0.13	6.0	0.65
Ecuador	Cubano Amarillo Duro	ECU 957	ICA	-1	-79.4	183	67.8	2.05	71.2	1.37	3.46	0.13	5.7	0.65
Ecuador	Cubano Cateto	ECU 877	ICA	-0.2	-79.3	229	68.3	2.05	72.7	1.37	4.35	0.13	6.2	0.65
Ecuador	Cubano Tuson	ECU 542	ICA	-1.1	-80.5	30	67.7	2.06	72.1	1.37	4.42	0.13	6.0	0.65

Supplemental Table 3.3 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	DTA	DTA SE	DTS	DTS SE	ASI	ASI SE	LODGE	LODGE SE
Ecuador	Cubano Tuson	ECU 660	ICA	-1.1	-80.5	30	67.5	2.05	72.4	1.37	4.96	0.13	5.8	0.65
Ecuador	Cubano Tuson	ECU 764	ICA	-1.1	-80.5	18	66.3	2.05	70.4	1.36	4.12	0.13	4.9	0.65
Ecuador	Enano Gigante	ECU Comp.	NCRPIS	-1.1	-78	916	68.7	2.05	72.8	1.36	4.10	0.13	6.4	0.65
Ecuador	Gallina	ECU 329	ICA	-1.9	-80	5	67.3	2.05	72.9	1.37	5.60	0.13	5.9	0.65
Ecuador	Huandango	ECU 735	NRC	0.8	-78	2287	68.2	2.05	72.8	1.37	4.55	0.13	6.3	0.65
Ecuador	Mishca	ECU 321	NRC	-1.7	-78.7	2241	65.8	2.05	70.4	1.36	4.65	0.13	6.3	0.65
Ecuador	Morochon	ECU 454B	NCRPIS	0	-78	2195	66.7	2.05	69.1	1.37	2.41	0.13	5.7	0.65
Ecuador	Patillo	ECU 417	ICA	-0.3	-78.6	2287	65.9	2.05	70.4	1.37	4.48	0.13	5.2	0.65
Ecuador	Pojoso Chico Ecuatorian	ECU 522	NCRPIS	-1	-77.8	530	65.8	2.05	70.0	1.37	4.23	0.13	5.1	0.65
Ecuador	Racimo de Uva	ECU 517	NRC	-1.7	-78.7	2287	65.6	2.05	69.5	1.36	3.95	0.13	5.8	0.65
Ecuador	Tusilla	ECU 569	ICA	-4.1	-79	274	67.8	2.05	72.8	1.37	4.94	0.13	5.4	0.65
Ecuador	Tuxpeno	ECU 942	ICA	-1	-79.4	184	67.2	2.05	72.7	1.37	5.51	0.13	5.8	0.65
Ecuador	Uchima	ECU 681	ICA	-4	-79.2	2152	67.6	2.05	72.0	1.36	4.41	0.13	6.9	0.65
Ecuador	Yungueno	ECU 572	ICA	-4.1	-79	1296	68.0	2.05	73.0	1.37	5.04	0.13	5.9	0.65
Ecuador	Yunquillano forma Andaqui	ECU 710	NCRPIS	-4.1	-79	1296	67.1	2.05	71.1	1.37	3.99	0.13	6.0	0.65
Ecuador	Yunquillano forma Andaqui	ECU 853	ICA	-3.5	-78.6	732	67.3	2.05	72.1	1.37	4.79	0.13	6.5	0.65
Ecuador	Yunquillano forma Andaqui	ECU 855	ICA	-3.5	-78.6	1098	67.2	2.05	70.9	1.37	3.67	0.13	5.8	0.65
El Salvad	Amarillo Salvadoreno	Comp.	NCRPIS	13.8	-89.3	721	65.6	2.05	69.3	1.36	3.72	0.13	5.4	0.65
Guatemala	Comiteco	GUA 418	INIFAP	15.4	-91.7	1768	67.9	2.05	72.7	1.36	4.87	0.13	6.0	0.65
Guatemala	Comiteco	GUA 515	NCRPIS	15.7	-91.6	1751	68.1	2.05	72.7	1.37	4.55	0.13	5.7	0.65
Guatemala	Comiteco	GUA 546	NCRPIS	15.7	-91.6	1751	68.7	2.06	73.1	1.37	4.42	0.13	6.1	0.65
Guatemala	Dzit Bacal	GUA 131	CIMMYT	14.3	-89.7	737	66.5	2.05	69.9	1.36	3.44	0.13	5.7	0.65
Guatemala	Imbricado	GUA 493	INIFAP	14.8	-91.6	2317	66.7	2.05	71.0	1.36	4.26	0.13	5.1	0.65
Guatemala	Imbricado	GUA 922	INIFAP	15.6	-91.5	2256	66.9	2.05	71.4	1.36	4.44	0.13	5.2	0.65
Guatemala	N de Chimaltenango	GUA 369	INIFAP	14.6	-90.9	2073	68.4	2.05	74.3	1.37	5.89	0.13	5.8	0.65
Guatemala	N de Chimaltenango	GUA 590	INIFAP	14.7	-90.9	2165	68.4	2.05	73.7	1.37	5.37	0.13	6.2	0.65

Supplemental Table 3.3 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	DTA	DTA SE	DTS	DTS SE	ASI	ASI SE	LODGE	LODGE SE
Guatemala	N de T Caliente	GUA 159	CIMMYT	14.6	-91.4	1067	66.5	2.05	69.8	1.36	3.29	0.13	5.5	0.65
Guatemala	N de T Fria	GUA 522	INIFAP	15.3	-91.5	1921	66.6	2.05	70.1	1.36	3.55	0.13	5.5	0.65
Guatemala	Nal Tel ATB	GUA 111	CIMMYT	14.6	-90.1	915	64.0	2.05	68.0	1.36	3.93	0.13	6.2	0.65
Guatemala	Nal Tel ATB	GUA 220	CIMMYT	14.6	-89.6	793	64.3	2.05	67.2	1.37	2.93	0.13	6.0	0.65
Guatemala	Nal Tel ATB	GUA 281	CIMMYT	14.3	-90.1	1113	65.6	2.05	69.1	1.36	3.55	0.13	5.4	0.65
Guatemala	Nal Tel BTA	GUA 20	INIFAP	14.6	-91.9	2439	68.5	2.09	72.0	1.60	3.48	0.13	6.6	0.74
Guatemala	Nal Tel BTB	GUA 145*	CIMMYT	15	-90.3	1006	64.5	2.05	68.1	1.36	3.62	0.13	5.6	0.65
Guatemala	Nal Tel BTB	GUA 280	CIMMYT	14.4	-89.9	1021	64.0	2.05	67.6	1.36	3.61	0.13	5.7	0.65
Guatemala	Nal Tel BTB	GUA 765*	CIMMYT	14.4	-89.9	1021	64.5	2.05	68.4	1.36	3.87	0.13	5.6	0.65
Guatemala	Oloton	GUA 383	NCRPIS	14.6	-90.6	1551	67.1	2.05	71.2	1.37	4.11	0.13	6.3	0.65
Guatemala	Quicheno Early	GUA 162	CIMMYT	15.1	-91.1	1860	67.2	2.05	71.1	1.37	3.95	0.13	6.0	0.65
Guatemala	Quicheno Late	GUA 863	INIFAP	15.4	-90.8	1829	68.7	2.06	75.0	1.37	6.38	0.13	5.0	0.65
Guatemala	Quicheno Late	GUA 877	NCRPIS	15.7	-91.5	2365	68.7	2.05	72.9	1.37	4.20	0.13	5.2	0.65
Guatemala	Salpor	GUA 476	INIFAP	14.9	-91.5	2317	68.1	2.05	73.6	1.37	5.48	0.13	5.4	0.65
Guatemala	Salpor Tardio	GUA 485	INIFAP	15	-91.8	2393	67.9	2.05	72.3	1.37	4.41	0.13	6.2	0.65
Guatemala	San Marceno	GUA 506	INIFAP	15.1	-91.7	2134	67.9	2.05	72.7	1.36	4.78	0.13	5.1	0.65
Guatemala	San Marceno	GUA 724	NCRPIS	14.7	-91	2304	68.6	2.05	72.8	1.37	4.20	0.13	5.7	0.65
Guatemala	Serrano	GUA 940	INIFAP	15	-91.8	3049	65.1	2.05	69.9	1.36	4.76	0.13	5.7	0.65
Guatemala	Tepecintle	GUA 597	CIMMYT	14.6	-91.7	427	67.3	2.05	70.9	1.37	3.56	0.13	5.8	0.65
Guatemala	Tepecintle	GUA 65	CIMMYT	14.6	-90.8	152	67.6	2.05	71.2	1.37	3.66	0.13	6.1	0.65
Guatemala	Tepecintle	GUA 651	CIMMYT	14.5	-91.4	290	67.4	2.05	72.9	1.37	5.57	0.13	5.3	0.65
Guatemala	Tepecintle	GUA 79	CIMMYT	15.4	-89.7	122	67.4	2.05	72.8	1.36	5.41	0.13	5.9	0.65
Guatemala	Tuxpeno	GUA 456	CIMMYT	16.5	-90.2	183	68.5	2.05	72.1	1.37	3.64	0.13	5.6	0.65
Guyana	Cateto Nortista	GIN 1	CIMMYT	6.8	-58.2	4	68.0	2.05	70.8	1.37	2.74	0.13	6.1	0.65
Haiti	Chandelle	HTI 14	INIFAP	19.5	-72	20	68.4	2.05	72.4	1.37	3.93	0.13	6.3	0.65
Haiti	Haitian Yellow	HTI 1	INIFAP	18.4	-74.3	580	67.2	2.05	70.9	1.37	3.74	0.13	6.1	0.65

Supplemental Table 3.3 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	DTA	DTA SE	DTS	DTS SE	ASI	ASI SE	LODGE	LODGE SE
Martinica	Early Carribean	Martinica 9	INIFAP	14.9	-61.1	90	66.4	2.05	69.7	1.36	3.36	0.13	5.7	0.65
Martinica	Unassigned	Martinica 12	NCRPIS	14.9	-61.1	90	66.3	2.05	69.0	1.36	2.70	0.13	5.8	0.65
Mexico	Apachito	CHH 138*	CIMMYT	29.7	-108.3	2210	63.0	2.05	67.2	1.37	4.20	0.13	4.8	0.65
Mexico	Apachito	CHH 166*	INIFAP	28	-107.6	2400	61.9	2.05	65.8	1.36	3.86	0.13	4.7	0.65
Mexico	Apachito	CHH 180*	INIFAP	27.8	-107.6	2180	61.9	2.05	65.2	1.36	3.27	0.13	5.0	0.65
Mexico	Apachito	CHH 207	CIMMYT	26.8	-107.3	2510	63.1	2.05	66.7	1.36	3.59	0.13	5.6	0.65
Mexico	Apachito	CHH 182	NCRPIS	27.8	-107.6	2368	63.1	2.05	67.1	1.37	4.02	0.13	5.0	0.65
Mexico	Arrocillo Amarillo	PUE 91	INIFAP	19.8	-97.6	2317	65.9	2.05	70.0	1.37	4.09	0.13	5.9	0.65
Mexico	Arrocillo Amarillo	VER 311*	INIFAP	19.8	-97.3	2220	66.0	2.05	70.0	1.36	4.03	0.13	5.1	0.65
Mexico	Azul	ACC 70-2	DHT	28.8	-107.7	1970	63.7	2.05	67.7	1.36	3.96	0.13	5.2	0.65
Mexico	Azul	CHH 158*	INIFAP	28.6	-107.5	2040	63.8	2.05	67.3	1.37	3.50	0.13	4.9	0.65
Mexico	Azul	CHH 220	INIFAP	28.7	-107.9	1900	64.1	2.05	68.2	1.36	4.08	0.13	5.9	0.65
Mexico	Azul	CHIH 218	NCRPIS	28.9	-107.8	1911	64.3	2.05	69.4	1.36	5.06	0.13	5.3	0.65
Mexico	Bofo	DGO 123	CIMMYT	25	-107	500	64.4	2.05	68.3	1.37	3.91	0.13	6.1	0.65
Mexico	Bofo	NAY 191*	CIMMYT	21.4	-104.1	1000	67.2	2.05	70.6	1.36	3.31	0.13	5.5	0.65
Mexico	Bofo	NAY 203	CIMMYT	21.1	-104.4	1850	66.9	2.05	71.3	1.36	4.40	0.13	5.9	0.65
Mexico	Bolita	OAX 44	INIFAP	17	-96.5	793	65.8	2.05	70.2	1.36	4.37	0.13	5.5	0.65
Mexico	Cacahuacintle	MEX 7	CIMMYT	19.3	-99.7	2652	65.4	2.05	68.8	1.36	3.46	0.13	4.7	0.65
Mexico	Cacahuacintle	PUE 552*	INIFAP	19	-97.4	2600	66.0	2.05	69.8	1.36	3.76	0.13	5.6	0.65
Mexico	Celaya	GTO 36*	INIFAP	20.2	-100.9	1799	67.7	2.05	71.8	1.37	4.16	0.13	6.1	0.65
Mexico	Celaya	GTO 69	INIFAP	20.5	-101	1812	67.8	2.05	71.2	1.36	3.42	0.13	5.7	0.65
Mexico	Celaya	GTO 88	INIFAP	20.2	-101	1768	67.5	2.05	74.1	1.37	6.59	0.13	5.9	0.65
Mexico	Chalqueno	HGO 7	NCRPIS	20.3	-98.9	2100	66.6	2.05	70.7	1.36	4.08	0.13	5.8	0.65
Mexico	Chapalote	SIN 2*	INIFAP	24.8	-107.4	61	65.0	2.05	67.5	1.36	2.48	0.13	5.3	0.65
Mexico	Chapalote	SIN 6	INIFAP	26.4	-108.6	115	64.9	2.05	69.0	1.36	4.18	0.13	6.0	0.65
Mexico	Chapalote	SIN 65	INIFAP	26	-107.4	750	65.8	2.05	69.1	1.37	3.35	0.13	5.4	0.65

Supplemental Table 3.3 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	DTA	DTA SE	DTS	DTS SE	ASI	ASI SE	LODGE	LODGE SE
Mexico	Conejo	GRO 129	INIFAP	17.7	-101.3	100	66.1	2.05	70.5	1.37	4.36	0.13	6.1	0.65
Mexico	Conejo	GRO 157	INIFAP	17.1	-100.5	30	65.8	2.05	69.0	1.36	3.28	0.13	5.7	0.65
Mexico	Conejo	GRO 17	INIFAP	17	-99.8	100	64.2	2.05	68.1	1.37	3.83	0.13	6.1	0.65
Mexico	Conico	PUE 116	NCRPIS	19.9	-97.7	2243	65.4	2.06	68.2	1.36	2.78	0.13	4.7	0.65
Mexico	Conico	PUE 48	NCRPIS	18.9	-97.9	1720	65.4	2.05	69.3	1.36	3.90	0.13	4.7	0.65
Mexico	Conico Norteno	ZAC 12	INIFAP	21.4	-102.9	1951	66.1	2.05	71.2	1.37	5.07	0.13	6.1	0.65
Mexico	Conico Norteno	ZAC 161*	NCRPIS	22.4	-102.9	1937	64.7	2.05	68.5	1.36	3.83	0.13	4.8	0.65
Mexico	Coscomatepec	VER 110*	INIFAP	19.2	-97	1320	68.2	2.05	71.8	1.37	3.66	0.13	5.9	0.65
Mexico	Coscomatepec	VER 110B*	NCRPIS	19.2	-97	1320	68.3	2.09	72.5	1.60	4.23	0.13	6.0	0.74
Mexico	Cristalino de Chihuahua	CHH 128*	INIFAP	29.2	-108.1	2095	63.6	2.05	67.0	1.36	3.45	0.13	4.8	0.65
Mexico	Cristalino de Chihuahua	CHH 154*	INIFAP	29.4	-107.8	2140	63.5	2.05	66.9	1.36	3.32	0.13	5.2	0.65
Mexico	Cristalino de Chihuahua	CHH 254	INIFAP	28.5	-107.4	1900	65.3	2.05	70.0	1.36	4.79	0.13	5.0	0.65
Mexico	Dulce de Jalisco	JAL304	INIFAP	22.1	-103.3	1700	65.6	2.05	68.8	1.36	3.21	0.13	4.7	0.65
Mexico	Dulce de Jalisco	JAL78	INIFAP	21.2	-102.9	1880	66.2	2.05	69.4	1.37	3.23	0.13	5.5	0.65
Mexico	Dulcillo del Noroeste	SIN 34	INIFAP	25.1	-107.5	500	66.5	2.05	69.5	1.36	3.02	0.13	5.2	0.65
Mexico	Dulcillo del Noroeste	SIN 79	INIFAP	26.4	-108.6	180	65.4	2.05	69.0	1.37	3.60	0.13	5.8	0.65
Mexico	Dulcillo del Noroeste	SON 57*	CIMMYT	26.4	-108.6	180	65.0	2.05	69.0	1.36	4.02	0.13	5.3	0.65
Mexico	Dzit Bacal	VER 96	INIFAP	18.9	-96.9	700	66.6	2.05	70.0	1.36	3.44	0.13	5.9	0.65
Mexico	Elotero de Sinaloa	NAY 32*	INIFAP	22.4	-105.5	100	65.5	2.05	69.1	1.36	3.55	0.13	5.7	0.65
Mexico	Elotero de Sinaloa	NAY 46	INIFAP	22	-105.2	100	65.3	2.05	69.8	1.36	4.45	0.13	5.2	0.65
Mexico	Elotero de Sinaloa	SIN 17	INIFAP	23.5	-106.3	200	65.5	2.05	70.0	1.36	4.51	0.13	5.3	0.65
Mexico	Elotes Occidentales	DGO 236*	NCRPIS	24.5	-104.8	1969	64.6	2.05	68.6	1.36	3.98	0.13	4.8	0.65
Mexico	Elotes Occidentales	GTO 191*	INIFAP	21.1	-101.7	1885	65.8	2.05	70.5	1.37	4.75	0.13	6.4	0.65
Mexico	Elotes Occidentales	NAY 29	INIFAP	22.4	-105.5	46	65.2	2.05	68.2	1.37	2.98	0.13	5.2	0.65
Mexico	Elotes Occidentales	NAY 38	INIFAP	21.9	-105.3	46	65.9	2.05	69.4	1.36	3.49	0.13	5.9	0.65
Mexico	Elotes Occidentales	ZAC 210*	INIFAP	21.6	-103	1500	65.5	2.05	69.8	1.37	4.29	0.13	5.1	0.65

Supplemental Table 3.3 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	DTA	DTA SE	DTS	DTS SE	ASI	ASI SE	LODGE	LODGE SE
Mexico	Gordo	CHH 131*	CIMMYT	29.2	-108.1	2095	63.8	2.05	68.3	1.36	4.58	0.13	5.1	0.65
Mexico	Gordo	CHH 160*	CIMMYT	28.6	-107.5	2040	64.5	2.05	68.6	1.37	4.09	0.13	4.9	0.65
Mexico	Gordo	CHH 214*	CIMMYT	28.6	-107.5	2040	64.1	2.05	68.0	1.37	3.88	0.13	5.0	0.65
Mexico	Gordo	CHH 256*	CIMMYT	28.5	-107.4	1900	64.3	2.05	67.9	1.37	3.62	0.13	5.4	0.65
Mexico	Harinoso de Ocho	NAY 24	INIFAP	22	-105.3	46	64.6	2.05	68.4	1.36	3.77	0.13	6.4	0.65
Mexico	Jala	JAL44*	CIMMYT	20	-104.3	1300	66.2	2.05	70.2	1.36	4.05	0.13	5.6	0.65
Mexico	Jala	NAY 130	INIFAP	21.1	-104.4	1095	68.4	2.05	72.9	1.37	4.49	0.13	5.8	0.65
Mexico	Mixteco	OAX 569	INIFAP	17.4	-97.4	2500	67.3	2.05	71.2	1.37	3.85	0.13	5.1	0.65
Mexico	Motozinteco	CHS 650	INIFAP	15.4	-92.3	1270	67.5	2.06	73.9	1.37	6.43	0.13	5.3	0.65
Mexico	Motozinteco	CHS 650B	NCRPIS	15.4	-92.3	1270	67.2	2.09	70.8	1.60	3.53	0.13	6.0	0.74
Mexico	Mushito	MIC 371	INIFAP	19.5	-101.6	2100	66.5	2.05	70.4	1.36	3.91	0.13	5.7	0.65
Mexico	Mushito	MIC 317*	NCRPIS	19.3	-101.5	2253	68.2	2.05	72.7	1.37	4.53	0.13	6.1	0.65
Mexico	Nal-Tel	CAM 48	INIFAP	19.8	-90.1	50	65.8	2.05	69.4	1.36	3.53	0.13	5.7	0.65
Mexico	Negrito	OAX 26*	INIFAP	17.2	-96.8	1640	64.3	2.06	68.2	1.37	3.87	0.13	4.6	0.65
Mexico	Olotillo	CHS 53	CIMMYT	16.8	-93.2	579	69.5	2.05	74.9	1.37	5.43	0.13	6.1	0.65
Mexico	Olotillo	CHS 81	INIFAP	16.6	-92.7	686	67.5	2.05	71.7	1.36	4.25	0.13	6.2	0.65
Mexico	Oloton	CHS 684	INIFAP	16.8	-92.5	2100	67.4	2.05	71.5	1.36	4.10	0.13	6.0	0.65
Mexico	Onaveno	SON 114	INIFAP	29	-109.4	410	64.4	2.05	67.5	1.36	3.03	0.13	5.0	0.65
Mexico	Onaveno	SON 24*	NCRPIS	30.8	-110.8	867	65.9	2.05	70.0	1.36	4.11	0.13	5.8	0.65
Mexico	Palomero de Jalisco	JAL154*	INIFAP	20	-103.7	2520	64.7	2.05	69.0	1.36	4.34	0.13	5.4	0.65
Mexico	Palomero Tipo Chihuahua	CHH 148*	INIFAP	29.4	-107.8	2140	64.0	2.05	66.9	1.36	2.84	0.13	5.2	0.65
Mexico	Palomero Tipo Chihuahua	CHH 201*	INIFAP	26.8	-107.1	2130	63.2	2.05	66.2	1.37	2.98	0.13	4.8	0.65
Mexico	Palomero Toluqueno	VER 35*	NCRPIS	19.6	-97.3	2391	64.5	2.05	67.5	1.36	3.04	0.13	5.4	0.65
Mexico	Pepitilla	GRO 3*	INIFAP	18.4	-99.5	747	69.4	2.05	74.3	1.37	4.96	0.13	5.9	0.65
Mexico	Raton	CHH 191*	NCRPIS	28.8	-106.4	1885	64.9	2.05	67.4	1.36	2.51	0.13	4.8	0.65
Mexico	Raton	NLE 9*	INIFAP	25.6	-99.3	250	64.0	2.05	68.4	1.36	4.41	0.13	5.4	0.65

