Reports of Meetings

Plant Genome III

Bruno Quebedeaux, Andrew Kalinski, Susan McCarthy, and Patrick Byrne

E-mail: smccarth@nalusda.gov

(BQ) Department of Horticulture, University of Maryland, College Park, MD 20742-5611, USA; (AK, SM) National Agricultural Library, USDA, Beltsville, MD 20705-2351, USA; (PB) University of Missouri, Columbia, MO 65211, USA

The Third Plant Genome International Conference on the Status of Plant Genome Research was held in San Diego, California, USA, on 15–19 January 1995. Plant Genome III presented the following areas of genome research and development: isolation and transformation of agriculturally important genes, comparative genetic mapping, chromosome structure, new instrumentation and automation technology. Plenary and general sessions and specific workshops were featured highlighting new computer tools, databases, nomenclature, gene-tagging for abiotic stress, or individual species: pine trees, arabidopsis, barley, tree fruits, maize, legumes, cotton and grass genome integration. The conference was sponsored and supported by the USDA Agricultural Research Service (ARS), the USDA National Agricultural Library (NAL), USDA Cooperative State, Research Education and Extension Service, National Research Initiative Competitive Grants Office, John Innes Centre (UK), the Rockefeller Foundation, and the International Society for Plant Molecular Biology. The meeting attracted over 660 participants from 25 countries; there was substantially increased participation from the European Community and Japan.

The plant genome research program is now entering its fifth year. Jerome Miksche, Director, USDA Plant Genome Research Program,

Abbreviations: DAF, DNA amplification fingerprinting; EST, expressed sequence tag; MAS, marker-assisted selection; QTL, quantitative trait locus; RAPD, random-amplified-polymorphic DNA; RFLP, restriction-fragment-length polymorphism.
commended conference participants for their efforts leading to development of new genomic information, new technologies, and international collaboration. He stressed the need for continued and expanded funding to support continued research efforts. He indicated that the program, using molecular genetics to search for genes of agricultural importance and to construct detailed maps, has already yielded a plentiful harvest of new information.

**Marker-Based Breeding**

Genetic improvement of crop plants depends upon genetic diversity. Intensive breeding for crop improvement has narrowed the diversity of many of our commercially important cultivars. For these crop species, additional genetic improvement will be increasingly difficult to achieve without the new approaches to breeding now under development.

Steve Tanksley (Cornell University, USA) discussed the need to develop new QTLs, and identified a strategy for advanced backcross analysis: nearly elite lines are matched with an exotic, or ancient, donor germplasm. The F1 progeny are backcrossed several times and rapidly screened for advantageous QTLs. Tanksley's approach is to develop QTL isogenic lines for rapid map-based plant breeding.

Marker-facilitated QTL manipulation has been successfully used to transfer traits between elite maize lines was reported by Charles Stuber (North Carolina State University, USA). The marker-assisted backcrossing was used in a complex breeding program which greatly accelerated the development of a new hybrid line. The two highest yielding hybrids afforded an improvement of 1.7 to 1.9 ton/hectare.

A Tree Fruit Workshop, organized for the first time at the conference, also announced accelerated breeding. Norman Weeden (Cornell University, USA) reported that high heterozygosity, characteristic of the apple genomes and related species within the Rosaceae family, permits genetic analysis of isolated genes approximately nine months after making a cross between two varieties. This technique can accelerate breeding by 5 to 15 years while reducing costs. Future breeding goals aim to develop cultivars with improved fruit quality, insect and disease resistance.

Maps with over 200 segregation markers for several major apple cultivars have already been completed. Weeden indicated that molecular techniques such as RAPD and RFLP markers and bulk segregant analysis are being incorporated into the apple breeding program at Cornell. Genes encoding fruit color, fruit size, columnar growth habit,