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Title

Comparative Genome Analysis between Agrostis stolonifera and Members of the Pooideae Subfamily Including Brachypodium distachyon

Authors

Loreto P. Araneda, *University of Massachusetts Amherst* Follow

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Abstract

Understanding of grass genome structure and evolution has been significantly advanced through comparative genomics. The genomes of most cool-season forage and turf grasses, belonging to the Pooideae subfamily of the grasses, remain understudied. Creeping bentgrass (*Agrostis stolonifera*) is one of the most important cool-season turfgrasses due to its low mowing tolerance and aggressive growth habit. An RFLP genetic map of creeping bentgrass using 229 RFLP markers derived from cereal and creeping bentgrass EST-RFLP probes was constructed for a comparative genome analysis. This genetic map was compared with those of perennial ryegrass, oat, wheat, and rice. Large-scale chromosomal rearrangements between the map of creeping bentgrass and the respective maps of the Triticeae, oat, and rice were observed. However, no evidence of chromosomal rearrangements between the maps of creeping bentgrass and perennial ryegrass was detected, suggesting that these recently domesticated species might be closely related than expected. Further comparative genome analysis of creeping bentgrass was performed with the genome sequences of *Brachypodium distachyon* using sequences of the above-mentioned RFLP mapped markers and 8,470 publicly available *A. stolonifera* EST (AgEST) sequences. A total of 24 syntenic blocks were identified between the *Agrostis* linkage groups and the *B. distachyon* chromosomes. Orthologous loci of AgESTs (678) were identified in the *B. distachyon* genome, and these loci can be utilized in further comparative mapping of Pooideae species. Insights from comparative genomics with *B. distachyon* will be useful for genetic improvement of *Agrostis* spp. and provide a better understanding of the evolution of the Pooideae species.

First Advisor

Geunhwa Jung

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