Supplemental Table 3.3 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	DTA	DTA SE	DTS	DTS SE	ASI	ASI SE	LODGE	LODGE SE
Mexico	Raton	TAM 25*	INIFAP	24.6	-99.6	290	65.8	2.05	68.9	1.36	3.06	0.13	5.5	0.65
Mexico	Reventador	NAY 15*	INIFAP	22.3	-105.4	46	65.7	2.05	69.1	1.37	3.40	0.13	5.6	0.65
Mexico	Reventador	NAY 39	INIFAP	21.9	-105.3	46	66.0	2.05	69.9	1.37	3.84	0.13	5.4	0.65
Mexico	Serrano de Jalisco	JAL133*	INIFAP	20	-103.8	2060	65.7	2.05	69.2	1.36	3.50	0.13	5.2	0.65
Mexico	Serrano de Jalisco	JAL146	INIFAP	20	-103.7	2520	63.8	2.05	68.5	1.36	4.69	0.13	5.8	0.65
Mexico	Serrano Mixe	OAX 565	INIFAP	17.1	-96	2350	68.7	2.05	72.8	1.37	4.16	0.13	5.7	0.65
Mexico	Tablilla de Ocho	JAL301	CIMMYT	22.1	-103.2	1700	65.9	2.05	69.7	1.36	3.74	0.13	5.2	0.65
Mexico	Tablilla de Ocho	NAY 185	CIMMYT	21.7	-104.1	1100	66.7	2.05	71.4	1.37	4.73	0.13	6.0	0.65
Mexico	Tablilla de Ocho	ZAC 187	NCRPIS	22.3	-103.6	2170	64.8	2.05	68.9	1.37	4.10	0.13	5.6	0.65
Mexico	Tabloncillo	JAL102	INIFAP	19.5	-103.3	1280	67.0	2.05	70.1	1.36	3.11	0.13	5.9	0.65
Mexico	Tabloncillo	JAL103*	NCRPIS	19	-103	1290	67.2	2.05	70.8	1.37	3.60	0.13	5.7	0.65
Mexico	Tabloncillo	JAL103B*	NCRPIS	19	-103	1290	65.9	2.09	70.0	1.59	4.09	0.13	5.5	0.74
Mexico	Tabloncillo Perla	NAY 12	INIFAP	22	-105.2	46	64.8	2.05	69.0	1.36	4.14	0.13	5.9	0.65
Mexico	Tabloncillo Perla	NAY 16	CIMMYT	22.1	-105.3	46	65.6	2.05	67.9	1.37	2.37	0.13	6.0	0.65
Mexico	Tehua	CHS 159	CIMMYT	16.5	-92.5	747	70.4	2.06	79.0	1.37	8.62	0.13	6.4	0.65
Mexico	Tehua	CHS 29	CIMMYT	15.8	-92.7	1000	69.1	2.05	73.3	1.37	4.27	0.13	5.9	0.65
Mexico	Tepecintle	CHS 76	INIFAP	16.5	-92.8	579	65.8	2.05	69.6	1.36	3.80	0.13	5.4	0.65
Mexico	Tuxpeno	VER 143*	NCRPIS	19.3	-96.5	141	67.3	2.05	71.1	1.37	3.74	0.13	6.0	0.65
Mexico	Tuxpeno Norteno	CHH 121	INIFAP	30.9	-108.2	1470	65.6	2.05	69.3	1.36	3.64	0.13	5.4	0.65
Mexico	Tuxpeno Norteno	CHH 287*	NCRPIS	30.4	-107.9	1456	63.9	2.06	67.1	1.36	3.20	0.13	6.1	0.66
Mexico	Tuxpeno Norteno	TAM 3*	INIFAP	23.3	-99	300	65.6	2.05	69.5	1.36	3.97	0.13	5.6	0.65
Mexico	Vandeno	GRO 96	NCRPIS	17.5	-101.3	61	68.4	2.06	71.9	1.37	3.52	0.13	5.4	0.65
Mexico	Zamorano Amarillo	GTO 1	INIFAP	21.1	-101.7	1870	65.5	2.05	69.5	1.36	3.96	0.13	5.7	0.65
Mexico	Zamorano Amarillo	MIC 66*	INIFAP	20.1	-102	1645	65.4	2.05	69.3	1.37	3.91	0.13	5.8	0.65
Mexico	Zapalote Chico	CHS 662	INIFAP	16.2	-94	100	63.3	2.05	67.4	1.36	4.02	0.13	5.9	0.65
Mexico	Zapalote Chico	OAX 48	CIMMYT	16.4	-94.2	50	62.8	2.06	66.2	1.37	3.42	0.13	5.8	0.65

Supplemental Table 3.3 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	DTA	DTA SE	DTS	DTS SE	ASI	ASI SE	LODGE	LODGE SE
Mexico	Zapalote Chico	OAX 50	CIMMYT	16.6	-94.6	107	64.8	2.05	68.5	1.36	3.63	0.13	5.7	0.65
Mexico	Zapalote Chico	OAX 70	CIMMYT	16.3	-95.2	46	63.7	2.05	66.4	1.37	2.71	0.13	5.3	0.65
Mexico	Zapalote Grande	CHS 104	INIFAP	15.3	-92.7	107	66.7	2.06	69.5	1.37	2.87	0.13	5.9	0.65
Mexico	Zapalote Grande	CHS 224	INIFAP	15.3	-92.7	91	66.5	2.05	70.1	1.36	3.60	0.13	5.6	0.65
Mexico	Zapalote Grande	CHS 236	INIFAP	16.7	-93.8	120	64.1	2.05	67.7	1.36	3.66	0.13	5.5	0.65
Mexico	Zapalote Grande	CHS 521	INIFAP	16.7	-93.7	730	65.6	2.05	68.9	1.36	3.28	0.13	6.0	0.65
Paraguay	Avati Moroti Guapi	PAG 139 (USDA)	NCRPIS	-25.5	-56.4	369	66.9	2.05	70.7	1.37	3.84	0.13	5.7	0.65
Paraguay	Avati Moroti Ti	PAG124 (USDA)	NCRPIS	-26.7	-57.2	276	67.6	2.05	71.6	1.37	4.03	0.13	6.3	0.65
Paraguay	Cateto Sabugo Grosso	PAG 422 (USDA)	NCRPIS	-26	-56.5	95	66.4	2.05	69.8	1.37	3.42	0.13	5.2	0.65
Paraguay	Moroti Guapi	PAG VI-A	NCRPIS	-26.1	-56.93	400	67.9	2.06	72.4	1.36	4.46	0.13	5.0	0.65
Paraguay	Semi Dente Paulista	PAG I*	CIMMYT	-26	-56	270	67.2	2.05	70.9	1.37	3.69	0.13	5.8	0.65
Peru	Alazan	LBQ 18	PCIM	-6.7	-79.8	50	67.8	2.05	72.4	1.36	4.54	0.13	5.5	0.65
Peru	Alazan	LIB 34	NCRPIS	-7.8	-79.3	80	67.7	2.05	75.4	1.37	7.65	0.13	6.2	0.65
Peru	Aleman	HCO 38*	NRC	-9.3	-76	700	66.7	2.05	70.1	1.36	3.34	0.13	5.4	0.65
Peru	Amarillo Huancabamba	PIU 17B	NCRPIS	-5	-79	2100	67.6	2.05	74.0	1.36	6.35	0.13	6.8	0.65
Peru	Amarillo Huancabamba	PIU 38B*	NCRPIS	-5.2	-79.5	2000	67.5	2.05	74.4	1.37	6.93	0.13	6.3	0.65
Peru	Ancashino	ANC 102*	NCRPIS	-9.1	-77.8	2600	67.4	2.05	71.5	1.36	4.03	0.13	6.0	0.65
Peru	Arequipeno	ARQ 1*	NCRPIS	-16.2	-71.3	2332	66.5	2.05	70.0	1.36	3.51	0.13	5.1	0.65
Peru	Arizona	LIB 16	NRC	-8.6	-78.8	100	66.1	2.05	69.4	1.37	3.28	0.13	4.9	0.65
Peru	Arizona	LIB 2*	NRC	-8.4	-78.8	80	66.6	2.05	71.1	1.36	4.52	0.13	6.3	0.65
Peru	Blanco Ayabaca	PIU 119	NCRPIS	-4.6	-79.7	2630	67.5	2.05	71.0	1.36	3.50	0.13	5.8	0.65
Peru	Chancayano Blanco	LIM 45*	PCIM	-11.1	-77.6	50	68.0	2.05	73.7	1.37	5.69	0.13	5.8	0.65
Peru	Chancayano Pintado	LIM 46*	NRC	-11.1	-77.6	50	67.7	2.05	71.8	1.37	4.10	0.13	5.8	0.65
Peru	Chaparreno	ARQ34*	PCIM	-17	-72	10	67.9	2.05	71.9	1.37	4.01	0.13	5.5	0.65
Peru	Chulpi	LIM 66*	NCRPIS	-11.4	-77.4	110	67.3	2.06	72.2	1.37	4.87	0.13	5.6	0.65
Peru	Chuncho	CUZ 112*	NCRPIS	-12.8	-72.7	1300	68.5	2.05	72.9	1.37	4.41	0.13	5.7	0.65

Supplemental Table 3.3 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	DTA	DTA SE	DTS	DTS SE	ASI	ASI SE	LODGE	LODGE SE
Peru	Colorado	LIB 8*	NCRPIS	-7.4	-79.5	51	67.1	2.09	70.8	1.59	3.69	0.13	5.5	0.74
Peru	Confite Morocho	AYA 20	PCIM	-12.9	-74.3	2500	64.3	2.05	69.4	1.36	5.12	0.13	5.8	0.65
Peru	Confite Puneno	APC 56	PCIM	-14.4	-72.9	3600	63.5	2.05	66.7	1.37	3.15	0.13	5.2	0.65
Peru	Confite Puntigudo	CAJ 27	NRC	-7.6	-78	2500	65.1	2.05	68.4	1.36	3.33	0.13	5.4	0.65
Peru	Confite Puntigudo	CUZ 13	NCRPIS	-15.5	-70.1	3832	65.0	2.05	69.3	1.36	4.36	0.13	5.9	0.65
Peru	Coruca	TAC 1*	PCIM	-18	-70.9	500	66.8	2.05	70.2	1.36	3.39	0.13	6.5	0.65
Peru	Cubano Amarillo	UCA 8*	NCRPIS	-5.2	-75.7	129	67.4	2.05	71.7	1.37	4.31	0.13	6.0	0.65
Peru	Cuzco Cristalino Amaril	CUZ 363	NCRPIS	-13.5	-72.1	3375	63.7	2.05	69.9	1.36	6.22	0.13	5.9	0.65
Peru	Cuzco Gigante	CAJ 17	PCIM	-7.2	-78.5	2800	67.1	2.05	70.1	1.36	3.04	0.13	6.0	0.65
Peru	Granada	ANC 57	PCIM	-9.3	-77.6	2600	65.9	2.05	70.4	1.36	4.50	0.13	5.6	0.65
Peru	Huachano	LIM 43*	NRC	-11.1	-77.6	40	67.0	2.05	70.6	1.36	3.55	0.13	5.8	0.65
Peru	Huancavelicano	HVC 179*	NCRPIS	-13	-75.1	4562	65.9	2.05	70.6	1.36	4.67	0.13	6.0	0.65
Peru	Huanuco	HCO 128B*	NCRPIS	-9	-76	2700	69.2	2.05	75.5	1.37	6.30	0.13	6.6	0.65
Peru	Huarmaca	PIU 72*	PCIM	-5.6	-79.5	2300	68.0	2.05	72.0	1.37	4.00	0.13	6.4	0.65
Peru	Huayleno	ANC 180x181	NCRPIS	-9	-77	2600	68.6	2.05	72.9	1.36	4.28	0.13	5.2	0.65
Peru	Huayleno	ANC 291*	NCRPIS	-9.5	-77.5	3059	66.2	2.05	70.2	1.36	4.03	0.13	5.7	0.65
Peru	Jora	ANC 1*	PCIM	-10.1	-78.2	100	68.5	2.05	74.4	1.36	5.98	0.13	6.3	0.65
Peru	Kculli	HVC 137	PCIM	-12.6	-74.9	3100	65.4	2.09	71.0	1.59	5.67	0.13	5.7	0.74
Peru	Maranon	LIB 63B	NCRPIS	-8	-77	2800	69.1	2.05	74.2	1.37	5.10	0.13	6.1	0.65
Peru	Mochero	LBQ 5*	NRC	-6.7	-79.9	25	66.8	2.05	69.3	1.36	2.55	0.13	5.1	0.65
Peru	Morado Canteno	Lima 55*	NCRPIS	-12	-77	60	65.7	2.05	69.8	1.36	4.11	0.13	5.4	0.65
Peru	Morochillo	PIU 96*	PCIM	-4.7	-79.7	2000	67.7	2.05	72.5	1.37	4.83	0.13	6.0	0.65
Peru	Morocho	APC 67*	NCRPIS	-13.6	-72.6	2750	65.6	2.05	69.7	1.36	4.13	0.13	6.3	0.65
Peru	Morocho	APC 77*	NCRPIS	-13.7	-73.1	2977	65.9	2.05	70.4	1.36	4.53	0.13	6.1	0.65
Peru	Morocho Cajabambino	LIB 62*	PCIM	-8.4	-77.3	2800	67.6	2.05	72.3	1.37	4.67	0.13	6.2	0.65
Peru	Pagaladroga	PIU 2	PCIM	-5.1	-80.2	520	67.9	2.05	73.7	1.37	5.85	0.13	6.0	0.65

Supplemental Table 3.3 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	DTA	DTA SE	DTS	DTS SE	ASI	ASI SE	LODGE	LODGE SE
Peru	Pardo	LIM 19*	NRC	-11.1	-77.6	40	67.5	2.05	71.5	1.36	4.00	0.13	5.9	0.65
Peru	Paro	CUZ 76	PCIM	-13.6	-71.7	3300	67.0	2.05	72.4	1.36	5.41	0.13	5.7	0.65
Peru	Perla	ANC 23*	NCRPIS	-10.1	-78.2	100	67.8	2.05	73.1	1.37	5.27	0.13	5.8	0.65
Peru	Perla	ANC 24*	NRC	-10.1	-78.2	50	67.9	2.05	74.0	1.37	6.03	0.13	5.9	0.65
Peru	Perla	LIM 50*	NRC	-12.1	-77.1	50	68.7	2.05	74.5	1.37	5.77	0.13	6.0	0.65
Peru	Piricincó	SM 8*	NCRPIS	-6.2	-76.6	940	67.5	2.05	72.3	1.36	4.80	0.13	6.2	0.65
Peru	Pisccorunto	APC 13	PCIM	-13.7	-73.4	2900	64.5	2.07	67.8	1.36	3.31	0.13	5.7	0.65
Peru	Pisccorunto	APC 13B	NCRPIS	-13.7	-73.4	2900	66.9	2.09	73.0	1.59	6.13	0.13	5.5	0.74
Peru	Rabo de Zorro	ANC 325*	NCRPIS	-8.5	-78.1	2600	67.2	2.05	70.0	1.36	2.85	0.13	5.6	0.65
Peru	Rienda	CAJ 80	PCIM	-7.6	-78	2000	67.9	2.05	71.8	1.36	3.89	0.13	5.6	0.65
Peru	San Geronimo Huancaveli	JUN 164	NCRPIS	-12	-75.2	3333	64.6	2.05	68.8	1.36	4.21	0.13	6.0	0.65
Peru	Sarco	ANC 184	NRC	-9.4	-77.2	3150	68.2	2.05	73.2	1.37	4.97	0.13	5.7	0.65
Peru	Shajatu	ANC 117	PCIM	-8.5	-77.9	2580	67.1	2.05	70.6	1.37	3.50	0.13	5.9	0.65
Trinidad	Tuson	TRN 1	INIFAP	10.5	-61.1	125	67.8	2.05	73.1	1.37	5.31	0.13	5.7	0.65
Trinidad	Tuson	TRN 10	INIFAP	10.6	-61.1	20	67.9	2.05	73.3	1.37	5.39	0.13	6.2	0.65
Trinidad U.S. Virgin Islands	St. Croix	IVC 2*	NRC	17.7	-64.7	150	66.9	2.05	71.5	1.37	4.55	0.13	5.5	0.65
Uruguay	Cateto Sulino	URG IV	CIMMYT	-31.7	-56	126	64.8	2.05	68.1	1.36	3.32	0.13	5.6	0.65
Uruguay	Cateto Sulino Escuro	URG V	CIMMYT	-31.7	-56	126	65.8	2.05	70.0	1.37	4.17	0.13	5.0	0.65
Uruguay	Cateto Sulino Grosso	URG III	CIMMYT	-31.7	-56	126	64.6	2.05	68.7	1.36	4.14	0.13	5.1	0.65
Uruguay	Dentado Branco	URZM 13010	NCRPIS	-34	-56	104	65.3	2.05	67.6	1.36	2.29	0.13	4.8	0.65
Uruguay	Semi-Dentado Rugoso	URZM 13052	NCRPIS	-30.8	-66.8	714	65.5	2.05	69.3	1.36	3.83	0.13	4.7	0.65
USA	Apache	PI 213731	NCRPIS	33.4	-110.4	1067	64.8	2.05	68.7	1.36	3.83	0.13	4.8	0.65
USA	Argentine Pop	PI 217404*	NCRPIS	-32	-58	305	66.4	2.05	68.7	1.36	2.31	0.13	5.1	0.65
USA	Bear Isl. Chippewa	PI 213801*	NCRPIS	47	-92.2	457	60.6	2.07	63.8	1.37	3.16	0.13	4.9	0.65
USA	Cherokee	PI 213744*	NCRPIS	36.7	-96	229	65.9	2.05	68.9	1.36	3.06	0.13	6.0	0.65
USA	Cochiti Pueblo	PI 218151*	NCRPIS	35.6	-106.4	1616	63.9	2.05	68.2	1.37	4.30	0.13	4.7	0.65

Supplemental Table 3.3 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	DTA	DTA SE	DTS	DTS SE	ASI	ASI SE	LODGE	LODGE SE
USA	Domingo Pueblo	PI 218130*	NCRPIS	35.5	-106.4	1585	65.2	2.05	69.2	1.37	4.01	0.13	4.7	0.65
USA	Gaspe Flint	PI 401757*	NCRPIS	48.8	-64.3	173	59.1	2.05	62.8	1.36	3.71	0.13	4.5	0.66
USA	Gourd Seed	PI 217405*	NCRPIS	33	-97.1	229	66.5	2.05	71.0	1.36	4.49	0.13	5.2	0.65
USA	Gourd Seed	PI 414183*	NCRPIS	32	-99	300	66.5	2.05	70.1	1.36	3.62	0.13	5.3	0.65
USA	Havasupai	PI 317675*	NCRPIS	36.3	-112.7	1303	63.9	2.05	67.0	1.37	3.14	0.13	5.1	0.65
USA	Havasupai	PI 317679*	NCRPIS	36.3	-112.7	1303	65.0	2.05	69.1	1.36	4.12	0.13	4.4	0.65
USA	Hopi	PI 213733*	NCRPIS	35.9	-110.7	1941	64.3	2.05	68.5	1.36	4.21	0.13	4.1	0.65
USA	Hualapai	PI 213741*	NCRPIS	35.5	-113.4	1067	64.1	2.05	66.6	1.36	2.46	0.13	4.5	0.65
USA	Isleta-Tiwa	PI 218148*	NCRPIS	34.9	-106.7	1509	66.1	2.06	69.9	1.36	3.71	0.13	4.4	0.65
USA	Jemez Pueblo	PI 218173*	NCRPIS	35.6	-106.7	1829	65.7	2.05	69.6	1.36	3.96	0.13	4.7	0.65
USA	Laguna Pueblo	PI 218169*	NCRPIS	35.1	-107.4	1768	64.6	2.05	68.8	1.36	4.12	0.13	4.6	0.65
USA	Laguna Pueblo	PI 218170*	NCRPIS	35.1	-107.4	1768	65.4	2.05	69.4	1.36	4.07	0.13	4.4	0.65
USA	Longfellow	PI 214195*	NCRPIS	43.6	-80.2	488	62.0	2.05	64.8	1.37	2.82	0.13	4.5	0.65
USA	Longfellow Flint	PI 217408*	NCRPIS	42.3	-71.5	99	60.8	2.05	64.5	1.37	3.71	0.13	4.1	0.65
USA	Mexican June	PI 221889*	NCRPIS	37	-93.2	213	65.9	2.05	69.7	1.37	3.81	0.13	5.1	0.65
USA	Mexican June	PI 311243*	NCRPIS	37	-77	305	65.4	2.05	68.6	1.37	3.25	0.13	5.9	0.65
USA	Moencopi Pueblo	PI 218175*	NCRPIS	36.1	-111.2	1311	64.4	2.05	68.2	1.37	3.80	0.13	4.7	0.65
USA	Moencopi Pueblo	PI 218177*	NCRPIS	36.1	-111.2	1311	65.1	2.05	68.2	1.36	3.06	0.13	4.5	0.65
USA	Mohave	PI 218187*	NCRPIS	34.2	-114.3	91	63.2	2.05	67.5	1.36	4.31	0.13	4.8	0.65
USA	Mohawk Round Nose	PI 483087*	NCRPIS	45	-74.7	59	64.0	2.05	67.3	1.37	3.24	0.13	4.7	0.65
USA	N.W. Dent	PI 217480*	NCRPIS	38.3	-104.7	1444	63.5	2.05	66.8	1.37	3.28	0.13	4.6	0.65
USA	Navajo	PI 218163*	NCRPIS	36.6	-110.6	1616	64.2	2.05	67.2	1.36	3.01	0.13	4.4	0.65
USA	Northeast Flint	WLB	NCRPIS	41.7	-71.7	130	63.6	2.05	66.6	1.37	3.06	0.13	4.4	0.65
USA	Papago-Pimans	PI 217410*	NCRPIS	32.3	-112	1067	65.1	2.05	67.0	1.36	1.94	0.13	4.3	0.65
USA	Pueblo 12-Row Hopi Koko	PI 503564*	NCRPIS	35.9	-110.7	1908	64.3	2.05	68.1	1.36	3.80	0.13	4.9	0.65
USA	Quapaw Red	PI 213757*	NCRPIS	37	-94.8	229	64.9	2.05	68.7	1.36	3.82	0.13	4.9	0.65

