INTRODUCTION

For plant genomics to affect economic and environmental benefits, the knowledge gained must be “translated” into crop varieties having desired characteristics. The discipline of plant breeding is the “translator” of new knowledge from emerging technologies into improved crop cultivars, or “varieties.” The AgGenomics section of the peer-reviewed Initiative for Future Agriculture and Food Systems [(IFAFS) offered by CSREES, USDA in 2000 and 2001] was one of the few sources of funding to date for integration of genomics and plant breeding. A symposium held 13 Nov. 2002 at the annual meetings of the Crop Science Society of America (CSSA), cosponsored by CSREES, USDA, and by CSSA Divisions C-1 and C-7, shared perspectives gained from IFAFS research on the value of genomics to plant breeding. A panel of IFAFS grantees representing genomics research experience and participate in a diversity of crops was invited to present summaries of research and to discuss questions designed to facilitate a panel discussion and an overall summary of the symposium’s main points, both prepared by the symposium editors.

Application of Genomic Technologies to Crop Plants: Opportunities and Challenges

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Enormous genomic resources have been developed for model plants such as Arabidopsis thaliana (L.) Heynh. and rice (Oryza sativa L.), including detailed genetic maps (Harushima et al., 1998), huge numbers of expressed sequence tags (ESTs) (Sasaki et al., 1994; Seki et al., 2002), deep-coverage large-insert libraries with extensive contig assemblies (Zhang et al., 1996; Mozo et al., 1998; Zhao et al., 2002), and both targeted and complete genome sequencing and annotation (Goff et al., 2002; Yu et al., 2002). These resources, coupled with the development of mutant stocks by knock-outs (Young et al., 2001) or targeted induced local lesions in genomes [TILLING (Till et al., 2003)], will allow for the efficient identification of gene(s) controlling phenotypes in model systems. However, it is not clear how these also condition economically important traits in crop plants. An example is the FLC locus controlling flowering in Arabidopsis (Michaels and Amasino, 1999) and in the closely related brassicas (Koornneef et al., 1995). Similar successes are readily communicated to the scientific community through publications; however, it will be difficult to publish, and therefore assess, the opposite scenario in which genes identified in model systems are not associated with similar traits in important plants. The purpose of this paper is to identify some potential inconsistencies between model systems and economically important plants with Allium cepa L.) as an example.

Recent studies have revealed that the Alliaceae and Asparagales are two strongly supported sister groups within the monocots...