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Ponderosa pine at Square S Gulch: photo provided by Jim Michels, White River Field Office, BLM.

Genetic Assessment of Ponderosa Pine (*Pinus ponderosa*) at the Square S Gulch Site, Rio Blanco County, Colorado

Part of NFGEL Project #232

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Ponderosa pine samples from the Square S Gulch site in Rio Blanco County, northwestern Colorado, were collected as part of the Wyoming BLM/USFS NFGEL Project 232. This project is the first range wide genetic sampling and analysis of ponderosa pine using standardized field and laboratory protocols. This allows for the standardized analysis of all samples collected across agency and landscape boundaries. The findings below are preliminary and may change with further analysis. However, the levels of genetic diversity that define the uniqueness of this stand will remain the same and can be used for planning and management purposes. When the final report is issued, any changes in the Square S Gulch analysis will be addressed.

Preliminary results from a single microsatellite molecular DNA marker locus (*PtTX2146)* suggest that the Square S Gulch population of ponderosa pine (*Pinus ponderosa* Dougl. ex Laws.) exhibits relatively high genetic variation. Twelve separate alleles at this locus were amplified from the 31 trees sampled, compared to an average of 9.9 alleles for 63 ponderosa pine populations sampled across the distribution of the species in the United States. The allelic richness of the Square S Gulch population, calculated as the number of alleles standardized to the smallest sample using rarefaction (El Mousadik and Petit 1996), was within the highest quartile of populations for this measure of genetic variation (allelic richness of 8.32 compared to the mean of 6.72). The population additionally contained two rare alleles, one that was present in fewer than 5 percent of the ponderosa pine populations, and another present in fewer than 10 percent of the populations.

The Square S Gulch population also had observed heterozygosity in the highest quartile of ponderosa pine populations (0.903 compared to the mean of 0.769), and exhibited higher-than-average heterozygosity under Hardy-Weinberg expectations (0.816 compared to 0.78). Unlike several other populations in Colorado, Utah and Wyoming, the Square S Gulch population was not inbred at this microsatellite locus.

The high levels of genetic variation in the Square S Gulch population are somewhat unexpected, because small and isolated populations tend to be more prone to genetic drift and inbreeding which cause a decrease in diversity (Savolainen and Kuittinen 2000, Young and others 1996). At the same time, the unusual soil conditions (the trees only successfully reproduce on 13 mile Tongue of the Green River Formation) suggest that the trees at Square S Gulch may possess adaptive traits controlled by functional genes that are uncommon in other populations. Similarly, variation in the number of needles per fascicle on sampled trees indicates the potential for within-population variation in other morphological traits and genes.

Additionally, sequencing a fragment of haploid mitochondrial DNA from trees across the range of ponderosa pine has yielded preliminary results illuminating evolutionary relationships among populations. Specifically, the trees at the Square S Gulch population share a mitochondrial haplotype (a ‘genetic type’) with other ponderosa pine populations stretching from Arizona, southern Nevada and western New Mexico through western Colorado and eastern Utah into north-central Wyoming. The Square S Gulch population, therefore, appears more closely related to populations in these areas than elsewhere across the range of the species.

Additional analyses could further quantify ponderosa pine genetic variation at the Square S Gulch stand and could clarify its evolutionary relationship with other ponderosa pine populations throughout the range of the species. Conservation biology emphasizes the maintenance of native gene pools as an important function in maintaining ecosystem and species integrity. Jackson and Betancourt (NSF-DEB-9815500) state that "Finally, our results underscore the growing need to focus more on genotypes than species in biogeographic modeling and ecological forecasting." With the growing awareness of climate change and its potential impacts on the outliers of a species, such as the Square S Gulch ponderosa pine population, the above statement underscores the long term need for appropriate management action.

Management and Silvicultural Considerations:

At this time only neutral markers can be analyzed using current laboratory techniques. Future work may identify the specific genes or gene complexes controlling the adaptations that have allowed this population of ponderosa pine to persist in the unusual conditions present at Square S Gulch. Until that time, it is recommended that the Square S Gulch population be managed as a genetically unique genotype of ponderosa pine. The lack of inbreeding in this population is significant in the fact that it is less likely to undergo inbreeding depression which would reduce the capability of the stand to be successful in regeneration and future adaptation.

Silvicultural recommendations include:

1. Maintain as much structural and age diversity within the stands as possible.
2. Actively manage the stands where appropriate to reduce the juniper (J*uniperus* spp.), pinyon pine (*Pinus edulis* Engelm.), and other woody species to (1) reduce fuel ladders that would intensify wildfire and threaten the ponderosa pine overstory, and (2) reduce competition for the ponderosa pine.
3. Maintain a basal area of between 40 and 60 to reduce the potential for mountain pine beetle infestations.
4. Collect seeds locally and store in long term storage, so locally adapted seed can be used for planting after a disturbance.
5. Maintain the older age cohorts as much as possible by limiting disturbance. Any soil compaction activities such as road/trail construction should be at least 50 feet from the edge of the tree canopy.
6. Prescribed fire activities should be undertaken with care and follow the recommendations listed in Hood (2010) for areas involving older cohort trees.

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