Supplemental Table 3.3 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	DTA	DTA SE	DTS	DTS SE	ASI	ASI SE	LODGE	LODGE SE
USA	Sac And Fox	PI 217411*	NCRPIS	42	-92.6	229	63.9	2.05	67.0	1.36	3.16	0.13	4.5	0.65
USA	San Lorenzo Pueblo	PI 218135	NCRPIS	36.1	-106.3	2104	62.8	2.05	67.7	1.36	4.92	0.13	4.7	0.65
USA	Santo Domingo Pueblo	PI 218143*	NCRPIS	35.5	-106.4	1585	65.1	2.05	70.1	1.36	4.92	0.13	4.3	0.65
USA	Seneca Hominy Corn	PI 401754*	NCRPIS	42.1	-78.9	431	61.1	2.05	64.3	1.37	3.15	0.13	4.3	0.65
USA	Shoshone	PI 213769*	NCRPIS	43	-112.4	229	61.1	2.05	65.2	1.37	4.07	0.13	4.0	0.65
USA	Smut Nose	PI 222490*	NCRPIS	42.7	-84.5	213	63.6	2.05	67.1	1.36	3.48	0.13	4.3	0.65
USA	Supergold Pop	PI 222648*	NCRPIS	38	-96	319	64.8	2.05	67.9	1.36	3.08	0.13	4.9	0.65
USA	Tennessee Red Cob	PI 311235*	NCRPIS	37.2	-80.4	305	65.0	2.05	69.0	1.36	4.04	0.13	5.6	0.65
USA	Tesuque Pueblo	PI 218137*	NCRPIS	35.8	-106	2073	64.7	2.05	69.6	1.36	4.87	0.13	3.6	0.65
USA	White Dent	PI 221885*	NCRPIS	39.1	-93.2	238	65.9	2.05	69.6	1.36	3.66	0.13	5.5	0.65
USA	White Dent	PI 311232*	NCRPIS	37	-77	305	64.9	2.05	69.7	1.36	4.79	0.13	5.2	0.65
USA	Winnebago	PI 213772*	NCRPIS	42.2	-96.5	229	63.3	2.05	66.6	1.36	3.33	0.13	4.5	0.65
USA	Winnebago	PI 213774*	NCRPIS	42.2	-96.5	229	63.4	2.05	66.8	1.37	3.46	0.13	4.0	0.65
USA	Zia Pueblo	PI 218139*	NCRPIS	35.5	-106.7	1829	65.7	2.05	69.8	1.36	4.14	0.13	4.9	0.65
Venezuela	Araguito	VEN 568	NRC	8.9	-64.2	183	64.1	2.05	67.1	1.36	3.03	0.13	6.0	0.65
Venezuela	Araguito	VEN 628	NRC	8.9	-64.2	183	63.0	2.05	66.4	1.36	3.35	0.13	5.7	0.65
Venezuela	Araguito	VEN 678	NCRPIS	8.9	-64.2	73	64.3	2.05	67.9	1.37	3.58	0.13	6.1	0.65
Venezuela	Araguito	VEN 760	NRC	9.6	-63.1	123	66.9	2.05	70.5	1.36	3.60	0.13	6.1	0.65
Venezuela	Cacao	VEN 630	NCRPIS	8.6	-71.2	201	68.6	2.05	72.6	1.37	3.99	0.13	6.5	0.65
Venezuela	Canilla	VEN 693	NRC	8.9	-64.2	91	68.3	2.05	72.8	1.37	4.49	0.13	6.2	0.65
Venezuela	Cariaco	VEN 408	ICA	10.4	-63.8	46	68.9	2.05	74.2	1.37	5.31	0.13	5.3	0.65
Venezuela	Cariaco	VEN 631	NRC	8.1	-63.6	366	68.7	2.05	74.6	1.37	5.98	0.13	6.5	0.65
Venezuela	Cariaco	VEN 639	NCRPIS	8.6	-70.2	194	68.0	2.05	72.7	1.37	4.67	0.13	6.0	0.65
Venezuela	Chandelle	VEN 409	ICA	10.1	-68.4	137	67.5	2.05	70.5	1.37	3.03	0.13	5.8	0.65
Venezuela	Chandelle	VEN 460	ICA	8.1	-63.6	229	67.8	2.05	72.0	1.37	4.25	0.13	5.9	0.65
Venezuela	Chirimito	VEN 703*	ICA	8.1	-63.6	229	67.5	2.05	71.3	1.36	3.87	0.13	5.6	0.65

Supplemental Table 3.3 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	DTA	DTA SE	DTS	DTS SE	ASI	ASI SE	LODGE	LODGE SE
Venezuela	Comun	VEN 448	ICA	7.6	-72	457	67.3	2.06	71.8	1.37	4.53	0.13	6.0	0.65
Venezuela	Comun	VEN 881	ICA	10	-69.3	607	67.6	2.06	72.7	1.37	5.02	0.13	6.0	0.65
Venezuela	Costeno	VEN 775	NCRPIS	9.2	-68.3	184	67.4	2.05	71.5	1.37	4.01	0.13	5.2	0.65
Venezuela	Cuba Yellow Flint	VEN 331	ICA	10	-68	46	67.6	2.06	72.5	1.37	4.89	0.13	6.2	0.65
Venezuela	Cuba Yellow Flint	VEN 650	ICA	8.9	-64.2	128	67.0	2.05	70.6	1.36	3.55	0.13	6.1	0.65
Venezuela	Guaribero	VEN 653	ICA	8.9	-64.2	73	66.0	2.05	71.0	1.36	4.94	0.13	6.0	0.65
Venezuela	Guaribero	VEN 733	ICA	8.9	-64.2	137	67.5	2.05	70.6	1.37	3.12	0.13	5.7	0.65
Venezuela	Huevito	VEN 396	ICA	8	-71.8	1052	69.7	2.05	76.0	1.37	6.24	0.13	5.7	0.65
Venezuela	Huevito	VEN 445	ICA	7.8	-72.3	823	67.2	2.05	71.0	1.36	3.76	0.13	5.7	0.65
Venezuela	Negrito	VEN 426	ICA	10.3	-67.5	384	68.0	2.05	72.7	1.36	4.66	0.13	5.9	0.65
Venezuela	Negrito	VEN 673	ICA	10.3	-67.5	384	68.3	2.05	74.0	1.37	5.70	0.13	6.3	0.65
Venezuela	Negrito	VEN 870	ICA	10.3	-67.5	384	68.3	2.05	73.4	1.37	5.14	0.13	5.6	0.65
Venezuela	Pira	VEN 457	ICA	8	-72	412	65.6	2.05	69.3	1.36	3.74	0.13	6.4	0.65
Venezuela	Pollo	VEN 310	NRC	8	-72	3088	66.0	2.05	71.2	1.36	5.24	0.13	6.2	0.65
Venezuela	Puya	VEN 946	ICA	9	-72	91	68.2	2.05	72.4	1.37	4.21	0.13	5.5	0.65
Venezuela	Puya Grande	VEN 345	ICA	10	-68	37	68.7	2.06	73.3	1.37	4.60	0.13	6.1	0.65
Venezuela	Puya Grande	VEN 651	NCRPIS	9.6	-63.1	203	67.7	2.05	71.9	1.36	4.26	0.13	5.9	0.65
Venezuela	Tuson	VEN 405	ICA	7.5	-72	389	68.0	2.05	72.5	1.37	4.54	0.13	5.6	0.65
Venezuela	Tuxpeno	VEN 598	ICA	9.5	-69.3	96	67.2	2.05	71.1	1.36	3.93	0.13	6.1	0.65
Venezuela	Tuxpeno	VEN 692	ICA	9.5	-69.3	199	67.6	2.05	72.1	1.37	4.45	0.13	6.3	0.65
Venezuela	Tuxpeno	VEN 891	ICA	10	-69.3	471	67.7	2.05	72.6	1.36	4.90	0.13	6.9	0.65

Notes:

†Most accessions were collected during the 1940s and 1950s; additional Mexican accessions were collected during the 1960s and 1970s by E. Hernández X. and R. Ortega P. Data on Altitude, Latitude and Longitude were obtained from Vigouroux et al (2008), from the Original Strains of Corn Vol I and Vol II (NSF-NRC, 1954) and from the studies of the accessions published by the National Academy of Sciences and Harvard (Brieger et al, 1958; Brown., 1960; Grant et. al., 1963; Grobman et al, 1961; Hatheway, 1957; Ramírez et. al., 1960; Roberts et al, 1957; Timothy et al, 1961, 1963; Wellhausen et al, 1952, 1957). Vigouroux et al (2008) notes that most accessions were originally acquired from national germplasm banks or CIMMYT in the 1960s and 1970s, but those labeled NRC were acquired directly from the original collections, either from the collections of William L. Brown (Pioneer Hi-Bred, Johnston, IA) or original backup seeds once held in storage at Glenn Dale, MD, by the USDA-ARS. (All those labeled NRC were increased by MMG and are now deposited with the NCRPIS at Ames, Iowa). Most eastern South American (Brazil, Paraguay, Uruguay, Guianas, some Argentine and a few Bolivian accessions: all have collections with roman numerals) were bulk samples of several accessions, and data shown are means of the accessions (Paterniani E and Goodman MM, 1977). Many accessions sourced from INIFAP are more recent Mexican collections (sometimes 1990s and later) made by J.J. Sánchez-Gonzalez, R. Ortega P., and collaborators, and generally have exact geographic coordinates (Sanchez G. JJ, 2000). Also occasionally seed from a given accession was sampled twice by the Goodman group at different times. These two samples were labeled sample A and B, these are not different accessions. Accessions labeled with an (USDA) indicate accessions from Argentina or Brazil which were once held in storage at Glenn Dale, MD, but not from the NRC. They were increased by MMG and are now deposited with the NCRPIS at Ames, Iowa. It is also noted that accessions noted with an asterisk (*) are those currently available from NCRPIS, unfortunately these number only 170 of the accessions used in this study.

‡Source abbreviations are as follows: Intentional Maize and Wheat Improvement Center (CIMMYT), North Central Regional Plant Introduction Station (NCRPIS), National Research Council (NRC), Columbian Agriculture Institute (ICA), National Research Institute for Forestry, Agriculture, and Livestock (INIFAP), National Center for Genetic Resources Preservation (NCGRP), Cooperative Program for Maize Investigations (PCIM), David Timothy personal collection (DHT), and William L. Brown personal collection (WLB).

Supplemental Table 3.4 Agronomic ratings for check hybrids

Line	Pedigree	Year Released	DTA	DTA SE	DTS	DTS SE	ASI	ASI SE	Lodging	Lodging SE
PHB47	((B37*3) ×SD105)	1984	67.06	2.02	70.27	1.22	3.21	0.11	4.85	0.59
PHB47xDJ7	(B73 x BS16 Synthetic) =DJ 7	1985	64.61	2.02	68.59	1.22	3.98	0.11	6.41	0.59
DKHBA1x PHB47	(Pioneer 3195 x Pioneer 3199) = DKHBA1	1985	65.13	2.02	67.57	1.22	2.44	0.11	7.57	0.59
NC296x PHB47	(Pioneer X105A x H5) = NC296	1990	65.54	2.02	68.35	1.22	2.81	0.11	7.92	0.59
Pioneer 3394	unavailable	1991	65.56	2.02	63.92	1.22	3.36	0.11	7.75	0.59
Pioneer 33M54	GE535764 xGE587284	2003	65.75	2.02	68.84	1.22	3.83	0.11	8.06	0.59

Note: DTA was scored as number of days after planting till 50% of plants in row showed pollen shed, DTS scored as number of days after planting till 50% of plants in row showed silk. ASI was the difference between DTS and DTA. Lodging was scored on a 1 to 9 scale with 9 being resistant.

Supplemental Table 3.5 Details of experimental units

Location	Row Length (m)	Alley Length (m)	Row Spacing (m)	Number Kernels Planted	Planting density (plants/ha)
Andrews, NC	3.5	0.8	0.76	15	46000
Cairo GA	3.9	0.8	0.76	25	70000
Clayton, NC	2.6	0.8	0.97	18	54600
Salisbury, NC	4.9	1	0.76	25	55800
Thomasboro, IL	3.7	1	0.76	20	56000
Windfall, IN	3.5	0.8	0.76	15	45900

Supplemental Table 3.6 Accessions for which no collection information could be found

Country	Race	Accession	Latitude	Longitude	Altitude (m)
Argentina	Cristalino Amarillo	AR21004	-38.1	-62.2	295
Bolivia	Checchi	BOV Comp.	-18.1	-65.8	2542
Bolivia	Huilcaparu Moteado	BOV Comp.	-16.9	-67.1	2760
Bolivia	Paru	BOV Comp.	-15.8	-68.7	2737
Bolivia	Uchuquilla	BOV318	-17.23	-66.11	1922
Brazil	Avati Pichinga	BR2760	-25.0	-56.0	366
Brazil	Avati Pichinga	BR2776	-25.0	-56.0	366
Brazil	Avati Pichinga Ihu	BR2830	-25.0	-56.0	366
Chile	Cristalino Chileno	CHI156	-38.1	-71.9	66
Colombia	Amagaceño	HUI317	2.5	-74.8	1554
Colombia	Harinoso Dentado	NAR326	1.4	-77.6	1400
Colombia	Montaña	NAR625	1.2	-77.3	2541.8
Colombia	Sabanero	ANT423	7.0	-75.7	1479.8
Colombia	Sabanero	CUN342	8.5	-75.5	250
Colombia	Comun	CAU454	2.2	-76.9	922
Ecuador	Chillo	ECU411	-0.3	-78.4	2510.3
Ecuador	Cubano Amarillo Duro	ECU326	-1.1	-80.5	40.8
Ecuador	Enano Gigante	ECU Comp.	-1.1	-78.0	915.6
El Salvador	Amarillo Salvadoreño	Comp.	13.8	-89.3	721
USA	Northeast Flint	WLB	41.7	-71.7	130
México	Raton	CHH191	28.8	-106.4	1885.3
Paraguay	Cateto Sabugo Grosso	PAG422	-26.0	-56.5	95
Peru	Amarillo Huancabamba	PIU38B	-5.2	-79.5	2000
Peru	Arequipeno	AREQ 1	-16.2	-71.3	2332
Peru	Chulpi	LIM66	-11.4	-77.4	110
Peru	Confite Puntigudo	CUZ13	-15.5	-70.1	3831.9
Peru	Cubano Amarillo	UCA8	-5.2	-75.7	129
Peru	Huancavelicano	HVC179	-13.0	-75.1	4562
Peru	Huayleno	ANC291	-9.53	-77.53	3059
Peru	Piricinco	SM8	-6.2	-76.6	940
Uruguay	Dentado Branco	URZM13010	-34.0	-56.0	104

Note: Coordinates are estimated from the publications of the Committee on Preservation of Indigenous Strains of Maize

Supplemental Table 3.7 Analysis of variance table for DTA

Source	DF	SS	MS	F Value	Pr > F
Model	2832	106037.94	37.44	24.5	<.0001
Error	2138	3267.3	1.53		
Total	4970	109305.25			
R-Square	Coeff Var	Root MSE	DTA Mean		
0.97	1.87	1.24	66.3		

Supplemental Table 3.8 DTA analysis of variance by sources of variation

Wald F statistics					
Source	NumDF	DenDF	F Value	P Value	
BC₁F_{1s}	482	2019.4	5.75	<.001	
Checks vs. BC₁F_{1s}	1	501.3	17.01	<.001	
Checks vs. Checks	5	489	5.24	0.01	
Random Effects					
Source	Component	Comp/SE	DF		
Env	19.58	1.4	4		
block(env)	0.55	2.07	15		
rep(block(env))	0.26	2.80	24		
col(env)	0.06	4.06	275		
row(env)	0.22	5.10	108		
line*env	0.44	10.16	1918		

Supplemental Table 3.9 Analysis of variance table for DTS

Source	DF	SS	MS	F Value	Pr > F
Model	1133	13783.92	12.17	6.28	<.0001
Error	864	1674.51	1.94		
Total	1997	15458.43			
R-Square	Coeff Var	Root MSE	DTS Mean		
0.89	1.98	1.39	70.38		

Supplemental Table 3.10 DTS analysis of variance by sources of variation

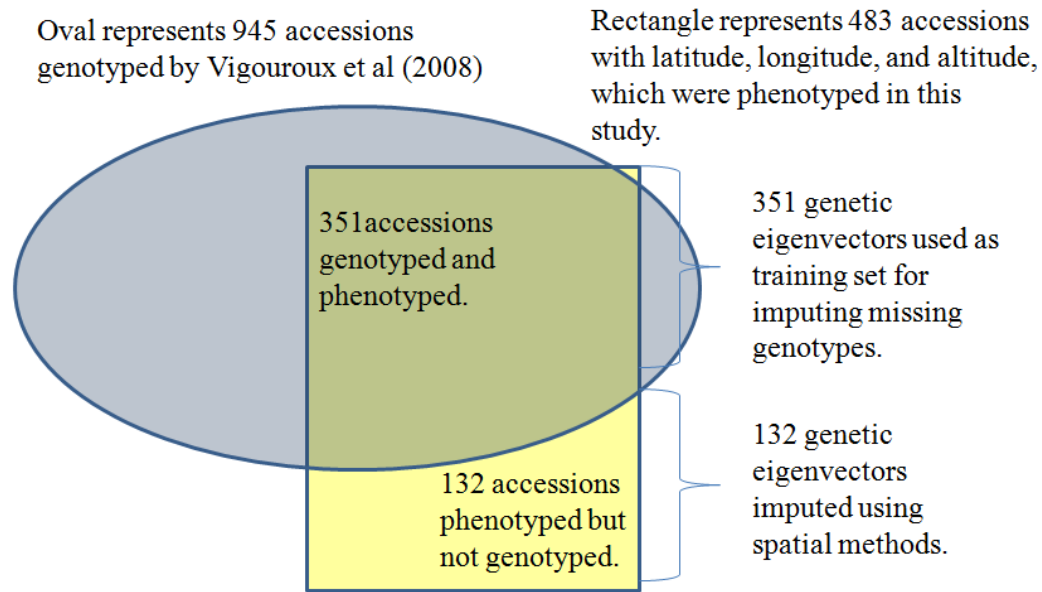
Wald F statistics				
Source	NumDF	DenDF	F Value	P Value
BC₁ F_{1s}	482	501.1	4.15	<.001
Checks vs. BC₁ F_{1s}	1	97.8	50.68	<.001
Checks vs. Checks	5	94.5	3.23	0.01
Random Effects				
Source	Component	Comp/SE	DF	
Env	2.3	0.69	1	
block(env)	0.38E-06	0.0	5	
rep(block(env))	0.43	2.42	128	
col(env)	0.12	3.14	111	
row(env)	0.093	2.41	46	
line*env	1.88	22.05	473	

Supplemental Table 3.11 Analysis of variance table for lodging

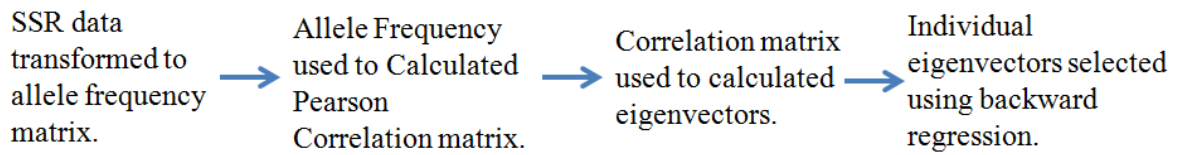
Source	DF	SS	MS	F Value	Pr > F
Model	3390	15176.2	4.48	4.48	<.0001
Error	2600	2867.33	1.1		
Total	5990	18043.5			
R-Square	Coeff Var	Root MSE	Lodging Mean		
0.84	18.58	1.05	5.65		

Supplemental Table 3.12 Lodging analysis of variance by sources of variation

Wald F statistics				
Source	NumDF	DenDF	F Value	P Value
BC₁ F_{1s}	432	2584.7	1.80	<.001
Checks vs. BC₁ F_{1s}	1	418.2	260.34	<.001
Checks vs. Checks	5	404.8	29.09	<.001
DTA	1	4620.3	16.00	<.001
Random Effects				
Source	Component	Comp/SE	DF	
Env	1.73	1.54	5	
block(env)	0.06	1.38	18	
rep(block(env))	0.09	2.87	24	
col(env)	0.13	7.88	328	
row(env)	0.06	4.59	131	
line*env	0.17	7.27	2395	



Process used to develop genetic covariates



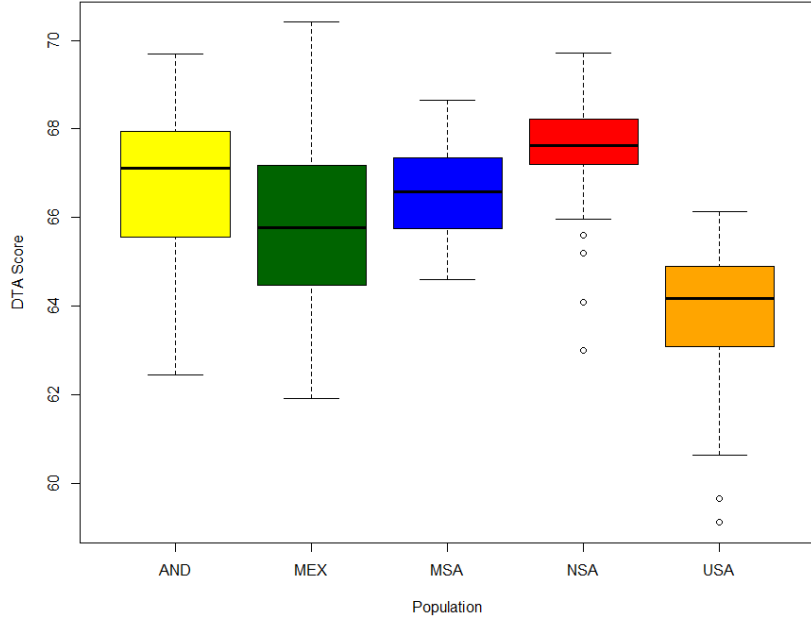
Supplemental Figure 3.1 Development of genotypes used as covariates in analysis.

Supplemental Table 3.13 Results from Tukey test for DTA scores in maize populations

Population	Mean	SE	Set[†]
NSA	67.5	0.16	a
AND	67.0	0.16	ab
MSA	66.5	0.16	bc
MEX	66.0	0.16	c
USA	63.5	0.27	d

HSD=0.77

[†]Groupings are based on Tukey HSD, and show which Populations are significantly different from one another at $\alpha=0.05$.



