

Origins, Adaptive Radiation, and Evolution of Switchgrass

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ABSTRACT

Switchgrass (*Panicum virgatum*), native to the central and Eastern USA, is highly valued as a component in tallgrass prairie and savanna restoration and conservation projects and as a potential bioenergy feedstock. The purpose of this study was to (1) identify regional diversity, gene pools, and centers-of-diversity of switchgrass to gain an understanding of its post-glacial evolution and (2) survey a broad array of putative upland and lowland accessions for the possible presence of natural hybrids or hybrid derivatives and evidence of historic gene flow between the two ecotypes. We sampled a total of 480 genotypes from 71 accessions that included the three main taxonomic groups of switchgrass (lowland 4x, upland 4x, and upland 8x) along with one accession possessing an intermediate phenotype. We identified primary centers of diversity for switchgrass in the eastern and western Gulf Coast regions. Migration, drift, and selection have led to adaptive radiation in switchgrass, creating regional gene pools within each of the main taxa. Genetic structure analysis revealed 21 individuals with strong evidence for inter-taxa hybrid origin and another 25 individuals with moderate evidence for inter-taxa hybrid origin. All but two of these individuals originated from remnant populations of the Central or Eastern Gulf Coast or along the Atlantic Seaboard, a region that is populated with significant quantities of both upland and lowland ecotypes. Gene flow has resulted in “hot spots” of genetic diversity in the southeastern USA and along the Atlantic Seaboard.

Fig. 1. Partial map of the USA, showing the approximate location of 67 switchgrass accessions and the probabilities of accession membership in one of 10 groups identified by STRUCTURE analysis. The size of each circle represents the sample size for each accession, with $n = 10$ shown in the legend. Each cultivar or accession is identified by a two- or three-character code from Zhang et al. (2011a). Each “slice of pie” represents the probability of membership in one of the 10 STRUCTURE groups shown in the legend. Figure is adapted from Zhang et al. (2011a).

