Improvement of orchardgrass germplasm through traditional and molecular approaches

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The objectives of our orchardgrass (*Dactylis glomerata* L.) genetics and breeding program are to 1) use molecular tools to characterize orchardgrass germplasm and genome structure, 2) identify the genetic determinants of agronomically important traits and strategically incorporate molecular markers in the breeding program, 3) phenotypically evaluate promising germplasm sources, and 4) develop elite breeding populations that possess increased winter hardiness, drought tolerance, persistence, forage yield, water soluble carbohydrate concentration, and high levels of nutritive value.

From our EST library, we developed over 1100 SSR markers. We used these markers to characterize the genetic diversity of both diploid and tetraploid subspecies of orchardgrass and to develop a genetic linkage map of an autotetraploid, biparental (subsp. *himalayensis* [late heading] x subsp. *aschersoniana* [early heading]) population of 284 genotypes. The linkage map showed high homology to physically mapped rice (*Oryza sativa* L.) genes and provided the background to map heading date QTL on three linkage groups. Ongoing efforts include candidate gene mapping studies to identify genes underlying heading date and freezing tolerance.

Evaluation of novel sources of orchardgrass germplasm, including its various subspecies, resulted in the identification of substantial levels of genetic variation for agronomic traits, including dry matter yield and heading date, under rainfed and irrigated conditions of the Intermountain U.S. Germplasm from the subsp. *woronowii* possessed particularly high forage yield potential. Additional germplasm evaluations focused on the half-sib and semi-hybrid progeny of nine specific populations, which originated from areas around the world. We identified substantial genetic variation for morphological traits and forage yield within the half-sib families (H^2 = 0.26 to 0.74) and individual families with superior trait values ($P < 0.05$) than the included commercial check cultivars. We identified differences ($P < 0.05$) among the semi-hybrid progenies of these germplasm sources and semi-hybrid populations that possessed higher forage yield than the included commercial check cultivars. We also found significant general and specific combining ability effects for dry matter yield. UTDG102, a breeding population derived from collections from the Altai region of Russia, possessed high overall general combining ability. UTDG101, a germplasm population collected from Xinjiang Province, China, possessed SCA when hybridized with IADG103 (Japan) and the cultivar Latar. However, UTDG101 possessed low GCA. These evaluations combined with molecular analyses allowed us to identify orchardgrass germplasm populations and potential heterotic groups. We also determined that within the untapped orchardgrass germplasm resides a substantial amount of genetic variation that we can exploit in our breeding program.