Supplemental Figure 3.2 Boxplot of DTA scores by maize Sub-population[†]

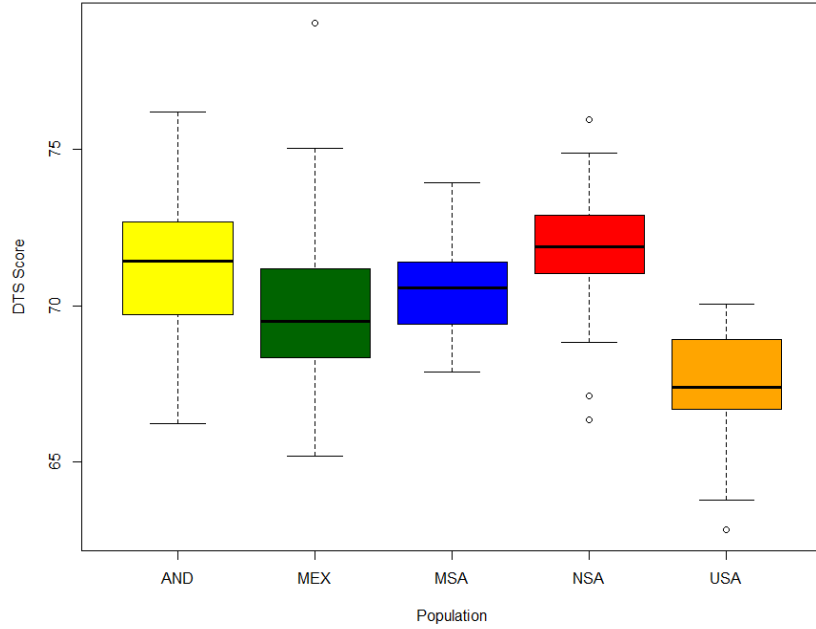
[†]Andean (AND), Mexican (MEX), Middle South America (MSA), Northern South America (NSA), and United States of America (USA). Bold line inside box represents the median, the bottom and top of the box are the first and third quartiles. Whiskers represent 1.5 times the first and third interquartile range. Circles represent scores outside this 1.5 inter quartile range.

Supplemental Table 3.14 Results from Tukey test for DTS scores in maize populations

Population	Mean	SE	Set[†]
NSA	72.0	0.25	a
AND	71.5	0.22	ab
MSA	70.5	0.21	bc
MEX	70.0	0.21	c
USA	67.5	0.29	d

HSD=1.02

[†]Groupings are based on Tukey HSD, and show which populations are significantly different from one another at $\alpha=0.05$.



Supplemental Figure 3.3 Boxplot of DTS scores by maize population[†]

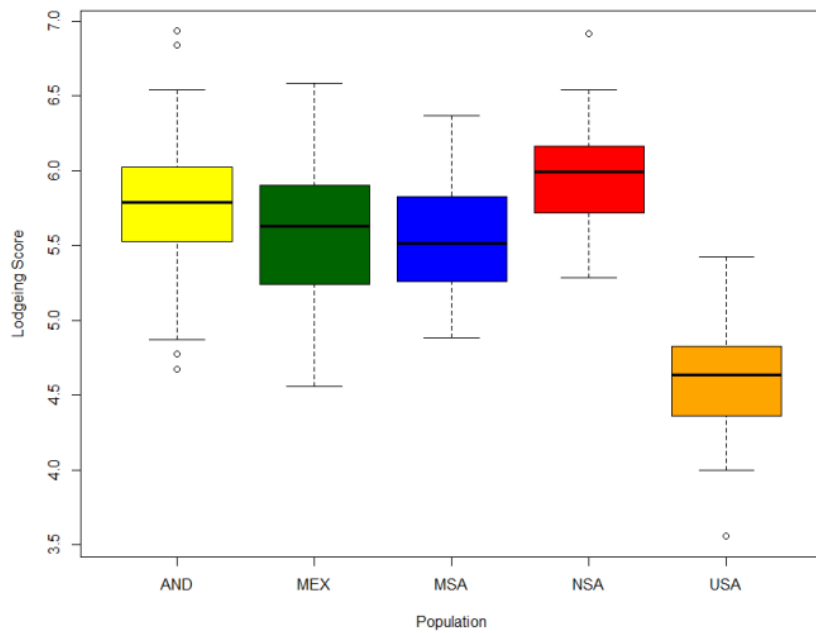
[†]Andean (AND), Mexican (MEX), Middle South America (MSA), Northern South America (NSA), and United States of America (USA). Bold line inside box represents the median, the bottom and top of the box are the first and third quartiles. Whiskers represent 1.5 times the first and third interquartile range. Circles represent scores outside this 1.5 inter quartile range.

Supplemental Table 3.15 Results from Tukey test for lodging (cm) in maize populations

Population	Mean	SE	Set[†]
NSA	5.97	0.05	a
AND	5.76	0.05	b
MEX	5.58	0.04	c
MSA	5.55	0.06	c
USA	4.58	0.06	d

HSD=0.21

[†]Groupings are based on Tukey HSD, and show which Populations are significantly different from one another at $\alpha=0.05$.



Supplemental Figure 3.4 Boxplot of lodging (cm) by maize population[†]

[†]Andean (AND), Mexican (MEX), Middle South America (MSA), Northern South America (NSA), and United States of America (USA). Bold line inside box represents the median, the bottom and top of the box are the first and third quartiles. Whiskers represent 1.5 times the first and third interquartile range. Circles represent scores outside this 1.5 inter quartile range.

Supplemental Table 3.16 Comparison of percent of variation accounted for by four different types of models

Trait	OLS	OLS w/ genetic covariates	Spatial	Spatial w/genetic covariates
DTS	6.9	38.4	20.5	37.8
DTA	7.2	42.5	20.1	42.4
Lodging	5.1	42	46.6	47.3

Note: Ordinary Least Squares (OLS), and Spatical methods, using latitude, longitude, and altitude, with and without genetic data used as covariates. Values calculated using the R^2 in the OLS models, and from the five-fold cross validation for the spatical methods.

Supplemental Table 3.17 Parameter estimates for the Matern spatial model developed for the three diseases

Model Parameters	DTA	DTS	Lodging
Intercept	66.34	70.66	4.72
Latitude [†]	0.01	0.008	0.0056
Longitude	-0.02	-0.009	-0.005
Altitude	0.00	0.0001	0.00
Eigenvector 1 [‡]	-4.46	-8.55	-1.64
Eigenvector 2	9.93	14.93	3.09
Eigenvector 3	3.81	4.52	0.88
Eigenvector 4	NA	3.63	-0.94
Eigenvector 5	NA	-3.20	NA
Sigmasq (partial sill) [§]	3.93	3.37	18.85
Phi (range) [¶]	738.5	12.39	337
Kappa [#]	0.08	0.052	0.96
Anisotropy angle ^{††}	0.70	0.708	1.858
Anisotropy ratio	4.19	7.92	1.81
Tau sq (nugget) ^{‡‡}	0.00	0.00	0.11

Note: [†]latitude, longitude, and altitude are all important covariates even though parameter estimates are close to zero.

[‡]For each disease a different set of genetic covariates were used in the spatial model. For the DTA the 2nd, 3rd, and 10th eigenvectors were used, for DTS the 2nd, 3rd, 10th, 49th, and 80th, and for lodging, the 2nd, 3rd, 11th, and 28th.

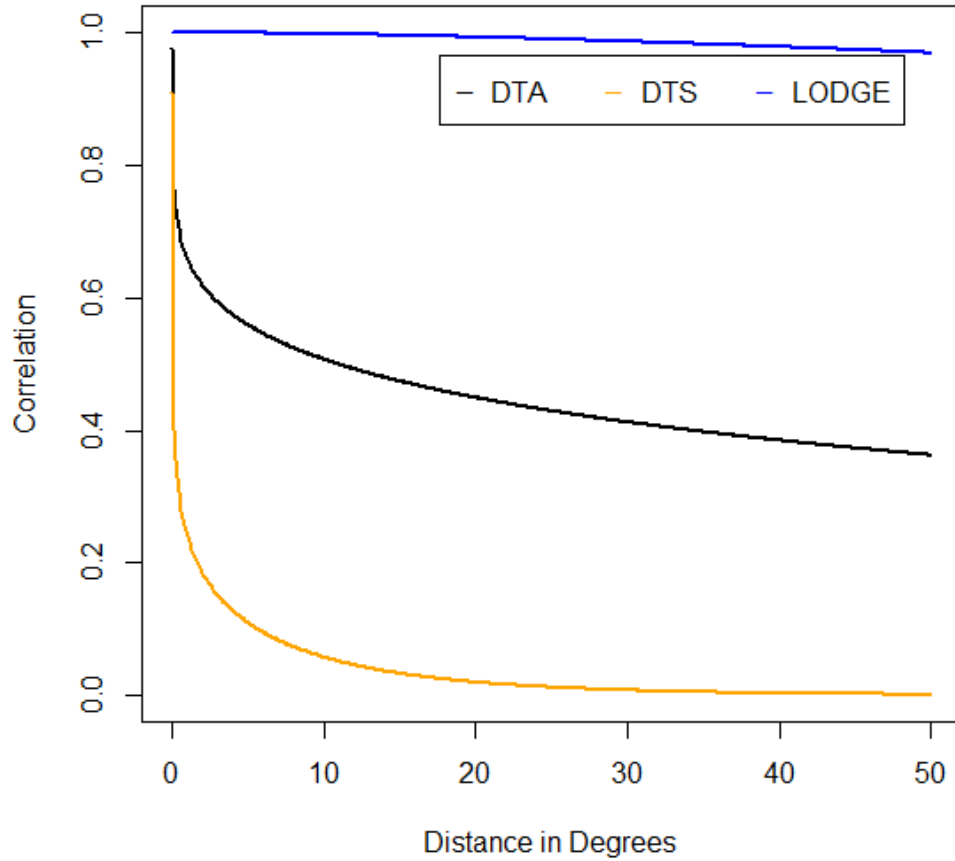
[§]Sigmasq or the partial sill is a parameter of the semivariogram model that represents the variance of agronomic scores spatially autocorrelated process without any nugget effect. In the semivariogram model, the partial sill is the difference between the nugget and the sill.

[¶]Phi (range) is a distance measure in degrees that represents a distance beyond which there is little or no autocorrelation among variables.

[#]Kappa is a smoothness parameter, explains how much the variances fluctuates over distance.

^{††}Anisotropy angle is the direction in which the data is varying. Anisotropy ratio regulates the dependency on anisotropy angle.

^{‡‡}Tau sq (nugget) is measurement error of sampling BC₁F₁s for agronomics at small distances.



Supplemental Figure 3.5 Covariance functions for Matérn models for DTA, DTS, and lodging[†]

[†]This figure gives us an indication of the spatial trends that these traits follow. The correlation between points decays quickly over distance for both DTA and DTS. This may be due to environment specific selection for flowering time, as an adaptive trait. Lodging decays more slowly and may have been under less selection than flowering time or selected for uniformly across geography.

Supplemental References

- Brieger FG, Gurgel JTA, Paterniani E, Blumenschein A, Alleoni MR, 1958. Races of maize in Brazil and other eastern South American countries. National Academy of Science-National Research Council Washington, DC, USA
- Brown WL, 1960. Races of maize in the West Indies. National Academy of Sciences. National Research Council, Washington, DC, USA
- Buckler ES, Holland JB, Bradbury PJ, Acharya CB, Brown PJ, Browne C, Ersoz E, Flint-Garcia S, Garcia A, Glaubitz JC, Goodman MM, Harjes C, Guill K, Kroon DE, Larsson S, Lepak NK, Li H, Mitchell SE, Pressoir G, Peiffer JA, Rosas MO, Rocheford TR, Romay MC, Romero S, Salvo S, Sanchez Villeda H, da Silva HS, Sun Q, Tian F, Upadyayula N, Ware D, Yates H, Yu J, Zhang Z, Kresovich S, McMullen MD, 2009. The genetic architecture of maize flowering time. *Science* 325:714-718
- Committee on Preservation of Indigenous Strains of Maize, 1954. Original Strains of Corn, I. National Academy of Sciences, National Research Council, Washington, D.C.
- Committee on Preservation of Indigenous Strains of Maize, 1955. Original strains of corn, II. National Academy of Sciences, National Research Council, Washington, D.C.
- Sanchez G. JJ, Goodman MM, Stuber C. 2000. Isozymatic and morphological diversity in the races of maize of Mexico. *Econ. Bot.* 54:43-59.
- Grant UJ, Hatheway WH, Timothy DH, Cassalet DC, Roberts LM, 1963. Races of maize in Venezuela. National Academy of Sciences. National Research Council, Washington, DC, USA
- Grobman A, Salhuana W, Sevilla R, with Mangelsdorf PC, 1961. Races of maize in Peru. National Academy of Sciences. National Research Council, Washington, DC, USA
- Hatheway WH, 1957. Races of maize in Cuba. National Academy of Sciences. National Research Council, Washington, DC, USA
- McMullen MD, Kresovich S, Villeda HS, Bradbury P, Li H, Sun Q, Flint-Garcia S, Thornsberry J, Acharya C, Bottoms C, Brown P, Browne C, Eller M, Guill K, Harjes C, Kroon D, Lepak N, Mitchell SE, Peterson B, Pressoir G, Romero S, Oropeza M, Rosas, Salvo S, Yates H, Hanson M, Jones E, Smith S, Glaubitz JC, Goodman MM, Ware D, Holland JB, Buckler ES, 2009. Genetic properties of the maize nested association mapping population. *Science* 325:737-740

- Paterniani E, Goodman MM, 1977. Races of maize in Brazil and adjacent areas. CIMMYT, Mexico City, Mexico.
- R. Ramírez E, Timothy DH, Díaz BE, Grant UJ, with GE Nickerson C, Anderson E, Brown W, 1960. Races of maize in Bolivia. National Academy of Sciences, National Research Council, Washington, DC, USA
- Roberts LM, Grant UJ, R. Ramírez E, Hatheway WH, Smith DL, Mangelsdorf PC, 1957. Races of maize in Colombia. National Academy of Sciences, National Research Council, Washington, DC, USA
- Timothy DH, Hatheway WH, Grant UJ, Torregroza CM, Sarria VD, Varela AD, 1963. Races of maize in Ecuador. National Academy of Sciences, National Research Council, Washington, DC, USA
- Timothy DH, Peña VB, R. Ramírez E, with Brown WL, Anderson E, 1961. Races of maize in Chile. National Academy of Sciences, National Research Council, Washington, DC, USA
- Wellhausen EJ, Fuentes OA, Hernández-Corzo A, with Mangelsdorf PC, 1957. Races of maize in Central America. National Academy of Sciences, National Research Council, Washington, DC, USA
- Wellhausen EJ, Roberts LM, E. Hernández X, with Mangelsdorf PC, 1952. Races of maize in Mexico: Their origin, characteristic and distribution. Bussey Institution of Harvard University, Cambridge, Massachusetts, USA

APPENDIX

Appendix

As part of the assessment of agronomic acceptability, plant height (PH) and ear height (EH) were measured. Plant and ear height are important as taller plants produce more dry matter, relative to the amount of grain produced. This reduction in harvested matter as compared to total matter produced is considered a waste of energy and resources on the part of the plant (Graham et al, 2007). In maize breeding programs there has been a trend for shorter plants that can withstand higher nitrogen applications and higher planting densities. Breeders also have concerns about the connection of plant height and lodging (Salas Fernandez et al, 2009). Like other traits examined in this study, the genes controlling PH and EH have been found to be randomly distributed though the genome (Appendix Table 1). This random distribution of genes allows the screening of BC₁ F₁s to be informative as to the variation of PH and EH in accessions (Peiffer et al, 2014).

PH and EH were measured in seven environments for this study: at Andrews, NC, and Windfall, IN, in 2012 and 2013, and at Cairo, GA, Salisbury, NC, and Thomasboro, IL, in 2013 using the same field locations, layout, and germplasm as was used in the assessment of other traits. Plant height was measured in centimeters (cm) as the visual average along the row of distance from the ground to the top of tassel. Ear height was measured in centimeters as the visual average along the row of distance from the ground to the node of the primary ear.

Data was analyzed using same ASReml model as was used to model days to anthesis (DTA). For both PH and EH, DTA was not used as a covariate as it was not significant when included. Population analysis was performed using the same five population designations as

were used for the other traits. Spatial analysis and cross validation was performed using the same methodology as used for other traits.

BC₁ F₁ effects were significant ($p < 0.001$) for both plant and ear height (Appendix Tables 2-5). A full table of the PH and EH estimates and their standard errors (SEs) is provided in Appendix Table 6. Plant height ranged from 233 cm for Gaspe Flint (PI 401757) to 326 cm for Olotillo (CHS 53). Ear height had a smaller range, from 71 cm for Gaspe Flint (PI 401757) to 144 cm for Moroti (PE I).

The pairwise phenotypic correlations of all the agronomic traits were moderate and significant ($p < 0.001$), with $r^2 = 0.82$ between PH and EH, $r^2 = 0.72$ between PH and DTA, and $r^2 = 0.76$ between EH and DTA. It is interesting to note the strong correlation between PH/EH and DTA, even though DTA was not a significant covariate in the analysis of PH and EH. Plots of pairwise correlations of all six agronomic traits measured in the BC₁ F₁s are provided in Appendix Figure 1. Of note is the positive correlations ($r^2 = 0.40$) between lodging and both PH and EH. In this sample of semi-exotic material, increased PH and EH do not seem to have much of an effect on lodging.

Population analysis with respect to average plant height showed the NSA population was the tallest with an average height of 299.1 cm, followed by AND at 298.7 cm, MSA at 294.0 cm, MEX at 292.9 cm, and USA the shortest at 264.4 cm, with a Tukey HSD at $\alpha = 0.05$ of 3.9 cm. This forms three groupings with NSA and AND in set A, MSA in sets A and B, MEX in set B, and USA in set C (Appendix Table 8 and Appendix Figure 2). The population differences in EH are slightly different with a Tukey HSD of 4.07 at $\alpha = 0.05$. This forms four sets, with the NSA population at 123.2 cm in set A, followed by AND at 119.7 cm

in both sets A and B, then MSA at 118.2 cm in sets B and C, MEX at 115.7cm in set C alone and USA at 96.7 cm in set D alone (Appendix Table 7 and Appendix Figure 3).

Raw point pattern data of PH and EH of the BC₁ F₁s can be observed in Appendix Figures 4 and 5. This data shows a spatial pattern which was used for modeling PH and EH at locations unsampled in this study. Spatial analyses shows PH and EH are predicted to be the highest around the equator, with a trend toward shorter plants farther north and south (Appendix Figures 6A and 7A). As with flowering time, locations that are at high altitude trend towards shorter plants. The spatial model without genotypic data accounted for 14% of the variation in PH and the full model with genotypic data accounted for 26% of the variation, while the reduced model accounted for 12% of the variation in EH and the full model accounted for 37%; both spacial models were an improvement over the variation that was captured using ordinary least squares. SEs of predictions for PH are similar to those of phenotypes ranging from 9.2 to 14.3, (Appendix Figure 6B). These prediction SEs are only slightly higher when compared to the SE of PH which ranged from 9.2 to 9.7. Ear height SEs show the same trend with predictions ranging from 5.6 to 8.2 (Appendix Figure 7B) with EH phenotypic SEs ranging from 5.4 to 5.9. This gives another indication that the spatial model is adequately describing the data as the ability to predict data is roughly the same as the ability to phenotype.

In the spatial analysis of PH and EH the 3rd and 10th eigenvectors were used as a covariate for PH while EH used the 3rd, 10th, 38th, and 55th eigenvectors. A full table of the model parameters for the Matérn model is given in Appendix Table 10. Appendix Table 11 gives the amount of variation different types of models account for, Ordinary Least Squares,

and Spatical methods, with and without the genetic covariates. The plots of the covariance functions for the Matérn models for PH and EH are given in Appendix Figure 8. This demonstrates that there are high correlations between locations with respect to PH and EH and may indicate that PH and EH are not under as much selection pressure for environmental adaptation as flowering time.

Appendix Table 1 Yates corrected Chi square tests for random distribution of QTL discovered in Nested Association Mapping Population studies for Plant Height (PH) and Ear Height (EH)

Chromosome	Proportion of Genome	Observed # of QTL PH	Expected# of QTL PH	PH Chi Square [†]
1	0.14	4	3.64	0.01
2	0.11	1	2.86	0.65
3	0.11	3	2.86	0.05
4	0.1	3	2.6	0.00
5	0.11	2	2.86	0.05
6	0.08	2	2.08	0.08
7	0.1	3	2.6	0.00
8	0.09	3	2.34	0.01
9	0.08	1	2.08	0.16
10	0.07	4	1.82	1.55
Total	1	26	26	2.56
w/9 df crit = 16.91				
Chromosome	Proportion of Genome	Observed # of QTL EH	Expected# of QTL EH	EH Chi Square [†]
1	0.14	4	3.08	0.06
2	0.11	5	2.42	1.79
3	0.11	2	2.42	0.00
4	0.1	1	2.2	0.22
5	0.11	2	2.42	0.00
6	0.08	1	1.76	0.04
7	0.1	2	2.2	0.04
8	0.09	1	1.98	0.12
9	0.08	1	1.76	0.04
10	0.07	3	1.54	0.60
Total	1	22	22	2.91
w/9 df crit = 16.91				

[†]Note: First, using the NAM map, the proportion of the genome for each chromosome was calculated (McMullen et al, 2009). Next, the numbers of QTL observed from the NAM mapping studies were counted on each chromosome (Peiffer et al, 2014). The expected number of QTL on each chromosome was calculated proportional to each chromosomes proportion of the genome. The observed QTL counts per chromosome were compared to expected counts with a Chi square test, with 9 df.

