An In Silico DNA Sequence Comparison of the Perennial Ryegrass and Rice Genomes

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Introduction Comparative mapping studies in the family Poaceae, which includes rice (a model species for this family) and perennial ryegrass (PRG) have indicated macro-colinearity of genes is generally conserved across different genomes. Genome mapping of simple sequence repeat markers derived from expressed sequence tags (EST-SSRs) for PRG (Faville *et al*., 2004) provides a vehicle for DNA sequence-based matching of mapped PRG genes to orthologous positions in the rice genome, which can be used to establish comparative relationships between these species' genomes. We have initiated such an analysis using an EST-SSR-based PRG genome map. Our objective was to assess this *in silico* approach as a tool for candidate gene identification from rice, and for targeting markers to specified PRG genome map regions based on rice genome position.

Materials and methods Two PRG bi-parental genetic linkage maps were combined to construct a consensus genome map (JoinMap 3.0) with 167 single locus EST-SSR locations. Potential rice orthologues of mapped PRG ESTs were identified by BLASTN analysis against a Rice Gene Index (http://www.tigr.org/tigr-scripts/tgi/T_index.cgi?species=rice). Criteria used were: E value $<e^{-20}$; sequence identity >85% over >100 bp alignment length. Rice tentative consensus (TC) sequences associated with map-ordered rice BAC (bacterial artificial chromosome) and PAC (P1-derived artificial chromosome) clones were identified, providing a rice genome position for their putative PRG orthologues.

Results Of 167 EST-SSRs used to construct a consensus PRG genome map, 37% were common to both PRG component maps. Common marker orders were conserved between component maps (r^2 0.93 across linkage groups), and component maps and the consensus map (r^2 0.98 for both). Under our BLASTN criteria, potential rice orthologues were identified for 136 mapped EST-SSRs. This information facilitates an overview of macro-colinearity between the PRG and rice genomes (Figure 1), with large portions of PRG linkage groups showing homology to 1-2 rice chromosomes. These relationships endorse earlier comparisons between the two species (Jones *et al*., 2002), and are concomitant with the wheat-rice relationship (Sorrells *et al*., 2003). Within macro-colinear blocks, apparent rearrangements of orthologous sequences were observed (data not shown). Verification of EST-SSR positions in more than one PRG mapping pedigree will confirm that these rearrangements are genuine and not due to ambiguous marker ordering.

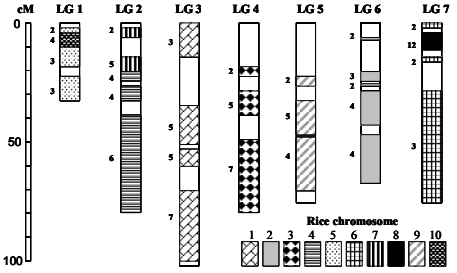

Figure 1. Perennial ryegrass (PRG) genome map-rice genome relationships. Patterned regions on the map represent macro-colinear blocks (intervals with ≥ 2 contiguous mapped PRG EST-SSRs matching rice sequences from one rice chromosome; no. matches indicated left of each block). White spaces contain EST-SSRs matches to one or no rice sequence. Macro-colinear blocks were not found for rice chromosomes 11 and 12. LG = linkage group; cM =centimorgans.

Conclusions The approach used was successful for identifying macro-colinearity between the PRG and rice genomes, and will improve by enhancing EST-SSR density and genome coverage. This information will be useful for selecting DNA sequence-derived markers targeted to broad PRG genome map regions. However, rice-PRG transfer of candidate gene information may be complicated by intrachromosomal rearrangements.

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