**Using patterns of genetic differentiation as the foundation for**

 **Presenter's Name:** Rob Massatti
**Presenter's Company/Employer:** U.S. Geological Survey
**Presenter's Title:** Research Ecologist
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 **Abstract:**Authors: R. Massatti[1], M.R. Jones[1], F.F. Kilkenny[2], & D.E. Winkler[3] [1]U.S. Geological Survey, Southwest Biological Science Center, Flagstaff, AZ 86001 USA [2]U.S.D.A. Forest Service Rocky Mountain Research Station, Boise, ID 83702 USA [3]U.S. Geological Survey, Southwest Biological Science Center, Moab, UT 84532 USA Presenting author's email: rmassatti@usgs.gov Abstract: As restoration needs for natural landscapes increase due to higher frequency and/or intensity disturbances, the establishment of invasive species, and impacts resulting from climate change, considerable time and resources are being invested to guide the development and deployment of native plant materials (NPMs) to improve restoration outcomes. For example, genetic sequence-based approaches are increasingly applied to restoration species to elucidate adaptation to environmental gradients, which can assist the development of seed transfer guidelines. However, the underlying patterns of genetic diversity within such datasets may also provide important knowledge to guide the use and development of NPMs. For example, natural patterns of genetic differentiation (e.g., a species' genetically defined populations), which are increasingly recognized as an inherently valuable resource, would best be protected by explicitly using them to create regional seed transfer boundaries. In turn, such genetic differentiation-informed boundaries may help mitigate other issues that can impact restoration outcomes, such as outbreeding depression or the decay of interactions among species within a community and the subsequent loss of community resilience. Here, we detail a new method that utilizes species distribution models, landscape resistance analyses, and empirical patterns of genetic differentiation to estimate the geographic distribution of genetically defined populations for two species, Pseudoroegneria spicata (bluebunch wheatgrass) and Hilaria jamesii (James' galleta grass). Furthermore, we use these boundaries to regionally constrain estimations of adaptation inferred either from common gardens (in the case of P. spicata) or from genetic sequencing data (in the case of H. jamesii). As such, we develop guidelines that can be used to minimize both genetic and adaptive differentiation during seed transfer or when selecting seed sources from which to generate new NPMs.