Appendix Table 2 Analysis of variance table for PH

Source	DF	SS	MS	F Value	Pr > F
Model	3953	5550820.29	1404.20	7.52	<.0001
Error	3069	573108.76	186.741		
Total	7022	6123929.04			
R-Square	Coeff Var	Root MSE	PH Mean		
0.91	4.66	13.67	293.12		

Appendix Table 3 PH analysis of variance by sources of variation

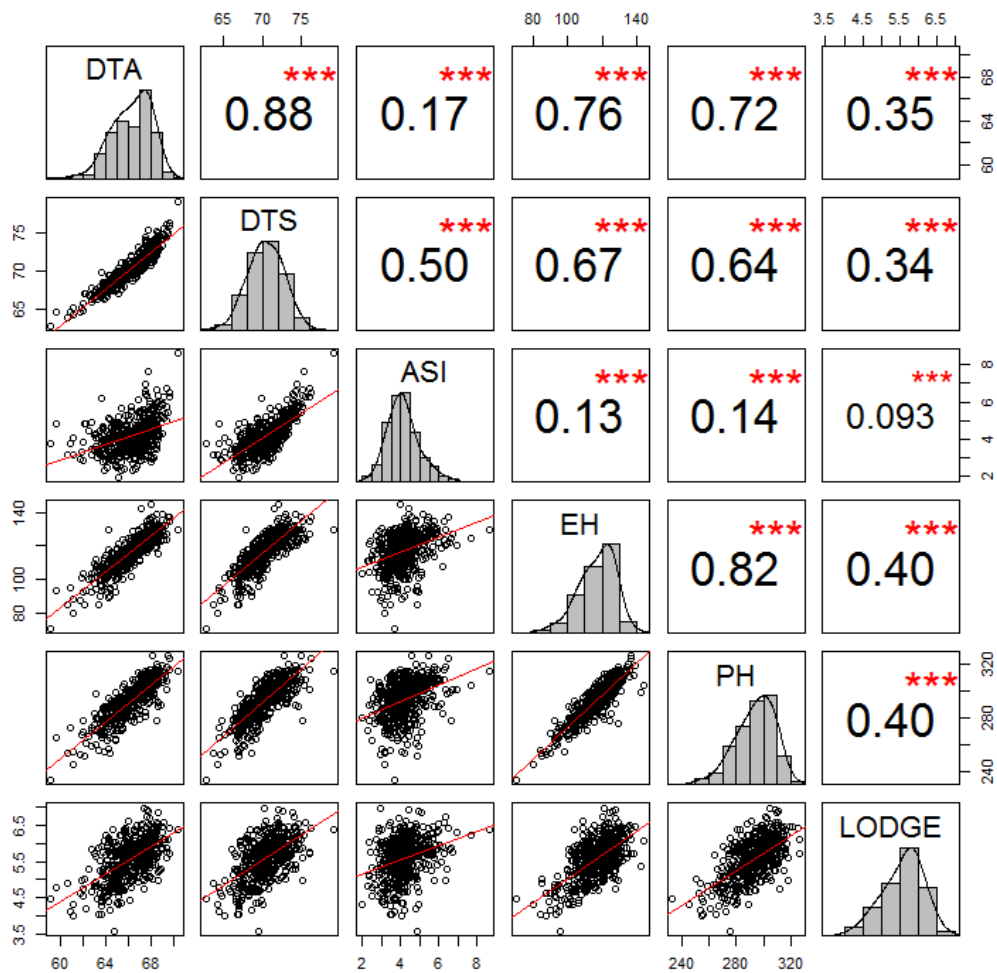
Wald F statistics				
Source	NumDF	DenDF	F Value	P Value
BC₁ F_{1s}	482	3290.2	7.96	<.001
Checks vs. BC₁ F_{1s}	1	397.6	55.01	<.001
Checks vs Checks	5	379.9	105.81	<.001
Random Effects				
Source	Component	Comp/SE	DF	
Env	639.86	1.85	6	
block(env)	13.68	2.27	20	
rep(block(env))	6.31	2.45	28	
col(env)	36.88	9.44	298	
row(env)	13.46	5.56	218	
line*env	18.31	5.14	2894	

Appendix Table 4 Analysis of variance table for EH

Source	DF	SS	MS	F Value	Pr > F
Model	3953	2346963.17	593.72	4.45	<.0001
Error	3070	409424.18	133.36		
Total	7023	2756387.35			
R-Square	Coeff Var	Root MSE	EH Mean		
0.85	9.87	11.55	116.95		

Appendix Table 5 EH analysis of variance by sources of variation

Wald F statistics				
Source	NumDF	DenDF	F Value	P Value
BC₁ F_{1s}	482	3510.7	6.20	<.001
Checks vs. BC₁ F_{1s}	1	328.0	55.49	<.001
Checks vs Checks	5	309.8	52.40	<.001
Random Effects				
Source	Component	Comp/SE	DF	
Env	217.45	1.84	6	
block(env)	4.92	1.83	20	
rep(block(env))	3.90	2.53	28	
col(env)	14.30	8.19	298	
row(env)	5.96	4.83	218	
line*env	6.65	3.04	2894	



Appendix Figure 1 Pairwise regression of DTA, DTS, ASI, EH, PH, and Lodging for the 483 BC₁F_{1s} screened.

Upper diagonal indicates significance (***) level of pairwise linear regression and pairwise r^2 . Diagonal shows distribution of scores for each trait. Below diagonal shows the pairwise linear regressions and scatter of points.

Appendix Table 6 List of accessions used country of origin, race name, accession name, source, and Latitude, Longitude, and Altitude at point of collection. Also given are the least square means and standard errors of plant height (PH) and ear height (EH)

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	PH	PH SE	EH	EH SE
Argentina	Amargo	ARZM 03014	NCRPIS	-32.2	-58.1	20	277	9.60	112	5.77
Argentina	Bola Blanca	ARG 532 (USDA)	NCRPIS	-23.2	-65.4	2287	280	9.24	111	5.39
Argentina	Calchaqui Small White	ARG 2420 (USDA)	NCRPIS	-32.7	-64.7	895	273	9.25	105	5.40
Argentina	Camelia	ARZM 03025	NCRPIS	-30.5	-58.3	68	290	9.22	118	5.37
Argentina	Canario de Formosa	ARZM 06016	NCRPIS	-1.7	-78.7	3050	281	9.22	117	5.36
Argentina	Canario de Ocho	ARG VI	CIMMYT	-32	-58	305	284	9.23	107	5.38
Argentina	Capia Blanco	ARG 499 (USDA)	NCRPIS	-23.2	-65.4	2287	295	9.23	121	5.37
Argentina	Capia Rosado	ARG 460 (USDA)	NCRPIS	-23.2	-65.4	2287	287	9.23	115	5.37
Argentina	Cateto Sulino	ARG I	CIMMYT	-32	-58	305	275	9.24	110	5.38
Argentina	Chulpi	ARG 484 (USDA)	NCRPIS	-23.2	-65.4	2287	289	9.24	114	5.38
Argentina	Cravo	ARZM 05071	NCRPIS	-33	-71.6	80	309	9.22	129	5.36
Argentina	Cristal Sulino	ARG III	CIMMYT	-29	-62	1554	288	9.23	119	5.37
Argentina	Cristalino Amarillo	AR 21004	NCRPIS	-38.1	-62.2	295	253	9.28	88	5.42
Argentina	Cristalino Amarillo	ARZM 19070	NCRPIS	-39.5	-69.3	381	266	9.25	94	5.39
Argentina	Cristalino Blanco	ARZM 19074	NCRPIS	-39.5	-69.3	381	273	9.25	97	5.39
Argentina	Cristalino Colorado	ARZM 16021	NCRPIS	-32.6	-69.3	1886	276	9.24	110	5.38
Argentina	Cuarentino	ARG 486 (USDA)*	NCRPIS	-34.9	-58	276	276	9.24	108	5.38
Argentina	Culli	ARG 471 (USDA)	NCRPIS	-23.2	-65.4	2287	271	9.26	103	5.40
Argentina	Dentado Amarillo	ARZM 16062	NCRPIS	-35	-67.7	474	281	9.22	109	5.37
Argentina	Dentado Blanco	ARZM 03056	NCRPIS	-39.2	-59.5	58	287	9.22	116	5.36
Argentina	Dentado Blanco Rugoso	ARZM 01149	NCRPIS	-38.2	-62.4	285	287	9.22	119	5.37
Argentina	Dulce	ARZM 20005B	NCRPIS	-40.8	-63	5	269	9.62	93	5.79
Argentina	Marron	ARG 468 (USDA)	NCRPIS	-23.8	-65.5	2359	279	9.61	105	5.79
Argentina	Oke	ARG 539 (USDA)	NCRPIS	-23.2	-65.4	2287	295	9.23	121	5.38
Argentina	Pisincho	ARG 481 (USDA)*	NCRPIS	-23.2	-65.4	2287	277	9.24	103	5.39
Argentina	Pisingallo	ARZM 13095	NCRPIS	-30.3	-66.3	457	280	9.24	106	5.38
Barbados	Tuson	BARBGP 2*	NCRPIS	13.1	-59.6	60	305	9.22	125	5.36
Bolivia	Altiplano	BOV 903	NRC	-21.8	-64.1	1976	282	9.23	110	5.38
Bolivia	Argentino	BOV 920	ICA	-21.8	-64.1	1829	297	9.22	116	5.36
Bolivia	Aysuma	BOV 331	ICA	-19	-65.3	2127	292	9.23	112	5.37
Bolivia	Camba	BOV 1131	ICA	-16.5	-68.2	1570	318	9.23	134	5.37
Bolivia	Cateto	BOV 1083	NRC	-11.3	-67.7	240	311	9.22	123	5.36
Bolivia	Cateto	BOV 317	NCRPIS	-17.8	-64.8	2843	298	9.22	123	5.36
Bolivia	Chake-Sara	BOV 520	NCRPIS	-17.5	-65.7	2395	291	9.23	112	5.38
Bolivia	Checchi	BOV 320	ICA	-17.4	-66.2	2080	297	9.22	115	5.36

Appendix Table 6 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	PH	PH SE	EH	EH SE
Bolivia	Cecchi	BOV Comp.	NCRPIS	-18.1	-65.8	2542	279	9.24	112	5.38
Bolivia	Cholito	BOV 309	NCRPIS	-18.1	-64.4	1581	312	9.22	128	5.36
Bolivia	Chuspillu	BOV 883	NCRPIS	-17.5	-65.7	2507	299	9.23	117	5.37
Bolivia	Coroico	BOV 1064	NCRPIS	-14	-65	92	304	9.22	122	5.36
Bolivia	Coroico Amarillo	BOV 405	NRC	-14.9	-65	160	301	9.22	122	5.36
Bolivia	Coroico Blanco	BOV 406	NCRPIS	-14.7	-65	130	298	9.22	123	5.36
Bolivia	Cubano Dentado	BOV 440	NRC	-17.8	-63.2	560	302	9.23	125	5.37
Bolivia	Cubano Dentado	BOV 585	NRC	-16.4	-61	330	309	9.22	124	5.36
Bolivia	Enano	BOV 1032	NCRPIS	-11	-68	180	298	9.22	127	5.36
Bolivia	Huilcaparu	BOV 685	ICA	-17.4	-65.9	2721	309	9.22	119	5.37
Bolivia	Huilcaparu Moteado	BOV Comp.	NCRPIS	-16.9	-67.1	2760	303	9.22	116	5.36
Bolivia	Karapampa	BOV 978	ICA	-21.8	-64.1	1976	290	9.23	112	5.37
Bolivia	Kcello	BOV 325	ICA	-17.4	-66.2	1400	288	9.23	112	5.37
Bolivia	Kcello	BOV 848	ICA	-19.6	-65.8	1801	289	9.22	114	5.37
Bolivia	Kcello	BOV 948	NRC	-19.6	-65.8	3256	275	9.24	104	5.38
Bolivia	Morado	BOV 567	ICA	-16.5	-67.5	2270	307	9.23	128	5.37
Bolivia	Ninuelo	BOV 1088	ICA	-17.8	-63.2	2201	302	9.22	123	5.36
Bolivia	Paru	BOV Comp.	NCRPIS	-15.8	-68.6	2737	299	9.37	142	5.53
Bolivia	Patillo Grande	BOV 649	ICA	-17.5	-65.7	2515	303	9.23	115	5.37
Bolivia	Perola	BOV 711	NRC	-21.3	-63.5	520	301	9.22	118	5.36
Bolivia	Pisankalla	BOV 344	ICA	-21.5	-64.8	1738	275	9.25	108	5.40
Bolivia	Pisankalla	BOV 864	ICA	-17.5	-65.7	2175	277	9.24	104	5.38
Bolivia	Pisankalla	BOV 965	ICA	-21.8	-64.1	1948	280	9.24	102	5.39
Bolivia	Pojoso Chico	BOV 800	NCRPIS	-17.7	-62.8	500	270	9.24	105	5.38
Bolivia	Pororo	BOV 583	ICA	-15.7	-67.3	330	293	9.22	123	5.36
Bolivia	Pororo	BOV 806	NRC	-18.3	-59.8	1400	294	9.38	118	5.54
Bolivia	Uchuquilla	BOV 318	NCRPIS	-17.2	-66.1	1922	298	9.22	111	5.36
Bolivia	Uchuquilla	BOV 954	ICA	-21.8	-64.1	1948	287	9.22	111	5.36
Bolivia	Yungueno	BOV 362	ICA	-21.8	-64.1	1052	305	9.22	124	5.36
Bolivia	Yungueno	BOV 716	ICA	-16.5	-68.2	1400	310	9.22	124	5.36
Brazil	Avati Pichinga	BR 2760 (USDA)	NCRPIS	-25	-56	366	294	9.22	122	5.36
Brazil	Avati Pichinga	BR 2776 (USDA)	NCRPIS	-25	-56	366	291	9.22	127	5.36
Brazil	Avati Pichinga Ihu	BR 2830 (USDA)	NCRPIS	-25	-56	366	283	9.22	125	5.36
Brazil	Caingang	PR III	CIMMYT	-23	-51	610	300	9.22	121	5.36
Brazil	Caingang	SP XIII	CIMMYT	-22	-51	407	293	9.22	113	5.37
Brazil	Caraja	1692 (USDA)	NCRPIS	-27.2	-49.6	433	315	9.22	134	5.36
Brazil	Cateto	BA II	CIMMYT	-12.5	-39	610	302	9.22	128	5.36

Appendix Table 6 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	PH	PH SE	EH	EH SE
Brazil	Cateto	CE I	CIMMYT	-3.8	-38.8	177	303	9.22	124	5.36
Brazil	Cateto Assis Brasil	RGS XIV	NCRPIS	-29	-53	274	299	9.28	114	5.43
Brazil	Cateto Grande	MT IV	CIMMYT	-20	-56	366	314	9.22	125	5.37
Brazil	Cateto Nortista Precoce	SUR I	CIMMYT	5.8	-55.2	61	303	9.22	127	5.36
Brazil	Cravo Paulista	SP I	CIMMYT	-22	-48	579	296	9.22	121	5.36
Brazil	Cravo Riograndense	RGS VII	CIMMYT	-30	-53	366	297	9.22	122	5.36
Brazil	Cristal	SP X	CIMMYT	-22	-48	803	300	9.22	131	5.36
Brazil	Cristal	SP XI	CIMMYT	-22	-48	803	310	9.22	132	5.36
Brazil	Cristal Inter. Perola	1115 (USDA)	NCRPIS	-28.4	-54.3	240	308	9.22	128	5.36
Brazil	Cristal Paraguay Paulis	2334 (USDA)	NCRPIS	-23.3	-46.1	582	305	9.22	125	5.36
Brazil	Dente Branco Paulista	SP V	CIMMYT	-22	-48	579	305	9.22	121	5.36
Brazil	Dente Branco R. G.	SC II	CIMMYT	-27	-52	892	290	9.23	112	5.37
Brazil	Dente Paulista	SP IV	CIMMYT	-22	-48	518	304	9.22	119	5.36
Brazil	Dente R. G. Liso	RGS VI	CIMMYT	-29	-52	366	300	9.22	124	5.36
Brazil	Dente R. G. Liso	SC I	CIMMYT	-27	-52	892	300	9.22	123	5.36
Brazil	Dente R. G. Rugoso	RGS II	CIMMYT	-30	-53	366	297	9.22	118	5.36
Brazil	Dourados Saboro	BR 50 (USDA)	NCRPIS	-22.3	-54.8	340	302	9.22	122	5.36
Brazil	Entrelacado	MT VI	CIMMYT	-18	-55	305	309	9.23	127	5.37
Brazil	Hickory King	RGS IX*	CIMMYT	-28.5	-51	366	294	9.22	120	5.36
Brazil	Moroti	MT I	CIMMYT	-20	-56	366	296	9.22	119	5.36
Brazil	Moroti	PE I	NCRPIS	-8	-36	344	305	9.23	144	5.37
Brazil	Moroti Precoce	BOL I	CIMMYT	-20	-58	457	264	9.23	100	5.38
Brazil	Semi Dente Paulista	SP IX	CIMMYT	-22	-48	305	305	9.22	129	5.36
Brazil	Semi Dente R. G.	RGS XV	CIMMYT	-30	-53	366	293	9.22	120	5.36
Brazil	Tuson	BAI III	CIMMYT	-12.5	-39	200	295	9.22	118	5.36
Brazil	Tuson	BAI IIIB	NCRPIS	-12.5	-39	200	293	9.59	118	5.76
Chile	Araucano	CHI 320*	NCGRP	-38.1	-72.3	417	251	9.28	85	5.43
Chile	Capia Chico Chileno	CHI 382*	NRC	-23.7	-70.4	40	267	9.64	100	5.81
Chile	Cristalino Chico	CHI 324	NCGRP	-38.1	-71.9	66	265	9.34	93	5.50
Chile	Cristalino Chileno	CHI 156	NCRPIS	-38.1	-71.9	66	286	9.23	106	5.38
Chile	Cristalino Grande	CHI 323*	NCRPIS	-37.5	-72.4	139	261	9.64	94	5.82
Chile	Curagua	CHI 301*	NRC	-33	-70.7	732	271	9.26	104	5.41
Chile	Curagua	CHI 314*	NCGRP	-33.2	-70.7	457	284	9.24	111	5.38
Chile	Curagua Grande	CHI 303	NRC	-33.2	-70.7	457	267	9.24	104	5.38
Chile	Dentado Comercial	CHI 326*	NCGRP	-38.1	-71.9	66	288	9.22	115	5.36
Chile	Dulce Evergreen	CHI 332*	NCGRP	-38.1	-71.9	66	284	9.24	104	5.38
Chile	Dulce Golden Bantam	CHI 335*	NCGRP	-38.1	-71.9	66	271	9.26	98	5.41

Appendix Table 6 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	PH	PH SE	EH	EH SE
Chile	Harinoso Tarapaqueno	CHI 421	NRC	-19.9	-69.5	1550	310	9.22	125	5.36
Colombia	Amagaceno	ANT 343*	NCRPIS	6.2	-75.8	1800	309	9.22	129	5.37
Colombia	Amagaceno	HUI 317*	NCRPIS	2.5	-74.8	1554	310	9.23	130	5.37
Colombia	Andaqui	CAQ 307*	NCRPIS	1.2	-75.9	490	308	9.23	132	5.37
Colombia	Andaqui	CAQ 333*	NRC	1.8	-75.6	500	298	9.22	122	5.36
Colombia	Cabuya	SAN 316*	NRC	7.4	-72.7	2100	302	9.22	125	5.36
Colombia	Cacao	SAS 327*	ICA	5.9	-73.7	1600	313	9.22	128	5.36
Colombia	Cacao	SAS 335*	NCGRP	6.4	-73.3	1300	297	9.22	125	5.37
Colombia	Capio	ANT 348*	ICA	5.9	-75.4	1966	278	9.22	124	5.36
Colombia	Capio	ANT 354	ICA	5.7	-75.3	2600	301	9.23	127	5.37
Colombia	Capio	NAR 315	ICA	1.2	-77.3	2360	325	9.23	137	5.37
Colombia	Caqueteno	CAQ 305*	ICA	1.5	-75.4	300	310	9.22	123	5.36
Colombia	Cariaco	COR 338*	NCGRP	8.8	-75.9	200	299	9.23	119	5.37
Colombia	Chococeno	CHO 340	NCRPIS	7.5	-77.1	30	319	9.22	139	5.37
Colombia	Clavo	NAR 329*	ICA	1.2	-77.3	2360	307	9.23	128	5.37
Colombia	Comun	CAU 454*	NCRPIS	7.5	-74.8	600	308	9.22	127	5.36
Colombia	Comun	NAR 330*	NCRPIS	1.5	-78.5	118	301	9.23	125	5.37
Colombia	Comun	VAL 374*	NCRPIS	3.6	-76.5	980	304	9.22	124	5.36
Colombia	Costeno	ANT 394*	NCRPIS	2.2	-76.9	922	305	9.22	121	5.36
Colombia	Costeno	ATL 314*	NCRPIS	10.9	-74.8	15	285	9.22	112	5.37
Colombia	Costeno	ATL 328*	NRC	10.4	-74.9	7	284	9.23	109	5.38
Colombia	Costeno	COR 320*	NCGRP	8.3	-75.2	100	301	9.23	123	5.37
Colombia	Guirua	MAG 469*	NCGRP	10.5	-73.3	1870	304	9.22	128	5.36
Colombia	Harin. Dent.	NAR 326*	NCRPIS	1.4	-77.6	1400	312	9.22	128	5.37
Colombia	Imbricado	NAR 389	ICA	0.8	-77.6	2000	314	9.22	131	5.37
Colombia	Montana	NAR 625*	NCRPIS	1.2	-77.3	2542	302	9.28	128	5.43
Colombia	Pira	CUN 327*	NRC	4.3	-74.4	1000	294	9.22	125	5.36
Colombia	Pira	CUN 480*	NRC	4.8	-74.7	1000	309	9.23	128	5.37
Colombia	Pira	TOL 405	NRC	4.2	-74.9	450	307	9.22	130	5.37
Colombia	Pollo	CUN 424	NCRPIS	4.8	-73.7	2000	298	9.22	120	5.36
Colombia	Pollo	CUN 443*	NRC	4.2	-74.4	1800	289	9.24	112	5.38
Colombia	Puya	MAG 355*	NRC	9.4	-75.7	27	297	9.22	119	5.36
Colombia	Puya Grande	SAN 347*	NCGRP	8.3	-73.3	1200	307	9.22	122	5.36
Colombia	Sabanero	ANT 423*	NCRPIS	7	-75.7	1480	297	9.22	125	5.36
Colombia	Sabanero	CUN 342*	NCRPIS	8.5	-75.5	250	311	9.23	130	5.37
Colombia	Sabanero	CUN 367	NCRPIS	4.3	-74	2110	311	9.22	136	5.36
Colombia	Sabanero	SAN 329	NRC	7.3	-72.5	2626	301	9.22	124	5.36

