Cytogenetics of Legumes

Cytogenetics played an essential role in studies of chromosome structure, behavior, and evolution in numerous plant species. Iwata et al. summarizes some of the achievements of cytogenetic studies in legumes in the Phaseoloid clade, which includes important legume crops such as common bean (Phaseolus vulgaris L.), cowpea (Vigna unguiculata [L.] Walp.), soybean (Glycine max [L.] Merr.), and pigeon pea (Cajanus cajan [L.] Huth). We also provide chromosome images of legume species mapped with their ribosomal DNAs using the fluorescence in situ hybridization technique. Molecular cytogenetics will continue to be an important tool in legume genetics and genomics, and we discuss future applications of molecular cytogenetics to better understand chromosome and genome structure and evolution in legumes.

World Cowpeas Go Wild

Cowpea is a major tropical legume crop grown in warm to hot areas throughout the world and is especially important to the people of sub-Saharan Africa. To date, relatively little is understood about the domestication history, worldwide dispersal, and distribution of genetic variation of this crop. Huynh et al. genotyped a worldwide collection of cowpea traditional cultivars (landraces) and African ancestral wild cowpea with more than 1200 gene-based markers. Two major subpopulations (gene pools) were found distributed in two distinct geographical zones of Africa separated by the Congo River basin and they were closely related to wild cowpea in the same geographic region. Representation of each gene pool also appeared dispersed throughout the rest of the world. This delineation of cowpea germplasm into groups of genetic relatedness will be valuable for guiding introgression efforts in breeding programs and for improving the efficiency of germplasm management.

Yield-related QTLs Identified in Soybean

Seed weight and plant height are two main traits which are related to the yield of soybean. Liu et al. identified 11 quantitative trait loci for plant height and 18 quantitative trait loci for seed weight across six diverse environments. Among them, two loci for plant height and five loci for seed weight were detected in four or more environments with a high value of phenotypic variation explained. Furthermore, 11 and 10 epistatic interactions of plant height and seed weight were also identified, respectively. These results will be useful for marker-assisted selection and should be targeted for future identification of candidate genes which can be used for increased yield of soybean.

Plants Have Conserved Flowering Genes

Plants exhibit great diversity in flowering strategies and growth habits. A limited number of studies have been undertaken to elucidate the molecular basis of flowering time in legumes. Kim et al. identified orthologous (or homologous) counterparts of approximately 200 Arabidopsis genes involved in the control of flowering time in three legume species, lotus corniculatus L var japonicus Regel, Medicago truncatula Gaertn., and soybean (Glycine max [L.] Merr.), of which the genomes have been sequenced. A large portion of the Arabidopsis flowering genes are represented in these legumes but several essential genes of flowering pathways are missing. These results suggest that basic flowering pathways are likely to be relatively well conserved between Arabidopsis and legumes.

Retrotransposon Tagging in Lotus

Legumes encompass a large number of crops. Legume species also have a characteristic feature, symbiotic nitrogen fixation, of which a deeper understanding is desired to achieve low input sustainable agriculture. Reflecting on the importance of symbiotic nitrogen fixation as a research subject, many research infrastructures have been established for legumes. In this review, Fukai et al. introduce one of them, the mutant library of model legume Lotus japonicus. The Lotus mutant library was developed using its endogenous retrotransposon as a mutagen. The methodology conducted in Lotus could be feasible in other crops, too.

Transcriptomics for Legume Functional Genomics

Legumes represent an important family of flowering plants for providing human nutrition and for their capacity to fix atmospheric nitrogen for agricultural sustainability. The recent availability of genome sequences of several legume plants has helped boost genomics research. In this review by Garg and Jain, various technologies available for transcriptome analyses and their usage in legume biology are discussed. The review focuses on the progress made.