Using a Barley Panel to Convert Association Mapping Information

The Plant Genome 2:11–22.

Association mapping is successfully used in the study of human genetics but it requires high marker density, potentially leading to many missing marker data and to high genotyping costs. In human genetics, methods exist to impute missing marker data and whole markers typed in a reference panel but not in the experimental dataset.

These researchers sought to determine if an imputation method developed for human data would function effectively in a barley panel. They found that despite a low number of marker tags, imputation accuracy was such that for about 80% of nontag markers, the correlation between imputed and true scores was 0.8 or higher.

When Diversity Arrays Technology markers were used as tags, single nucleotide polymorphism markers were attributed with similar accuracy, suggesting that the method can convert association information from one marker system (such as Diversity Arrays Technology) to another marker system (such as single nucleotide polymorphism). The researchers suggest that marker imputation methods will have an important future in association studies as a component of tagging methods and in reducing problems due to missing data. ■

Exploring the Apple Genome

The Plant Genome 2:23–38.

In this study, 34 apple cDNA libraries were constructed from root, leaf, bud, shoot, flower, and fruit tissues, at various developmental stages and conditions, and of several genotypes. The researchers then coalesced these into 23,442 tentative contigs and 9843 singletons, for a total of 33,825 apple unigenes. Of these apple unigenes, 8437 (25%) had no detectable homologs in the *Arabidopsis* genome.

When the entire apple unigene set was compared with the entire citrus unigene set and the poplar predicted proteome, both members of the core eudicot and rosids clade, 13,521 of apple unigenes matched one or more sequences in citrus, while 25,817 had counterparts in the poplar protein database.

The researchers found that apple–*Arabidopsis*–citrus–poplar comparisons revealed closer evolutionary relationships between apple and poplar than with the other two species. However, genes involved in basic metabolic pathways appear to be largely conserved among apple, citrus, poplar, and *Arabidopsis*. ■

Using a Reverse Genetic Technique to Discover Useful Wheat Traits

The Plant Genome 2:39–47.

The large genome and polyploidy of wheat makes it difficult to identify desirable genetic changes based on phenotypic screening due to gene redundancy. This also makes forward genetics more difficult in wheat than in diploid plants.

Researchers from the University of Sydney and the Value Added Wheat Cooperative Research Centre, Australia explored the use of a modified TILLING (Targeting Induced Local Lesions IN Genomes) method to detect useful mutants for wheat grain quality. This is a general reverse genetic technique that uses traditional chemical mutagenesis methods to create libraries of mutagenized individuals that are screened for mutations.

They found a hard grain variant of a soft cultivar due to a mutation in a puroindoline gene caused by a premature stop codon. The researchers state that with the increasing information of wheat genetics, many potential target genes of interest can be screened for mutations with this technique. ■

Making Sweet Sorghum Sweeter

The Plant Genome 2:48–62.

Sweet sorghum, like its close relative, sugarcane, has been breed to accumulate high levels of edible sugars in the stem. Sweet sorghums are tall and produce high biomass in addition to sugar. However, there is little documentation about the genetic relationships and diversity within sweet sorghums and how sweet sorghums relate to grain sorghum racial types.

Researchers from Cornell and Texas A&M genotyped with simple sequence repeats and single nucleotide polymorphisms a diverse panel of 125 (mostly sweet) sorghums.

Using both distance-based and model-based methods, the researchers identified three main genetic groupings of sweet sorghums. Based on observed phenotypes and known origins, these were classified as historical and modern syrup, modern sugar/energy, and amber types.

Three significant associations for height were detected. Two of these, on chromosomes 9 and 6, support published studies. One significant association for brix, on chromosome 1, was detected. ■

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Analyzing diverse genome sets with kinship construction

The Plant Genome 2:63–77.

Analyzing traits with association mapping provides a powerful complement to traditional linkage analysis. It requires deciding the number of background markers, which is a common issue that needs to be addressed in many association mapping studies.

In this study, a diverse group of researchers show that the adequacy of markers in relationship estimation influences the maximum likelihood of the model explaining phenotypic variation and demonstrated this influence with a series of computer simulations with different trait architectures.

They then used computer simulations to analyze two different data sets: one from a diverse set of maize inbred lines with a complex population structure and familial relatedness, and the other from a group of crossbred dogs.

Their results showed that the likelihood-based model-fitting approach can be used to quantify the robustness of genetic relationships derived from molecular marker data. They also found that kinship estimation was more sensitive to the number of markers used than population structure estimation in terms of model fitting.

Kinship construction with subsets of the whole marker panel and subsequent model testing with multiple phenotypic traits could provide ad hoc information on whether the number of markers is sufficient to quantify genetic relationships among individuals. ■

Tomato genome being sequenced

The Plant Genome 2:78–92.

A very large team of researchers from an international consortium of 10 countries (Korea, China, the United Kingdom, India, the Netherlands, France, Japan, Spain, Italy, and the United States) is working to sequence the tomato genome. The team is part of the larger "International Solanaceae Genome Project (SOL): Systems Approach to Diversity and Adaptation" initiative.

The tomato genome sequencing project uses an ordered bacterial artificial chromosome approach to generate a high-quality tomato euchromatic genome sequence for use as a reference genome for the Solanaceae and euasterids.

A Solanaceae reference genome will be an invaluable resource in addressing two fundamental biological questions: first, how genomes code for extensive phenotypic differences using relatively conserved sets of genes; and second, how phenotypic diversity can be harnessed for the improvement of agricultural products. The reference euchromatic tomato sequence is expected to be near completion by 2010. ■

Sequencing strawberries is sweet

The Plant Genome 2:93–101.

Strawberries, genus Fragaria, are an important commercial fruit crop, widely grown in all temperate regions of the world. The genus is an important clade within the family Rosaceae. The Rosaceae family includes many domesticated fruit and nut crops, such as peach, apple, and almond. Given their economic importance and relative small genomes, multiple sequencing projects and comparative analyses would be highly justified in this family.

These researchers undertook the application of the GeneTrek approach to *Fragaria vesca*, which contains one of the smallest genomes in any of the flowering plants and is a putative ancestor to the domesticated strawberry.

The results indicate that *F. vesca* contains about 30,500 genes and that they are mostly arranged in gene-rich regions (~1 gene per 5.7 kb) that would be open to a whole genome shotgun sequencing analysis.

The researchers indicate that this example supports the method of using GeneTrek on a great number of genomes, sampled from a phylogenetic perspective, allowing identification of lineages where dramatic changes have occurred in the rates of gene or genome evolution, such as in genome instability, gene loss, or gene duplication, and may pinpoint species deserving additional genomic investigation. ■