Appendix Table 6 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	PH	PH SE	EH	EH SE
Colombia	Yucatan	TOL 389*	ICA	5	-74.9	450	299	9.22	121	5.36
Colombia	Yucatan	TOL 399*	NCRGP	4.6	-74.9	500	303	9.22	123	5.36
Costa Rica	Huesillo	CRI 370*	NCRPIS	9.9	-83.9	1500	296	9.59	125	5.76
Cuba	Argentino	CUB 113*	NCRPIS	20.3	-76.9	25	298	9.22	120	5.36
Cuba	Chandelle	CUB 54*	CIMMYT	20.9	-76.7	305	298	9.22	122	5.36
Cuba	Chandelle	CUB 68	NCRPIS	20.7	-76.1	369	298	9.22	117	5.36
Cuba	Cuban Flint	CUB 63*	CIMMYT	20.7	-75.7	15	299	9.72	120	5.90
Cuba	Maiz Criollo	CUB 136*	NCRPIS	22.9	-82.3	84	301	9.22	123	5.36
Cuba	Tuson	CUB 67*	CIMMYT	20.9	-76.5	305	304	9.22	125	5.36
Ecuador	Blanco Blandito	ECU 523	NRC	0.4	-78.4	2122	310	9.22	130	5.36
Ecuador	Blanco Harinoso Dentado	ECU 640	ICA	-4	-79.2	1921	308	9.22	126	5.36
Ecuador	Candela	ECU 344*	ICA	-0.7	-80.1	55	305	9.22	125	5.36
Ecuador	Candela	ECU 531	ICA	-1.1	-80.5	27	292	9.22	122	5.36
Ecuador	Candela	ECU 699	NCRPIS	-1.1	-80.5	50	285	9.22	120	5.37
Ecuador	Canguil	ECU 500	NRC	0.2	-78.4	2213	288	9.23	113	5.37
Ecuador	Canguil Grueso	ECU 443	NCRPIS	0	-78.5	2838	291	9.23	109	5.37
Ecuador	Canguil Grueso	ECU 447	ICA	0.1	-78.2	2579	290	9.23	111	5.37
Ecuador	Chillo	ECU 411	ICA	-0.3	-78.4	2510	306	9.22	129	5.36
Ecuador	Chillo	ECU 458	NRC	-2.9	-78.7	2195	310	9.24	124	5.38
Ecuador	Chillo	ECU 480B	NCRPIS	0	-78	2241	316	9.22	129	5.36
Ecuador	Cholito	ECU 718	ICA	-4.1	-79	1296	313	9.22	130	5.36
Ecuador	Chulpi Chico	ECU 424	NRC	0.1	-78.2	2600	299	9.22	117	5.36
Ecuador	Clavito	ECU 884	ICA	-1.3	-78.5	1646	301	9.22	123	5.36
Ecuador	Conico Dentado	ECU 427	ICA	0.1	-78.4	2058	312	9.22	132	5.37
Ecuador	Cubano Amarillo Duro	ECU 326	ICA	-1.1	-80.5	41	301	9.22	120	5.36
Ecuador	Cubano Amarillo Duro	ECU 327	NCRPIS	-2.2	-80.1	46	321	9.22	135	5.36
Ecuador	Cubano Amarillo Duro	ECU 698	ICA	-1.1	-80.5	50	296	9.22	120	5.36
Ecuador	Cubano Amarillo Duro	ECU 957	ICA	-1	-79.4	183	299	9.22	121	5.36
Ecuador	Cubano Cateto	ECU 877	ICA	-0.2	-79.3	229	309	9.22	128	5.37
Ecuador	Cubano Tuson	ECU 542	ICA	-1.1	-80.5	30	307	9.22	127	5.36
Ecuador	Cubano Tuson	ECU 660	ICA	-1.1	-80.5	30	299	9.22	119	5.36
Ecuador	Cubano Tuson	ECU 764	ICA	-1.1	-80.5	18	299	9.22	120	5.36
Ecuador	Enano Gigante	ECU Comp.	NCRPIS	-1.1	-78	916	311	9.22	129	5.36
Ecuador	Gallina	ECU 329	ICA	-1.9	-80	5	313	9.22	131	5.36
Ecuador	Huandango	ECU 735	NRC	0.8	-78	2287	300	9.23	122	5.37
Ecuador	Mischa	ECU 321	NRC	-1.7	-78.7	2241	299	9.22	119	5.37
Ecuador	Morochon	ECU 454B	NCRPIS	0	-78	2195	309	9.23	123	5.37

Appendix Table 6 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	PH	PH SE	EH	EH SE
Ecuador	Patillo	ECU 417	ICA	-0.3	-78.6	2287	296	9.22	118	5.37
Ecuador	Pojoso Chico Ecuatorian	ECU 522	NCRPIS	-1	-77.8	530	282	9.23	111	5.37
Ecuador	Racimo de Uva	ECU 517	NRC	-1.7	-78.7	2287	305	9.23	117	5.37
Ecuador	Tusilla	ECU 569	ICA	-4.1	-79	274	308	9.22	126	5.37
Ecuador	Tuxpeno	ECU 942	ICA	-1	-79.4	184	308	9.22	126	5.36
Ecuador	Uchima	ECU 681	ICA	-4	-79.2	2152	308	9.22	127	5.36
Ecuador	Yungueno	ECU 572	ICA	-4.1	-79	1296	306	9.22	129	5.36
Ecuador	Yunquillano forma Andaqui	ECU 710	NCRPIS	-4.1	-79	1296	304	9.22	126	5.36
Ecuador	Yunquillano forma Andaqui	ECU 853	ICA	-3.5	-78.6	732	306	9.22	124	5.36
Ecuador	Yunquillano forma Andaqui	ECU 855	ICA	-3.5	-78.6	1098	305	9.22	123	5.36
El Salvad	Amarillo Salvadoreno	Comp.	NCRPIS	13.8	-89.3	721	304	9.23	123	5.37
Guatemala	Comiteco	GUA 418	INIFAP	15.4	-91.7	1768	310	9.22	124	5.36
Guatemala	Comiteco	GUA 515	NCRPIS	15.7	-91.6	1751	326	9.22	137	5.37
Guatemala	Comiteco	GUA 546	NCRPIS	15.7	-91.6	1751	315	9.22	133	5.37
Guatemala	Dzit Bacal	GUA 131	CIMMYT	14.3	-89.7	737	307	9.22	125	5.37
Guatemala	Imbricado	GUA 493	INIFAP	14.8	-91.6	2317	304	9.22	126	5.36
Guatemala	Imbricado	GUA 922	INIFAP	15.6	-91.5	2256	304	9.22	121	5.36
Guatemala	N de Chimaltenango	GUA 369	INIFAP	14.6	-90.9	2073	316	9.22	130	5.37
Guatemala	N de Chimaltenango	GUA 590	INIFAP	14.7	-90.9	2165	310	9.22	130	5.36
Guatemala	N de T Caliente	GUA 159	CIMMYT	14.6	-91.4	1067	293	9.22	119	5.36
Guatemala	N de T Fria	GUA 522	INIFAP	15.3	-91.5	1921	297	9.22	122	5.36
Guatemala	Nal Tel ATB	GUA 111	CIMMYT	14.6	-90.1	915	289	9.25	114	5.39
Guatemala	Nal Tel ATB	GUA 220	CIMMYT	14.6	-89.6	793	280	9.24	110	5.38
Guatemala	Nal Tel ATB	GUA 281	CIMMYT	14.3	-90.1	1113	286	9.22	112	5.36
Guatemala	Nal Tel BTA	GUA 20	INIFAP	14.6	-91.9	2439	310	9.60	130	5.77
Guatemala	Nal Tel BTB	GUA 145*	CIMMYT	15	-90.3	1006	288	9.24	110	5.39
Guatemala	Nal Tel BTB	GUA 280	CIMMYT	14.4	-89.9	1021	284	9.25	106	5.39
Guatemala	Nal Tel BTB	GUA 765*	CIMMYT	14.4	-89.9	1021	289	9.24	115	5.38
Guatemala	Oloton	GUA 383	NCRPIS	14.6	-90.6	1551	304	9.22	125	5.36
Guatemala	Quicheno Early	GUA 162	CIMMYT	15.1	-91.1	1860	305	9.22	124	5.36
Guatemala	Quicheno Late	GUA 863	INIFAP	15.4	-90.8	1829	318	9.22	130	5.36
Guatemala	Quicheno Late	GUA 877	NCRPIS	15.7	-91.5	2365	315	9.23	127	5.37
Guatemala	Salpor	GUA 476	INIFAP	14.9	-91.5	2317	309	9.23	127	5.37
Guatemala	Salpor Tardio	GUA 485	INIFAP	15	-91.8	2393	310	9.22	132	5.36
Guatemala	San Marceno	GUA 506	INIFAP	15.1	-91.7	2134	300	9.23	127	5.37
Guatemala	San Marceno	GUA 724	NCRPIS	14.7	-91	2304	312	9.23	131	5.37
Guatemala	Serrano	GUA 940	INIFAP	15	-91.8	3049	295	9.23	114	5.37

Appendix Table 6 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	PH	PH SE	EH	EH SE
Guatemala	Tepecintle	GUA 597	CIMMYT	14.6	-91.7	427	303	9.22	127	5.36
Guatemala	Tepecintle	GUA 65	CIMMYT	14.6	-90.8	152	309	9.22	126	5.36
Guatemala	Tepecintle	GUA 651	CIMMYT	14.5	-91.4	290	308	9.22	124	5.36
Guatemala	Tepecintle	GUA 79	CIMMYT	15.4	-89.7	122	302	9.22	126	5.36
Guatemala	Tuxpeno	GUA 456	CIMMYT	16.5	-90.2	183	309	9.22	131	5.37
Guyana	Cateto Nortista	GIN I	CIMMYT	6.8	-58.2	4	298	9.22	126	5.36
Haiti	Chandelle	HTI 14	INIFAP	19.5	-72	20	308	9.22	125	5.36
Haiti	Haitian Yellow	HTI 1	INIFAP	18.4	-74.3	580	302	9.22	120	5.36
Martinica	Early Carribean	Martinica 9	INIFAP	14.9	-61.1	90	281	9.22	111	5.36
Martinica	Unassigned	Martinica 12	NCRPIS	14.9	-61.1	90	292	9.22	115	5.36
Mexico	Apachito	CHH 138*	CIMMYT	29.7	-108.3	2210	283	9.26	110	5.41
Mexico	Apachito	CHH 166*	INIFAP	28	-107.6	2400	269	9.28	104	5.43
Mexico	Apachito	CHH 180*	INIFAP	27.8	-107.6	2180	267	9.28	101	5.43
Mexico	Apachito	CHH 207	CIMMYT	26.8	-107.3	2510	280	9.26	107	5.41
Mexico	Apachito	CHH 182	NCRPIS	27.8	-107.6	2368	298	9.26	112	5.41
Mexico	Arrocillo Amarillo	PUE 91	INIFAP	19.8	-97.6	2317	288	9.22	113	5.37
Mexico	Arrocillo Amarillo	VER 311*	INIFAP	19.8	-97.3	2220	300	9.22	125	5.36
Mexico	Azul	ACC 70-2	DHT	28.8	-107.7	1970	278	9.24	101	5.39
Mexico	Azul	CHH 158*	INIFAP	28.6	-107.5	2040	286	9.25	103	5.39
Mexico	Azul	CHH 220	INIFAP	28.7	-107.9	1900	278	9.24	107	5.39
Mexico	Azul	CHIH 218	NCRPIS	28.9	-107.8	1911	269	9.24	105	5.39
Mexico	Bofo	DGO 123	CIMMYT	25	-107	500	290	9.24	112	5.38
Mexico	Bofo	NAY 191*	CIMMYT	21.4	-104.1	1000	310	9.22	125	5.36
Mexico	Bofo	NAY 203	CIMMYT	21.1	-104.4	1850	314	9.22	129	5.36
Mexico	Bolita	OAX 44	INIFAP	17	-96.5	793	289	9.22	116	5.37
Mexico	Cacahuacintle	MEX 7	CIMMYT	19.3	-99.7	2652	280	9.23	106	5.37
Mexico	Cacahuacintle	PUE 552*	INIFAP	19	-97.4	2600	289	9.22	115	5.36
Mexico	Celaya	GTO 36*	INIFAP	20.2	-100.9	1799	297	9.22	123	5.36
Mexico	Celaya	GTO 69	INIFAP	20.5	-101	1812	307	9.22	118	5.36
Mexico	Celaya	GTO 88	INIFAP	20.2	-101	1768	299	9.22	122	5.36
Mexico	Chalqueno	HGO 7	NCRPIS	20.3	-98.9	2100	307	9.22	119	5.37
Mexico	Chapalote	SIN 2*	INIFAP	24.8	-107.4	61	291	9.23	114	5.37
Mexico	Chapalote	SIN 6	INIFAP	26.4	-108.6	115	287	9.23	112	5.38
Mexico	Chapalote	SIN 65	INIFAP	26	-107.4	750	292	9.23	111	5.37
Mexico	Conejo	GRO 129	INIFAP	17.7	-101.3	100	300	9.23	123	5.37
Mexico	Conejo	GRO 157	INIFAP	17.1	-100.5	30	298	9.23	122	5.37
Mexico	Conejo	GRO 17	INIFAP	17	-99.8	100	295	9.31	118	5.46

Appendix Table 6 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	PH	PH SE	EH	EH SE
Mexico	Conico	PUE 116	NCRPIS	19.9	-97.7	2243	294	9.23	118	5.37
Mexico	Conico	PUE 48	NCRPIS	18.9	-97.9	1720	293	9.23	115	5.37
Mexico	Conico Norteno	ZAC 12	INIFAP	21.4	-102.9	1951	294	9.23	117	5.37
Mexico	Conico Norteno	ZAC 161*	NCRPIS	22.4	-102.9	1937	284	9.23	116	5.38
Mexico	Coscomatepec	VER 110*	INIFAP	19.2	-97	1320	304	9.22	127	5.37
Mexico	Coscomatepec	VER 110B*	NCRPIS	19.2	-97	1320	310	9.59	126	5.76
Mexico	Cristalino de Chihuahua	CHH 128*	INIFAP	29.2	-108.1	2095	270	9.25	99	5.39
Mexico	Cristalino de Chihuahua	CHH 154*	INIFAP	29.4	-107.8	2140	277	9.25	100	5.39
Mexico	Cristalino de Chihuahua	CHH 254	INIFAP	28.5	-107.4	1900	282	9.23	107	5.37
Mexico	Dulce de Jalisco	JAL304	INIFAP	22.1	-103.3	1700	273	9.23	105	5.37
Mexico	Dulce de Jalisco	JAL78	INIFAP	21.2	-102.9	1880	278	9.22	102	5.36
Mexico	Dulcillo del Noroeste	SIN 34	INIFAP	25.1	-107.5	500	277	9.22	109	5.36
Mexico	Dulcillo del Noroeste	SIN 79	INIFAP	26.4	-108.6	180	287	9.23	117	5.37
Mexico	Dulcillo del Noroeste	SON 57*	CIMMYT	26.4	-108.6	180	294	9.23	118	5.38
Mexico	Dzit Bacal	VER 96	INIFAP	18.9	-96.9	700	302	9.22	121	5.36
Mexico	Elotero de Sinaloa	NAY 32*	INIFAP	22.4	-105.5	100	289	9.23	106	5.37
Mexico	Elotero de Sinaloa	NAY 46	INIFAP	22	-105.2	100	283	9.23	112	5.37
Mexico	Elotero de Sinaloa	SIN 17	INIFAP	23.5	-106.3	200	294	9.23	113	5.37
Mexico	Elotes Occidentales	DGO 236*	NCRPIS	24.5	-104.8	1969	289	9.24	106	5.38
Mexico	Elotes Occidentales	GTO 191*	INIFAP	21.1	-101.7	1885	295	9.22	109	5.37
Mexico	Elotes Occidentales	NAY 29	INIFAP	22.4	-105.5	46	295	9.23	115	5.37
Mexico	Elotes Occidentales	NAY 38	INIFAP	21.9	-105.3	46	295	9.22	113	5.37
Mexico	Elotes Occidentales	ZAC 210*	INIFAP	21.6	-103	1500	271	9.23	100	5.38
Mexico	Gordo	CHH 131*	CIMMYT	29.2	-108.1	2095	287	9.25	109	5.39
Mexico	Gordo	CHH 160*	CIMMYT	28.6	-107.5	2040	288	9.24	107	5.38
Mexico	Gordo	CHH 214*	CIMMYT	28.6	-107.5	2040	289	9.25	110	5.39
Mexico	Gordo	CHH 256*	CIMMYT	28.5	-107.4	1900	280	9.24	105	5.39
Mexico	Harinoso de Ocho	NAY 24	INIFAP	22	-105.3	46	281	9.24	104	5.39
Mexico	Jala	JAL44*	CIMMYT	20	-104.3	1300	291	9.22	112	5.36
Mexico	Jala	NAY 130	INIFAP	21.1	-104.4	1095	310	9.22	129	5.37
Mexico	Mixteco	OAX 569	INIFAP	17.4	-97.4	2500	302	9.22	120	5.36
Mexico	Motozinteco	CHS 650	INIFAP	15.4	-92.3	1270	298	9.22	121	5.36
Mexico	Motozinteco	CHS 650B	NCRPIS	15.4	-92.3	1270	301	9.60	125	5.77
Mexico	Mushito	MIC 371	INIFAP	19.5	-101.6	2100	292	9.22	121	5.36
Mexico	Mushito	MIC 317*	NCRPIS	19.3	-101.5	2253	302	9.22	125	5.36
Mexico	Nal-Tel	CAM 48	INIFAP	19.8	-90.1	50	285	9.22	117	5.36
Mexico	Negrilo	OAX 26*	INIFAP	17.2	-96.8	1640	276	9.24	108	5.38

Appendix Table 6 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	PH	PH SE	EH	EH SE
Mexico	Olotillo	CHS 53	CIMMYT	16.8	-93.2	579	326	9.23	137	5.37
Mexico	Olotillo	CHS 81	INIFAP	16.6	-92.7	686	313	9.22	123	5.36
Mexico	Oloton	CHS 684	INIFAP	16.8	-92.5	2100	302	9.22	126	5.36
Mexico	Onaveno	SON 114	INIFAP	29	-109.4	410	288	9.24	111	5.38
Mexico	Onaveno	SON 24*	NCRPIS	30.8	-110.8	867	287	9.22	106	5.37
Mexico	Palomero de Jalisco	JAL154*	INIFAP	20	-103.7	2520	279	9.24	110	5.39
Mexico	Palomero Tipo Chihuahua	CHH 148*	INIFAP	29.4	-107.8	2140	280	9.24	101	5.38
Mexico	Palomero Tipo Chihuahua	CHH 201*	INIFAP	26.8	-107.1	2130	279	9.26	108	5.40
Mexico	Palomero Toluqueno	VER 35*	NCRPIS	19.6	-97.3	2391	290	9.24	116	5.38
Mexico	Pepitilla	GRO 3*	INIFAP	18.4	-99.5	747	308	9.23	124	5.37
Mexico	Raton	CHH 191*	NCRPIS	28.8	-106.4	1885	282	9.23	112	5.37
Mexico	Raton	NLE 9*	INIFAP	25.6	-99.3	250	276	9.24	106	5.39
Mexico	Raton	TAM 25*	INIFAP	24.6	-99.6	290	288	9.22	118	5.37
Mexico	Reventador	NAY 15*	INIFAP	22.3	-105.4	46	290	9.23	110	5.37
Mexico	Reventador	NAY 39	INIFAP	21.9	-105.3	46	295	9.22	113	5.36
Mexico	Serrano de Jalisco	JAL133*	INIFAP	20	-103.8	2060	292	9.22	114	5.37
Mexico	Serrano de Jalisco	JAL146	INIFAP	20	-103.7	2520	279	9.25	105	5.40
Mexico	Serrano Mixe	OAX 565	INIFAP	17.1	-96	2350	306	9.23	124	5.37
Mexico	Tablilla de Ocho	JAL301	CIMMYT	22.1	-103.2	1700	289	9.22	112	5.36
Mexico	Tablilla de Ocho	NAY 185	CIMMYT	21.7	-104.1	1100	303	9.22	121	5.37
Mexico	Tablilla de Ocho	ZAC 187	NCRPIS	22.3	-103.6	2170	290	9.23	110	5.37
Mexico	Tabloncillo	JAL102	INIFAP	19.5	-103.3	1280	286	9.22	112	5.36
Mexico	Tabloncillo	JAL103*	NCRPIS	19	-103	1290	306	9.22	120	5.36
Mexico	Tabloncillo	JAL103B*	NCRPIS	19	-103	1290	291	9.59	108	5.76
Mexico	Tabloncillo Perla	NAY 12	INIFAP	22	-105.2	46	299	9.24	113	5.38
Mexico	Tabloncillo Perla	NAY 16	CIMMYT	22.1	-105.3	46	290	9.23	111	5.37
Mexico	Tehua	CHS 159	CIMMYT	16.5	-92.5	747	316	9.23	130	5.38
Mexico	Tehua	CHS 29	CIMMYT	15.8	-92.7	1000	315	9.24	132	5.38
Mexico	Tepecintle	CHS 76	INIFAP	16.5	-92.8	579	292	9.29	117	5.37
Mexico	Tuxpeno	VER 143*	NCRPIS	19.3	-96.5	141	306	9.22	125	5.36
Mexico	Tuxpeno Norteno	CHH 121	INIFAP	30.9	-108.2	1470	294	9.23	114	5.37
Mexico	Tuxpeno Norteno	CHH 287*	NCRPIS	30.4	-107.9	1456	288	9.31	113	5.46
Mexico	Tuxpeno Norteno	TAM 3*	INIFAP	23.3	-99	300	289	9.23	117	5.37
Mexico	Vandeno	GRO 96	NCRPIS	17.5	-101.3	61	307	9.22	128	5.36
Mexico	Zamorano Amarillo	GTO 1	INIFAP	21.1	-101.7	1870	287	9.23	111	5.37
Mexico	Zamorano Amarillo	MIC 66*	INIFAP	20.1	-102	1645	296	9.23	112	5.37
Mexico	Zapalote Chico	CHS 662	INIFAP	16.2	-94	100	279	9.26	106	5.41

