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Synteny in cereals

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It is now 20 years since the first "comparative maps" began to provide evidence for extensive synteny – the conservation of gene content and order – between plant genomes. Early work linked the genomes of the three major cereals – wheat, maize and rice. Subsequently, similar relationships were extended to the genomes of foxtail millet, sugar cane, sorghum, pearl millet and oats. These studies have been extended recently to tef, finger millet and the forage grasses, ryegrass and meadow fescue and brachypodium, the emerging Pooideae model genome. Similar relationships are apparent in broad leafed crop groups, particularly the Solanaceae, the legumes and brassicas. Although no comparisons have yet linked the grasses with other monocots, the genome sequences now available for rice and arabidopsis have been used to demonstrate residual synteny over the monocot-eudicot divide.

The extensive genomic DNA sequence of crop plants now available has provided evidence for evolutionary processes and mechanisms that tend to disrupt synteny. The discovery of a major polyploidisation event followed by only partial diploidisation preceding the divergence of the grasses 60 million years has added considerable interest to the analysis.

In crop research and breeding applications of synteny abound. The syntenous relationships that link the economic grasses with genomes ranging in size from 400 to 7000 Mb and basic chromosome numbers of 5 to 12 provide key data for evolutionary studies. There are interesting distinctions observed between actual and evolutionary time and the extensive rearrangements between some genomes of close relatives in the Triticeae still defy explanation.

The major early-identified application of synteny was "cross genome" gene isolation, i.e. using the extensive genomic resources of models such as rice to predict and isolate adaptive genes in the more intractable genomes, such as wheat and barley. Early failures were followed by stunning successes in barley and rye. The recent synteny-based isolation of the wheat chromosome pairing gene, *Ph*, has nicely demonstrated the added power of synteny when triangulated with rice and brachypodium.

Yet another application envisaged early on was the potential to extend the range of alleles of key genes available to breeders beyond their own crops to those discovered in other crops. A first example, the transfer of wheat "Green Revolution" dwarfing control, to rice by engineering an orthologous rice gene has now been achieved. The possibilities afforded by this approach are extensive.