PGDD: A Database for Investigations into the Functional and Evolutionary Consequences of Gene and Genome Duplication, using Angiosperms as a Model

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Plant Genome Duplication Database (PGDD)

• To provide genome alignments from a single resource based on uniform standards, we built the PGDD providing synteny information in terms of colinearity between chromosomes.
• At present, it provides data for 26 plants and 4 plants are being prepared.
• http://chibba.pgml.uga.edu/duplication/

The number of plants in PGDD

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Diagram of current PGDD server

• Determining colinearity blocks
• Post processing colinear data
• Finding homolog sequences
• Preparing data files

Colinear block data is useful in plant genome research

• Genome duplication (GD) is highly related with the architecture and function of many higher eukaryotic genomes.
• The flowering plants are outstanding models in which to elucidate consequences of GD for higher eukaryotes.
• The colinear block data based on alignments of plant genome sequences can provide the foundation for investigations into GD of the genome.
Plans to enhance PGDD

- Adopting Django as a development framework and redesigning the database to contain new types of data such as structure of chromosome sequence
- Displaying multiple alignment of synteny regions to compare multiple genomes at once
- Developing a set of open APIs in order to share PGDD information with other services

http://chibba.pgml.uga.edu/duplication/

DEMONSTRATION OF PGDD

Example of multiple alignment of synteny regions

Example of a downloaded file.

Acknowledgement

Thank you.
Plant Genome Duplication Database

The Plant Genome Mapping Laboratory

THE UNIVERSITY OF GEORGIA

Homepage of PGDD

Dot Plot

Locus Search

Map View

Downloads