Appendix Table 6 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	PH	PH SE	EH	EH SE
Mexico	Zapalote Chico	OAX 48	CIMMYT	16.4	-94.2	50	273	9.26	101	5.41
Mexico	Zapalote Chico	OAX 50	CIMMYT	16.6	-94.6	107	283	9.24	111	5.38
Mexico	Zapalote Chico	OAX 70	CIMMYT	16.3	-95.2	46	288	9.25	107	5.39
Mexico	Zapalote Grande	CHS 104	INIFAP	15.3	-92.7	107	300	9.22	123	5.36
Mexico	Zapalote Grande	CHS 224	INIFAP	15.3	-92.7	91	294	9.22	116	5.36
Mexico	Zapalote Grande	CHS 236	INIFAP	16.7	-93.8	120	282	9.24	109	5.38
Mexico	Zapalote Grande	CHS 521	INIFAP	16.7	-93.7	730	282	9.22	116	5.37
Paraguay	Avati Moroti Guapi	PAG 139 (USDA)	NCRPIS	-25.5	-56.4	369	298	9.22	116	5.36
Paraguay	Avati Moroti Ti	PAG124 (USDA)	NCRPIS	-26.7	-57.2	276	302	9.22	124	5.36
Paraguay	Cateto Sabugo Grosso	PAG 422 (USDA)	NCRPIS	-26	-56.5	95	296	9.22	120	5.36
Paraguay	Moroti Guapi	PAG VI-A	NCRPIS	-26.1	-56.93	400	292	9.22	121	5.36
Paraguay	Semi Dente Paulista	PAG I*	CIMMYT	-26	-56	270	305	9.22	125	5.36
Peru	Alazan	LBQ 18	PCIM	-6.7	-79.8	50	309	9.22	128	5.36
Peru	Alazan	LIB 34	NCRPIS	-7.8	-79.3	80	304	9.22	125	5.36
Peru	Aleman	HCO 38*	NRC	-9.3	-76	700	299	9.22	119	5.36
Peru	Amarillo Huancabamba	PIU 17B	NCRPIS	-5	-79	2100	301	9.22	120	5.36
Peru	Amarillo Huancabamba	PIU 38B*	NCRPIS	-5.2	-79.5	2000	301	9.22	120	5.36
Peru	Ancashino	ANC 102*	NCRPIS	-9.1	-77.8	2600	292	9.22	118	5.36
Peru	Arequipeno	ARQ 1*	NCRPIS	-16.2	-71.3	2332	291	9.22	112	5.37
Peru	Arizona	LIB 16	NRC	-8.6	-78.8	100	293	9.22	114	5.36
Peru	Arizona	LIB 2*	NRC	-8.4	-78.8	80	303	9.22	122	5.36
Peru	Blanco Ayabaca	PIU 119	NCRPIS	-4.6	-79.7	2630	312	9.22	128	5.36
Peru	Chancayano Blanco	LIM 45*	PCIM	-11.1	-77.6	50	297	9.22	119	5.36
Peru	Chancayano Pintado	LIM 46*	NRC	-11.1	-77.6	50	298	9.22	116	5.36
Peru	Chaparreno	ARQ34*	PCIM	-17	-72	10	311	9.22	132	5.37
Peru	Chulpi	LIM 66*	NCRPIS	-11.4	-77.4	110	313	9.22	126	5.37
Peru	Chuncho	CUZ 112*	NCRPIS	-12.8	-72.7	1300	312	9.22	139	5.36
Peru	Colorado	LIB 8*	NCRPIS	-7.4	-79.5	51	300	9.59	125	5.76
Peru	Confite Morocho	AYA 20	PCIM	-12.9	-74.3	2500	278	9.24	103	5.39
Peru	Confite Puneno	APC 56	PCIM	-14.4	-72.9	3600	283	9.25	108	5.40
Peru	Confite Puntiajudo	CAJ 27	NRC	-7.6	-78	2500	287	9.23	113	5.38
Peru	Confite Puntiajudo	CUZ 13	NCRPIS	-15.5	-70.1	3832	270	9.23	104	5.38
Peru	Coruca	TAC 1*	PCIM	-18	-70.9	500	298	9.23	115	5.37
Peru	Cubano Amarillo	UCA 8*	NCRPIS	-5.2	-75.7	129	300	9.22	126	5.36
Peru	Cuzco Cristalino Amaril	CUZ 363	NCRPIS	-13.5	-72.1	3375	283	9.25	107	5.40
Peru	Cuzco Gigante	CAJ 17	PCIM	-7.2	-78.5	2800	295	9.23	119	5.37
Peru	Granada	ANC 57	PCIM	-9.3	-77.6	2600	296	9.23	118	5.37

Appendix Table 6 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	PH	PH SE	EH	EH SE
Peru	Huachano	LIM 43*	NRC	-11.1	-77.6	40	295	9.22	115	5.36
Peru	Huancavelicano	HVC 179*	NCRPIS	-13	-75.1	4562	290	9.22	106	5.36
Peru	Huanuco	HCO 128B*	NCRPIS	-9	-76	2700	309	9.23	124	5.37
Peru	Huarmaca	PIU 72*	PCIM	-5.6	-79.5	2300	304	9.22	122	5.36
Peru	Huayleno	ANC 180x181	NCRPIS	-9	-77	2600	292	9.22	115	5.36
Peru	Huayleno	ANC 291*	NCRPIS	-9.5	-77.5	3059	287	9.22	112	5.36
Peru	Jora	ANC 1*	PCIM	-10.1	-78.2	100	309	9.22	122	5.36
Peru	Kculli	HVC 137	PCIM	-12.6	-74.9	3100	296	9.60	116	5.77
Peru	Maranon	LIB 63B	NCRPIS	-8	-77	2800	314	9.23	126	5.37
Peru	Mochero	LBQ 5*	NRC	-6.7	-79.9	25	295	9.22	117	5.37
Peru	Morado Canteno	Lima 55*	NCRPIS	-12	-77	60	280	9.23	108	5.37
Peru	Morochillo	PIU 96*	PCIM	-4.7	-79.7	2000	302	9.22	124	5.36
Peru	Morocho	APC 67*	NCRPIS	-13.6	-72.6	2750	294	9.23	112	5.37
Peru	Morocho	APC 77*	NCRPIS	-13.7	-73.1	2977	302	9.23	115	5.37
Peru	Morocho Cajabambino	LIB 62*	PCIM	-8.4	-77.3	2800	307	9.22	126	5.36
Peru	Pagaladroga	PIU 2	PCIM	-5.1	-80.2	520	305	9.22	127	5.36
Peru	Pardo	LIM 19*	NRC	-11.1	-77.6	40	305	9.22	118	5.36
Peru	Paro	CUZ 76	PCIM	-13.6	-71.7	3300	309	9.22	124	5.36
Peru	Perla	ANC 23*	NCRPIS	-10.1	-78.2	100	304	9.22	121	5.36
Peru	Perla	ANC 24*	NRC	-10.1	-78.2	50	309	9.22	125	5.36
Peru	Perla	LIM 50*	NRC	-12.1	-77.1	50	317	9.22	130	5.37
Peru	Piricincó	SM 8*	NCRPIS	-6.2	-76.6	940	315	9.22	129	5.36
Peru	Pisccorunto	APC 13	PCIM	-13.7	-73.4	2900	293	9.39	104	5.55
Peru	Pisccorunto	APC 13B	NCRPIS	-13.7	-73.4	2900	291	9.59	118	5.76
Peru	Rabo de Zorro	ANC 325*	NCRPIS	-8.5	-78.1	2600	303	9.22	122	5.36
Peru	Rienda	CAJ 80	PCIM	-7.6	-78	2000	296	9.22	122	5.36
Peru	San Geronimo Huancaveli	JUN 164	NCRPIS	-12	-75.2	3333	292	9.24	109	5.38
Peru	Sarco	ANC 184	NRC	-9.4	-77.2	3150	306	9.22	126	5.36
Peru	Shajatu	ANC 117	PCIM	-8.5	-77.9	2580	313	9.22	121	5.36
Trinidad	Tuson	TRN 1	INIFAP	10.5	-61.1	125	301	9.22	127	5.36
Trinidad	Tuson	TRN 10	INIFAP	10.6	-61.1	20	317	9.22	136	5.36
U.S. Virgin Islands	St. Croix	IVC 2*	NRC	17.7	-64.7	150	294	9.22	125	5.36
Uruguay	Cateto Sulino	URG IV	CIMMYT	-31.7	-56	126	275	9.24	109	5.38
Uruguay	Cateto Sulino Escuro	URG V	CIMMYT	-31.7	-56	126	280	9.22	108	5.36
Uruguay	Cateto Sulino Grosso	URG III	CIMMYT	-31.7	-56	126	270	9.24	106	5.38
Uruguay	Dentado Branco	URZM 13010	NCRPIS	-34	-56	104	270	9.23	111	5.37
Uruguay	Semi-Dentado Rugoso	URZM 13052	NCRPIS	-30.8	-66.8	714	278	9.23	110	5.37

Appendix Table 6 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	PH	PH SE	EH	EH SE
USA	Apache	PI 213731	NCRPIS	33.4	-110.4	1067	263	9.23	93	5.37
USA	Argentine Pop	PI 217404*	NCRPIS	-32	-58	305	289	9.22	121	5.36
USA	Bear Isl. Chippewa	PI 213801*	NCRPIS	47	-92.2	457	254	9.46	85	5.62
USA	Cherokee	PI 213744*	NCRPIS	36.7	-96	229	295	9.23	114	5.37
USA	Cochiti Pueblo	PI 218151*	NCRPIS	35.6	-106.4	1616	287	9.25	103	5.40
USA	Domingo Pueblo	PI 218130*	NCRPIS	35.5	-106.4	1585	282	9.23	105	5.38
USA	Gaspe Flint	PI 401757*	NCRPIS	48.8	-64.3	173	233	9.34	71	5.50
USA	Gourd Seed	PI 217405*	NCRPIS	33	-97.1	229	292	9.22	115	5.36
USA	Gourd Seed	PI 414183*	NCRPIS	32	-99	300	286	9.22	110	5.36
USA	Havasupai	PI 317675*	NCRPIS	36.3	-112.7	1303	268	9.24	94	5.39
USA	Havasupai	PI 317679*	NCRPIS	36.3	-112.7	1303	272	9.23	100	5.37
USA	Hopi	PI 213733*	NCRPIS	35.9	-110.7	1941	254	9.24	90	5.38
USA	Hualapai	PI 213741*	NCRPIS	35.5	-113.4	1067	263	9.24	93	5.38
USA	Isleta-Tiwa	PI 218148*	NCRPIS	34.9	-106.7	1509	281	9.22	106	5.36
USA	Jemez Pueblo	PI 218173*	NCRPIS	35.6	-106.7	1829	285	9.22	111	5.37
USA	Laguna Pueblo	PI 218169*	NCRPIS	35.1	-107.4	1768	280	9.24	103	5.38
USA	Laguna Pueblo	PI 218170*	NCRPIS	35.1	-107.4	1768	281	9.23	106	5.37
USA	Longfellow	PI 214195*	NCRPIS	43.6	-80.2	488	278	9.28	93	5.43
USA	Longfellow Flint	PI 217408*	NCRPIS	42.3	-71.5	99	272	9.30	95	5.46
USA	Mexican June	PI 221889*	NCRPIS	37	-93.2	213	301	9.22	117	5.36
USA	Mexican June	PI 311243*	NCRPIS	37	-77	305	283	9.23	110	5.37
USA	Moencopi Pueblo	PI 218175*	NCRPIS	36.1	-111.2	1311	265	9.24	94	5.39
USA	Moencopi Pueblo	PI 218177*	NCRPIS	36.1	-111.2	1311	280	9.23	101	5.37
USA	Mohave	PI 218187*	NCRPIS	34.2	-114.3	91	259	9.26	95	5.41
USA	Mohawk Round Nose	PI 483087*	NCRPIS	45	-74.7	59	273	9.25	100	5.39
USA	N.W. Dent	PI 217480*	NCRPIS	38.3	-104.7	1444	268	9.25	90	5.40
USA	Navajo	PI 218163*	NCRPIS	36.6	-110.6	1616	256	9.25	89	5.39
USA	Northeast Flint	WLB	NCRPIS	41.7	-71.7	130	278	9.25	104	5.40
USA	Papago-Pimans	PI 217410*	NCRPIS	32.3	-112	1067	280	9.23	103	5.38
USA	Pueblo 12-Row Hopi Koko	PI 503564*	NCRPIS	35.9	-110.7	1908	265	9.24	95	5.39
USA	Quapaw Red	PI 213757*	NCRPIS	37	-94.8	229	277	9.24	109	5.38
USA	Sac And Fox	PI 217411*	NCRPIS	42	-92.6	229	255	9.24	98	5.39
USA	San Lorenzo Pueblo	PI 218135	NCRPIS	36.1	-106.3	2104	259	9.27	92	5.41
USA	Santo Domingo Pueblo	PI 218143*	NCRPIS	35.5	-106.4	1585	289	9.24	101	5.38
USA	Seneca Hominy Corn	PI 401754*	NCRPIS	42.1	-78.9	431	245	9.30	80	5.45
USA	Shoshone	PI 213769*	NCRPIS	43	-112.4	229	255	9.30	88	5.45
USA	Smut Nose	PI 222490*	NCRPIS	42.7	-84.5	213	267	9.25	96	5.39

Appendix Table 6 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	PH	PH SE	EH	EH SE
USA	Supergold Pop	PI 222648*	NCRPIS	38	-96	319	277	9.24	115	5.38
USA	Tennessee Red Cob	PI 311235*	NCRPIS	37.2	-80.4	305	284	9.23	108	5.37
USA	Tesuque Pueblo	PI 218137*	NCRPIS	35.8	-106	2073	275	9.24	96	5.38
USA	White Dent	PI 221885*	NCRPIS	39.1	-93.2	238	286	9.22	114	5.37
USA	White Dent	PI 311232*	NCRPIS	37	-77	305	287	9.24	113	5.38
USA	Winnebago	PI 213772*	NCRPIS	42.2	-96.5	229	271	9.25	101	5.40
USA	Winnebago	PI 213774*	NCRPIS	42.2	-96.5	229	256	9.25	85	5.40
USA	Zia Pueblo	PI 218139*	NCRPIS	35.5	-106.7	1829	291	9.22	105	5.37
Venezuela	Araguito	VEN 568	NRC	8.9	-64.2	183	276	9.24	109	5.38
Venezuela	Araguito	VEN 628	NRC	8.9	-64.2	183	274	9.26	104	5.41
Venezuela	Araguito	VEN 678	NCRPIS	8.9	-64.2	73	275	9.24	129	5.39
Venezuela	Araguito	VEN 760	NRC	9.6	-63.1	123	294	9.22	118	5.36
Venezuela	Cacao	VEN 630	NCRPIS	8.6	-71.2	201	314	9.23	131	5.37
Venezuela	Canilla	VEN 693	NRC	8.9	-64.2	91	300	9.22	125	5.36
Venezuela	Cariaco	VEN 408	ICA	10.4	-63.8	46	290	9.22	123	5.36
Venezuela	Cariaco	VEN 631	NRC	8.1	-63.6	366	288	9.23	122	5.37
Venezuela	Cariaco	VEN 639	NCRPIS	8.6	-70.2	194	298	9.22	127	5.36
Venezuela	Chandelle	VEN 409	ICA	10.1	-68.4	137	281	9.22	121	5.36
Venezuela	Chandelle	VEN 460	ICA	8.1	-63.6	229	305	9.22	126	5.36
Venezuela	Chirimito	VEN 703*	ICA	8.1	-63.6	229	298	9.22	121	5.36
Venezuela	Comun	VEN 448	ICA	7.6	-72	457	302	9.23	123	5.37
Venezuela	Comun	VEN 881	ICA	10	-69.3	607	303	9.22	126	5.36
Venezuela	Costeno	VEN 775	NCRPIS	9.2	-68.3	184	298	9.22	118	5.36
Venezuela	Cuba Yellow Flint	VEN 331	ICA	10	-68	46	311	9.22	129	5.36
Venezuela	Cuba Yellow Flint	VEN 650	ICA	8.9	-64.2	128	279	9.22	121	5.36
Venezuela	Guaribero	VEN 653	ICA	8.9	-64.2	73	285	9.22	116	5.37
Venezuela	Guaribero	VEN 733	ICA	8.9	-64.2	137	299	9.22	128	5.36
Venezuela	Huevito	VEN 396	ICA	8	-71.8	1052	316	9.23	134	5.37
Venezuela	Huevito	VEN 445	ICA	7.8	-72.3	823	298	9.22	125	5.36
Venezuela	Negrito	VEN 426	ICA	10.3	-67.5	384	303	9.22	129	5.36
Venezuela	Negrito	VEN 673	ICA	10.3	-67.5	384	309	9.23	128	5.37
Venezuela	Negrito	VEN 870	ICA	10.3	-67.5	384	307	9.23	131	5.37
Venezuela	Pira	VEN 457	ICA	8	-72	412	283	9.22	114	5.37
Venezuela	Pollo	VEN 310	NRC	8	-72	3088	294	9.23	115	5.37
Venezuela	Puya	VEN 946	ICA	9	-72	91	305	9.22	126	5.36
Venezuela	Puya Grande	VEN 345	ICA	10	-68	37	312	9.23	132	5.37
Venezuela	Puya Grande	VEN 651	NCRPIS	9.6	-63.1	203	314	9.23	134	5.37

Appendix Table 6 Continued

Country	Race	Accession [†]	Source [‡]	Latitude	Longitude	Altitude (m)	PH	PH SE	EH	EH SE
Venezuela	Tuson	VEN 405	ICA	7.5	-72	389	307	9.22	125	5.36
Venezuela	Tuxpeno	VEN 598	ICA	9.5	-69.3	96	303	9.22	126	5.36
Venezuela	Tuxpeno	VEN 692	ICA	9.5	-69.3	199	294	9.22	126	5.36
Venezuela	Tuxpeno	VEN 891	ICA	10	-69.3	471	311	9.22	126	5.36

Notes:

†Most accessions were collected during the 1940s and 1950s; additional Mexican accessions were collected during the 1960s and 1970s by E. Hernández X. and R. Ortega P. Data on Altitude, Latitude and Longitude were obtained from Vigouroux et al (2008), from the Original Strains of Corn Vol I and Vol II (NSF-NRC, 1954) and from the studies of the accessions published by the National Academy of Sciences and Harvard (Brieger et al, 1958; Brown., 1960; Grant et al, 1963; Grobman et al, 1961; Hatheway, 1957; Ramírez et al, 1960; Roberts et al, 1957; Timothy et al, 1961; Timothy et al, 1963; Wellhausen et al, 1952; Wellhausen et al, 1957). Vigouroux et al (2008) notes that most accessions were originally acquired from national germplasm banks or CIMMYT in the 1960s and 1970s, but those labeled NRC were acquired directly from the original collections, either from the collections of William L. Brown (Pioneer Hi-Bred, Johnston, IA) or original backup seeds once held in storage at Glenn Dale, MD, by the USDA-ARS. (All those labeled NRC were increased by MMG and are now deposited with the NCRPIS at Ames, Iowa). Most eastern South American (Brazil, Paraguay, Uruguay, Guianas, some Argentine and a few Bolivian accessions: all have collections with Roman numerals) were bulk samples of several accessions, and data shown are means of the accessions (Paterniani E and Goodman MM, 1977). Many accessions sourced from INIFAP are more recent Mexican collections (sometimes 1990s and later) made by J.J. Sánchez-Gonzalez, R. Ortega P., and collaborators, and generally have exact geographic coordinates (Sanchez G. JJ, 2000). Also occasionally seed from a given accession was sampled twice by the Goodman group at different times. These two samples were labeled sample A and B, these are not different accessions. Accessions labeled with (USDA) indicate accessions from Brazil which were once held in storage at Glenn Dale, MD, but not from the NRC. They were increased by MMG and are now deposited with the NCRPIS at Ames, Iowa. Accessions noted with an asterisk (*) are those currently available from NCRPIS, unfortunately these number only 170 of the 483 accessions used in this study.

‡Source abbreviations are as follows: Intentional Maize and Wheat Improvement Center (CIMMYT), North Central Regional Plant Introduction Station (NCRPIS), National Research Council (NRC), Columbian Agriculture Institute (ICA), National Research Institute for Forestry, Agriculture, and Livestock (INIFAP), National Center for Genetic Resources Preservation (NCGRP), Cooperative Program for Maize Investigations (PCIM), David Timothy personal collection (DHT), and William L. Brown personal collection (WLB).

Appendix Table 7 Checks used in experiments, their pedigrees, year of release, and least square mean estimate of PH and EH and their standard errors

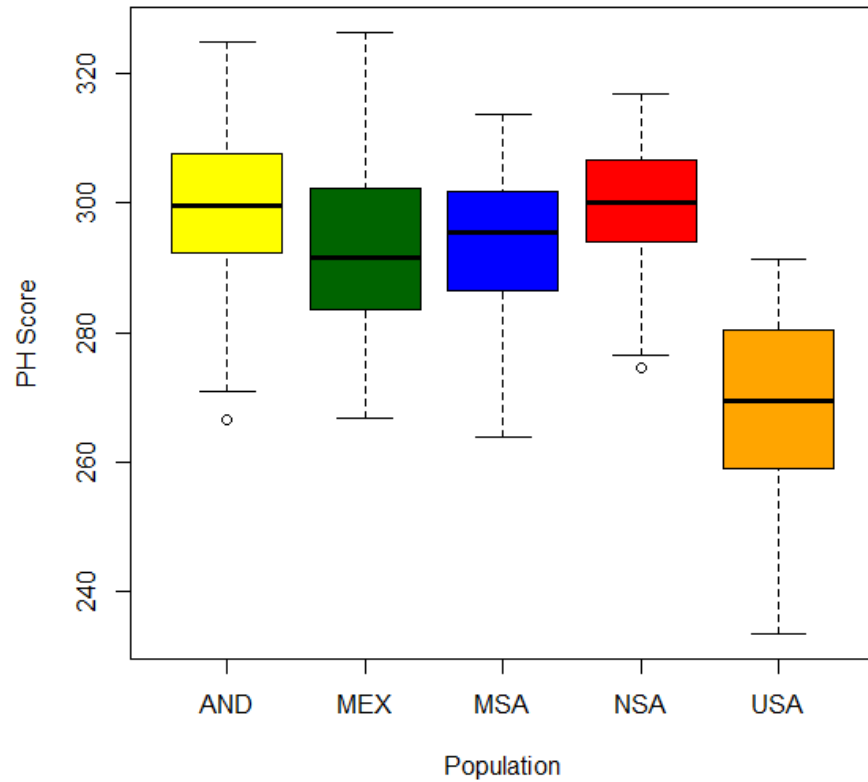
Line	Pedigree	Year Released	PH	PH SE	EH	EH SE
PH B47	((B37*3) xSD105)	1984	237.47	8.61	88.61	4.61
PH B47xDJ7	(B73 x BS16 Synthetic) = DJ 7	1985	285.95	8.63	112.39	4.63
DK HBA1xPH B47	(Pioneer 3195 x Pioneer 3199) =DKHBA1	1985	294.76	8.63	111.12	4.62
NC296xPH B47	(Pioneer X105A x H5) = NC 296	1990	305.54	8.62	124.56	4.61
Pioneer 3394	unavailable	1991	293.03	8.62	120.67	4.62
Pioneer 33M54	GE535764 xGE587284	2003	299.75	8.62	107.41	4.62

Appendix Table 8 Results from Tukey test for PH (cm) in maize populations

Population	Mean	SE	Set[†]
NSA	299.1	1.41	a
AND	298.7	1.19	a
MSA	294	1.63	ab
MEX	292.9	1.19	b
USA	269.4	2.11	c

HSD= 3.88

[†]Groupings are based on Tukey HSD, and show which populations are significantly different from one another at $\alpha=0.05$.



