



ABSTRACT

“Transferring gene functions between different plant species using PLAZA 2.0”

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PLAZA is an online comparative genomics platform where data generated by different plant sequencing initiatives is integrated and combined with advanced methods for data mining. This resource includes structural and functional annotation of published plant genomes together with a large set of interactive tools to study gene function and gene and genome evolution. Pre-computed data sets cover homologous gene families, multiple sequence alignments, phylogenetic trees, intra-species whole-genome dot plots, and genomic colinearity between species. The Workbench provides an efficient environment to analyze user-defined gene sets using PLAZA's interface including GO enrichment analysis for all species.

The second release of this resource integrates whole-genome information from 23 plants covering 11 dicots, 5 monocots, 2 (club-)mosses and 5 algae (>840,000 genes stored in >22,000 multi-species gene families). New features include functional gene clustering based on GO annotations, interactive Synteny plots to study the gene organization of homologous genes and the reliable identification of orthologous genes (through the integration of a complementary set of data types). During this presentation I will elaborate on different methodologies to identify orthologous genes in different species, discuss pitfalls inherent to simple *ad-hoc* approaches to identify 'functional homologs' and demonstrate how PLAZA 2.0 can facilitate the transfer of functional information between plants. PLAZA 2.0 is available at <http://bioinformatics.psb.ugent.be/plaza/>.