

Local population differentiation in *Bromus tectorum* L. in relation to habitat-specific selection regimes

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Abstract A central question of invasion biology is how an exotic species invades new habitats following its initial establishment. Three hypotheses to explain this expansion are: (1) the existence of ‘general purpose’ genotypes, (2) the in situ evolution of novel genotypes, and (3) the dispersal of existing specialized genotypes into habitats for which they are pre-adapted. *Bromus tectorum* is a selfing exotic winter annual grass that has achieved widespread dominance in semiarid western North America and that is actively invading salt desert habitats. We examined mechanisms driving this invasion in three complementary studies. In reciprocal seeding experiments with ten populations from saline playa, salt desert shrubland, and upland sagebrush communities along a salinity gradient in western Utah, we found that seeds from the playa population were able to establish better than those of most other populations across all habitats, including two highly saline sites. Seeds of one of the two seed sources from upland big sagebrush communities established best on the site of origin, while the seeds of the other source established well across a range of non-saline sites. In a greenhouse experiment with playa and upland seed sources, we found evidence of adaptation to high salinity in the playa source. Playa plants were larger than upland plants in control treatments and invested less in root. They maintained vigor and seed production at high salinity better than upland plants. Molecular genetic analysis showed that the playa population was dominated by a single SSR genotype absent from upland big sagebrush populations, which were comprised of SSR genotypes generally rare or absent in populations from salt desert shrubland sites. Our results demonstrate local population differentiation in *B. tectorum*, resulting at least in part from differential selection on pre-adapted genotypes with characteristic marker fingerprints. We found little evidence for selection favoring novel genotypes.