Appendix Figure 2 Boxplot of PH (cm) by maize population[†]

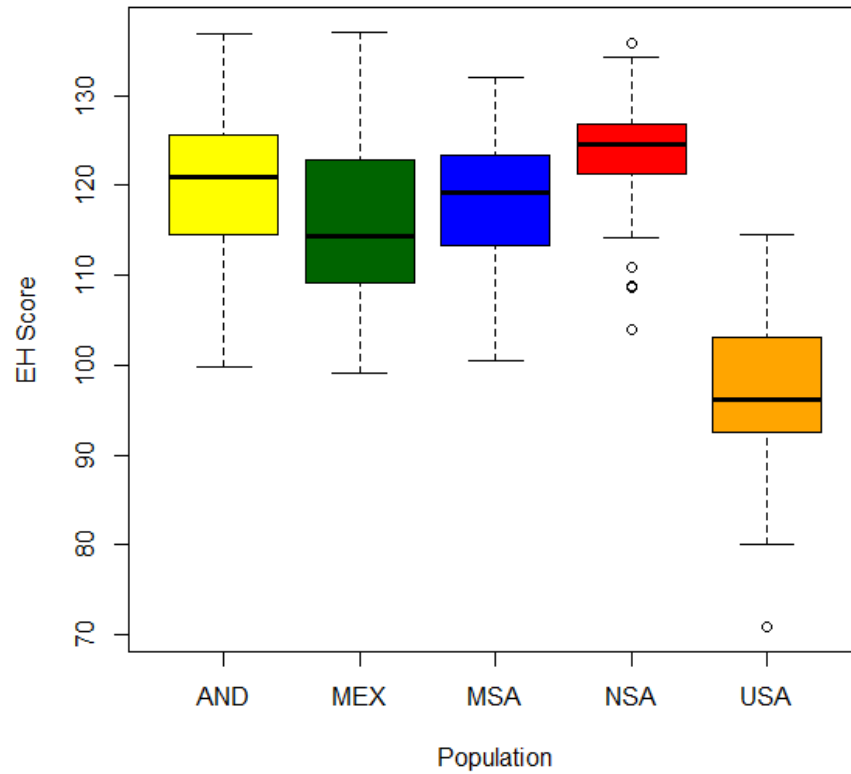
[†]Andean (AND), Mexican (MEX), Middle South America (MSA), Northern South America (NSA), and United States of America (USA). Bold line inside box represents the median, the bottom and top of the box are the first and third quartiles. Whiskers represent 1.5 times the first and third interquartile range. Circles represent scores outside this 1.5 inter quartile range.

Appendix Table 9 Results from Tukey test for EH (cm) in maize populations

Population	Mean	SE	Set[†]
NSA	123.2	0.87	a
AND	119.7	0.84	ab
MSA	118.2	1.022	bc
MEX	115.7	0.82	c
USA	96.67	1.40	d

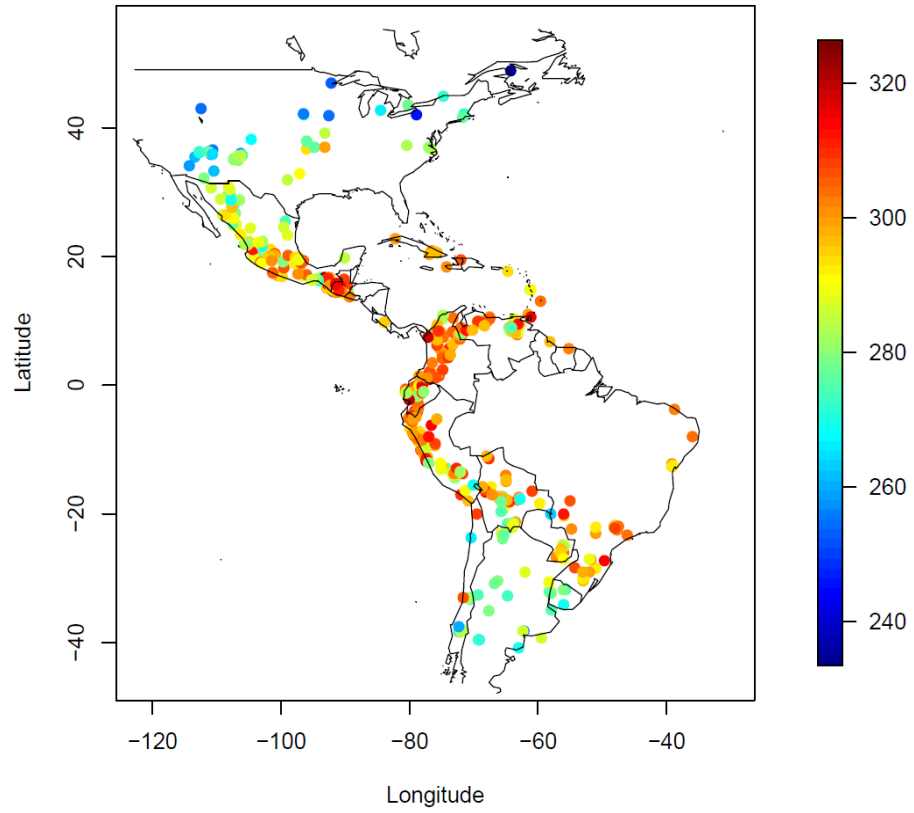
HSD=4.07

[†]Groupings are based on Tukey HSD, and show which populations are similar or different from one another at $\alpha=0.05$.

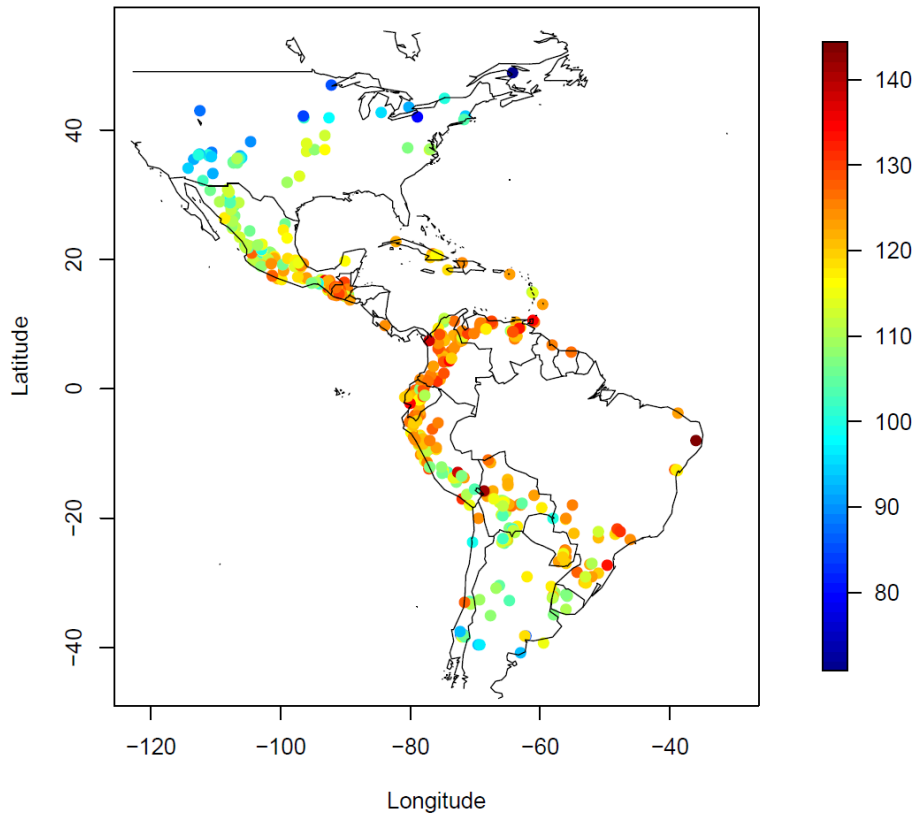


Appendix Figure 3 Boxplot of EH (cm) by maize population[†]

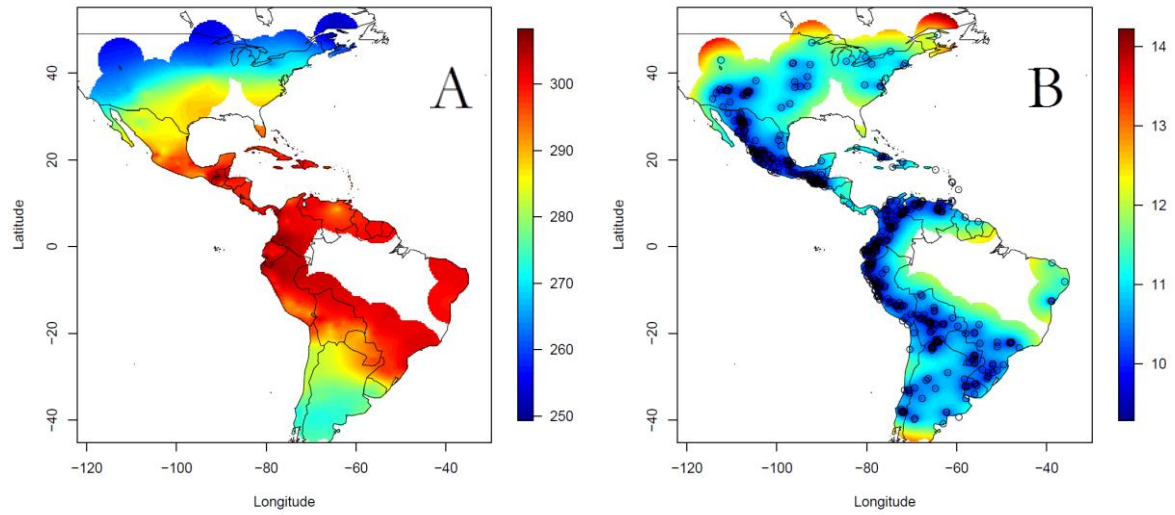
[†]Andean (AND), Mexican (MEX), Middle South America (MSA), Northern South America (NSA), and United States of America (USA). Bold line inside box represents the median, the bottom and top of the box are the first and third quartiles. Whiskers represent 1.5 times the first and third interquartile range. Circles represent scores outside this 1.5 inter quartile range.



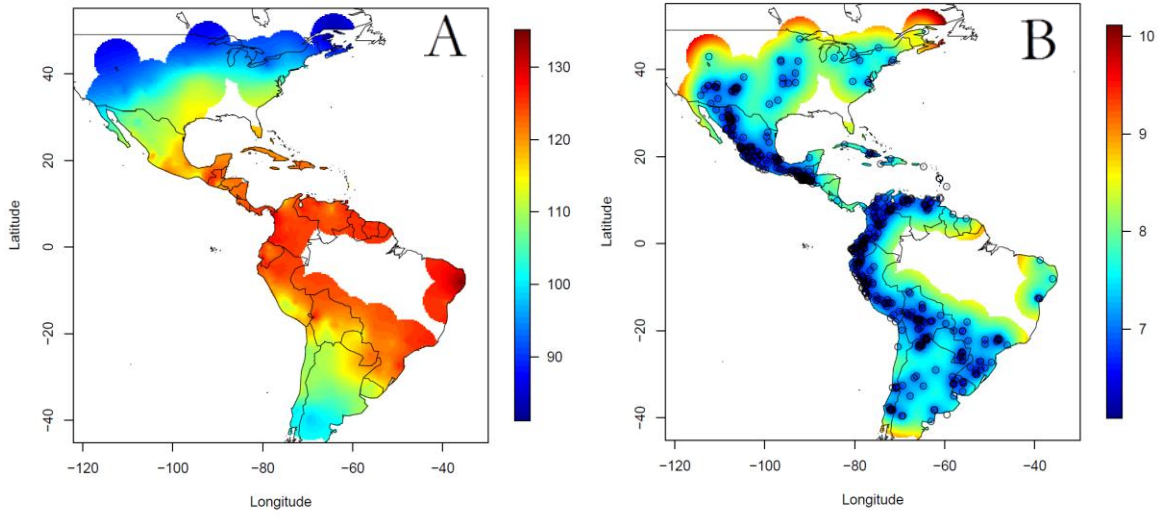
Appendix Figure 4 Raw point pattern data of PH measurements (cm) of BC₁ F₁S at point of collection of donor landraces



Appendix Figure 5 Raw point pattern data of EH measurements (cm) of BC₁ F₁s at point of collection of donor landraces



Appendix Figure 6A-B 6A shows predicted PH of $BC_1 F_1$ s with donor parents collected at unsampled locations across the Americas; 6B shows the standard errors of the PH estimates



Appendix Figure 7A-B 7A shows predicted EH of $BC_1 F_1$ s with donor parents collected at un-sampled locations across the Americas; 7B shows the standard errors of the EH estimates

Appendix Table 10 Parameter estimates for the Matérn Spatial model developed for PH and EH

Model Parameters	PH	EH
Intercept	284.03	114.66
Latitude [†]	0.107	0.17
Longitude	-0.29	-0.21
Altitude	-0.001	-0.0008
Eigenvector 1 [‡]	25.31	30.17
Eigenvector 2	22.76	20.40
Eigenvector 3	NA	14.19
Eigenvector 4	NA	15.10
Sigma_{sq} (partial sill) [§]	1050	750
Phi (range) [¶]	801.6	484.3
Kappa [#]	0.27	0.38
Anisotropy angle ^{††}	4.66	6.28
Anisotropy ratio	1.28	1
Tau sq (nugget) ^{**}	72.52	35.58

Note: [†]When examining the global disease distributions Latitude, Longitude, and Altitude are all important covariates in explaining the distribution of disease scores. Kriging defines and models the disease scores at a local neighborhood, thus Latitude, Longitude, and Altitude are not significant in the spatial analysis.

[‡]For each trait a different set of genetic covariates were used in the spatial model. For PH the 3rd, 10th eigenvectors were used, for EH the 3rd, 10th, 38th, and 55th.

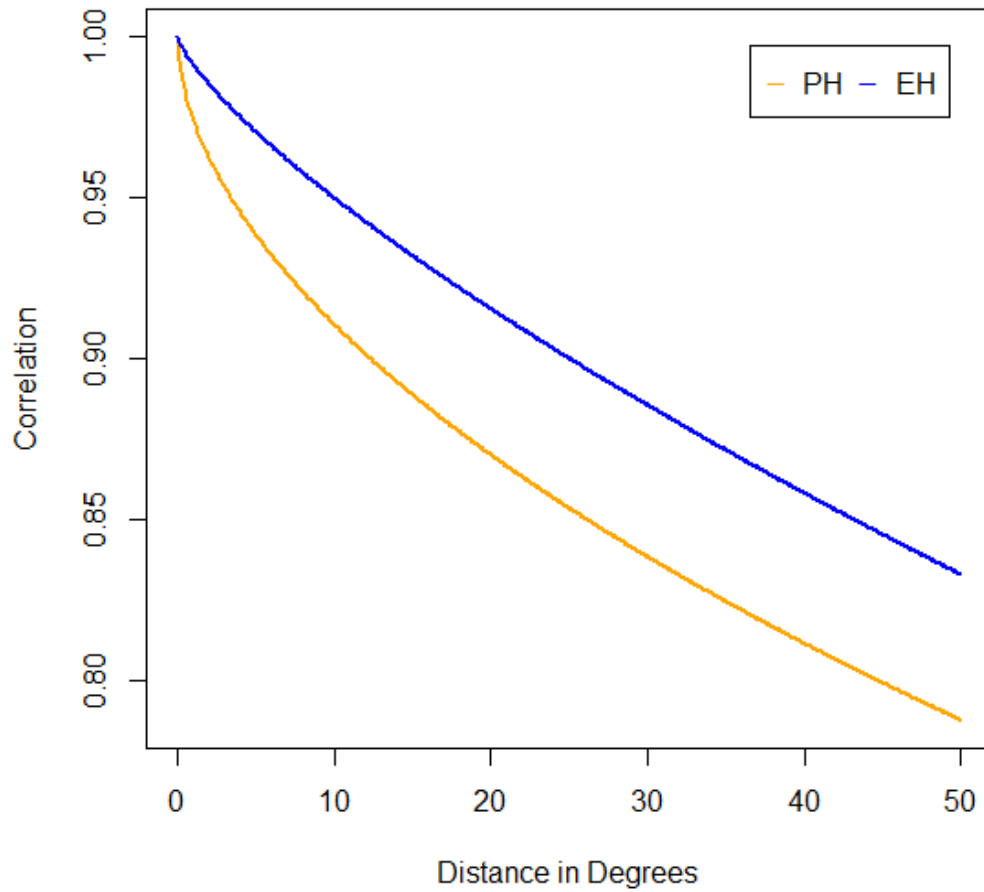
[§]Sigma_{sq} or the partial sill is a parameter of the semivariogram model that represents the variance of the height scores in the spatially autocorrelated process without any nugget effect. In the semivariogram model, the partial sill is the difference between the nugget and the sill.

[¶]Phi (range) is a distance measure in degrees that represents a distance beyond which there is little or no autocorrelation among variables.

[#]Kappa is a smoothness parameter, explains how much the variances fluctuates over distance. Using a Matern model is more flexible than an exponential model, and less computationally intense than a Gaussian model.

^{††}Anisotropy angle is the direction in which the data is varying. Anisotropy ratio regulates the dependency on anisotropy angle.

^{**}Tau sq (nugget) is measurement error of sampling BC₁F₁s for agronomics at small distances.



Appendix Figure 8 Covariance functions for the Matérn models for Plant Height and Ear Height[†]

[†]This gives us an indication of the spatial trends in these traits. The correlation between points decays moderately over distance for both PH and EH. PH and EH are connected with environmental adaptation, and thus may have been selected for differently across environments.

Appendix Table 11 Comparison of percent of variation accounted for by four different types of models

Trait	OLS	OLS with genetic covariates	Spatial	Spatial with genetic covariates
PH	3.8	24.3	13.9	25.6
EH	9.2	37.0	12.1	36.9

Note: Ordinary Least Squares (OLS), and Spatial methods, using latitude, longitude, and altitude, with and without genetic data used as covariates.

Values calculated using the R^2 in the OLS models, and from the five-fold cross validation for the spatial methods

Appendix Table 12 Summary of number of accessions used from each country and the number of which are currently available from NCRPIS

Country	No. of Accessions Used	No. of Accessions Available
Argentina	26	2
Bolivia	38	0
Brazil	33	1
Chile	12	8
Colombia	38	30
Costa Rica	1	1
Cuba	6	5
Ecuador	38	1
El Salvador	1	0
Guatemala	31	2
Guyana	1	0
Haiti	2	0
Martinica	2	0
Mexico	108	43
Paraguay	5	1
Peru	54	31
Uruguay	5	0
USA	45	42
Venezuela	33	1
West Indies	4	2
Total	483	170

Appendix References

- Brieger FG, Gurgel JTA, Paterniani E, Blumenschein A, Alleoni MR, 1958. Races of maize in Brazil and other eastern South American countries. National Academy of Science-National Research Council Washington, DC, USA
- Brown WL, 1960. Races of maize in the West Indies National Academy of Sciences. National Research Council, Washington, DC, USA
- Committee on Preservation of Indigenous Strains of Maize, 1954. Original Stains of Corn, I. National Academy of Sciences, National Research Council, Washington, D.C.
- Committee on Preservation of Indigenous Strains of Maize, 1955. Original strains of corn, II. National Academy of Sciences, National Research Council, Washington, D.C.
- Sanchez G. JJ, Goodman MM, Stuber C. 2000. Isozymatic and morphological diversity in the races of maize of Mexico. *Econ Bot* 54:43-59
- Graham RL, Nelson R, Sheehan J, Perlack R, Wright LL, 2007. Current and potential US corn stover supplies. *Agron J* 99:1-11
- Grant UJ, Hatheway WH, Timothy DH, Cassalet DC, Roberts LM, 1963. Races of maize in Venezuela National Academy of Sciences. National Research Council, Washington, DC, USA
- Grobman A, Salhuana W, Sevilla R, with Mangelsdorf PC, 1961. Races of maize in Peru. National Academy of Sciences. National Research Council, Washington, DC, USA
- McMullen MD, Kresovich S, Villeda HS, Bradbury P, Li H, Sun Q, Flint-Garcia S, Thornsberry J, Acharya C, Bottoms C, Brown P, Browne C, Eller M, Guill K, Harjes C, Kroon D, Lepak N, Mitchell SE, Peterson B, Pressoir G, Romero S, Oropeza M Rosas, Salvo S, Yates H, Hanson M, Jones E, Smith S, Glaubitz JC, Goodman MM, Ware D, Holland JB, Buckler ES, 2009. Genetic properties of the maize nested association mapping population. *Science* 325:737-740
- Paterniani E, Goodman MM, 1977. Races of maize in Brazil and adjacent areas. CIMMYT, Mexico City, Mexico.
- Peiffer JA, Romay MC, Gore MA, Flint-Garcia SA, Zhang Z, Millard MJ, Gardner CA, McMullen MD, Holland JB, Bradbury PJ, Buckler ES, 2014. The genetic architecture of maize height. *Genetics* 196:1337-1356

Ramírez ER, Timothy DH, Díaz BE, Grant UJ, with GE Nickerson C, Anderson E, Brown W, 1960. Races of maize in Bolivia. National Academy of Sciences, National Research Council, Washington, DC, USA

Roberts LM, Grant UJ, R. Ramírez E, Hatheway WH, Smith DL, with Mangelsdorf PC, 1957. Races of maize in Colombia. National Academy of Sciences, National Research Council, Washington, DC, USA

Salas Fernandez MG, Becraft PW, Yin Y, Lübberstedt T, 2009. From dwarves to giants? Plant height manipulation for biomass yield. *Trends Plant Sci* 14:454-461

Timothy DH, Hatheway WH, Grant UJ, Torregroza CM, Sarria VD, Varela AD, 1963. Races of maize in Ecuador. National Academy of Sciences, National Research Council, Washington, DC, USA

Timothy DH, Peña VB, R. Ramírez E, with Brown WL, Anderson E, 1961. Races of maize in Chile. National Academy of Sciences, National Research Council, Washington, DC, USA

Wellhausen EJ, Fuentes OA, Hernández-Corzo A, with Mangelsdorf PC, 1957. Races of maize in Central America. National Academy of Sciences, National Research Council, Washington, DC, USA

Wellhausen EJ, Roberts LM, E. Hernández X, with Mangelsdorf PC, 1952. Races of maize in Mexico: Their origin, characteristic and distribution. Bussey Institution of Harvard University, Cambridge, Massachusetts, USA