

RFLP Marker based Comparative Linkage Maps of the Lolium and Poaceae Genomes. (C07-sim220120-Oral)

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Abstract:

Ryegrass (*Lolium* spp.) is a major turf and forage grass species grown throughout the world. Ryegrass has not been studied extensively in terms of genome analysis, compared with other major cereal crops such as rice, wheat, and oat. Recent studies described construction of molecular marker based genetic maps of perennial ryegrass and comparative mapping with other Poaceae genomes. However, the density of the current map is not sufficient to observe the genomic rearrangements. Our study was conducted to construct a high-density RFLP linkage map of ryegrass and to understand the evolutionary chromosomal rearrangements. A genetic mapping population consisting of 156 F2 pseudo-testcross progenies was derived from a pair cross between the highly heterozygous ryegrass clones, MFA and MFB, from interspecific crosses, annual x perennial ryegrass. For RFLP analysis, oat cDNA (CDO), barley cDNA (BCD), and rice cDNA (RZ) clones were screened to detect polymorphism using parental genomic DNAs digested with five restriction enzymes (BamHI, DraI, HindIII, EcoRI, and EcoRV). Polymorphic probes were tested on a progeny set of up to 89 individuals. The comparative mapping of the *Lolium* and Poaceae genomes will be discussed.

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