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Using common gardens and AFLP analyses to identify metapopulations of indigenous plant materials for rangeland revegetation in western USA

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Introduction

Past mismanagement, overgrazing, invasive weedy species, wildfires, marginal crop production, mineral and energy extraction, recreation and global climate change are challenges currently facing rangelands (Pierson *et al.* 2011). These disturbances may lead to long-term reductions in biodiversity, altered nutrient and water cycling, diminished forage production for livestock and wildlife, increased wildfire frequency and increased soil erosion and stream sedimentation (Sheley *et al.* 2008). Rangeland revegetation with desirable plant materials may be required to improve degraded conditions, speed recovery, and prevent further erosion and degradation. There is a critical need for plant materials to restore and revegetate rangeland ecosystems. Legumes indigenous to western North America are of particular interest for revegetation because they provide biologically fixed nitrogen, increase plant production, enhance forage quality and provide food sources for grazing animals and pollinators. Some land managers in the USA are concerned with the genetic identity of populations used for revegetation. To balance concerns of genetic identity, ecological adaptation, and economical seed production, we assessed genetic variation and its phenotypic expression in *Astragalus filipes* Torr. ex A. Gray (basalt milkvetch), *Dalea ornata* (Douglas) Eaton & Wright (western prairie clover) and *D. searlsiae* (A. Gray) Barneby (Searls' prairie clover) using common-garden and AFLP (amplified fragment length polymorphism) techniques. These data were used to define population structures (genetically differentiated groups) within each species, which served as a basis for commercial release and rangeland revegetation (Johnson *et al.* 2012).

Methods and Materials

Details concerning the procedures for the phenotypic and genetic characterization of the three species are in the following publications for each species: basalt milkvetch (Bhattarai *et al.* 2008; Bushman *et al.* 2010), western prairie clover (Bhattarai *et al.* 2010), and Searls' prairie clover (Bhattarai *et al.* 2011). Briefly, seeds were collected and bulked from at least 100 plants for individual wildland sites across the range of each legume species. Seeds from each collection site were germinated in a greenhouse, and seedlings then transplanted to two common-garden sites in northern Utah. After an establishment year, field data were collected for a wide range of morphological and phenotypic

traits for two years. In addition, a genetic fingerprinting technique that used AFLP markers was used to determine genetic diversity and population structure in the three species (Meudt and Clarke 2007). Modified procedures of Vos *et al.* (1995) were used to genotype between 474 to 1,194 AFLP marker bands for each species. Analysis of variance procedures, neighbour-joining cluster dendrograms, model-based Bayesian structure analysis, and the Mantel and partial Mantel tests were used to detect relationships among genetic, geographic provenance, phenotypic, and climatic characteristics at the collection sites. Data from these common-garden studies and AFLP analyses were used to group collections (populations) into metapopulations.

Results

For basalt milkvetch, one metapopulation was identified in British Columbia, Canada; a second in central Nevada; and a third that covers portions of Oregon, Idaho, northern Nevada, California, and Washington (Fig. 1). A pre-variety germplasm (NBR-1 Germplasm) was released to the commercial seed trade to represent the third (and largest) metapopulation (Johnson *et al.* 2008). An additional release of basalt milkvetch is in the process of being developed for central Nevada. For western prairie clover, two metapopulations were detected (Fig. 2): one encompassing collections in the Deschutes River watershed in Oregon and a second for the remainder of the distribution in Oregon,

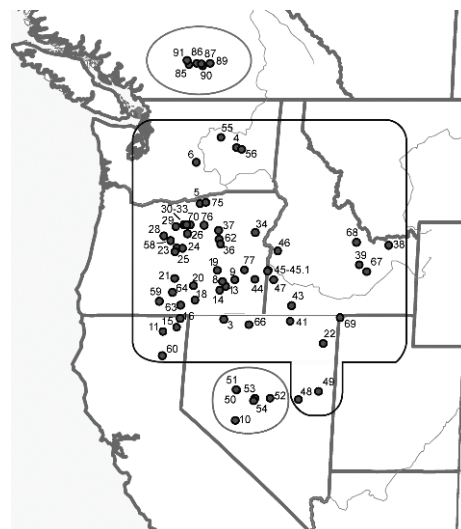


Figure 1. Basalt milkvetch.

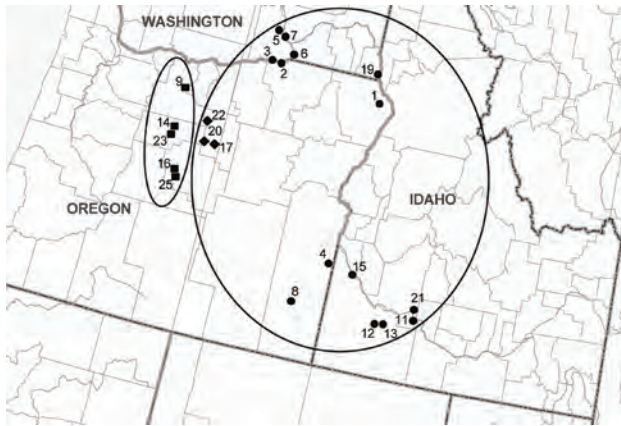


Figure 2. Western prairie clover.

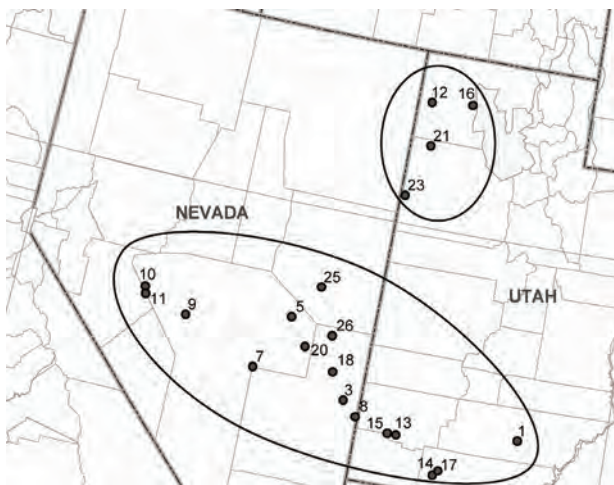


Figure 3. Searls' prairie clover.

Washington, and Idaho. Accordingly, one pre-variety germplasm was released for the Deschutes River watershed (Majestic Germplasm) and another for sites across Washington, Oregon, and Idaho (Spectrum Germplasm) (Johnson *et al.* 2011). For Searls' prairie clover, collections from north-western Utah were genetically differentiated from those in southern Utah and Nevada. Consequently, we are in the process of releasing one population of Searls' prairie clover for southern Nevada and Utah and another for north-western Utah (Fig. 3).

Discussion and Conclusions

The procedures used in our studies to analyse the genetic and phenotypic diversity in basalt milkvetch, western

prairie clover, and Searls' prairie clover were used to identify metapopulations for release to the commercial seed trade and subsequent use in rangeland revegetation. These techniques may be applicable in developing plant materials of other insect-pollinated, herbaceous plant species for the restoration and revegetation of degraded rangelands in other parts of the world.

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