

# Gramene: A Resource For Comparative Genomics in Plants

Marcela K. Monaco<sup>1</sup>, Vindhya Amarasinghe<sup>2</sup>, Ed Buckler<sup>2,3</sup>, Terry Casstevens<sup>4</sup>, Charles Chen<sup>4</sup>, Genevieve DeClerck<sup>4</sup>, Palitha Dharmawardhana<sup>5</sup>, Pankaj Jaiswal<sup>5</sup>, AS Karthikeyan<sup>4</sup>, Sunita Kumari<sup>1</sup>, Susan R McCouch<sup>4</sup>, Shiran Pasternak<sup>1</sup>, Will Spooner<sup>1</sup>, Joshua Stein<sup>1</sup>, Jim Thomason<sup>1</sup>, Sharon Wei<sup>1</sup>, Jon Zhang<sup>2</sup>, Ken Youens-Clark<sup>1</sup>, Doreen Ware<sup>1,3</sup>

<sup>1</sup>Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, USA; <sup>2</sup>Institute for Genomic Diversity, Cornell University, Ithaca, NY, 14853, USA; <sup>3</sup>USDA ARS NAA Robert W. Holley Center for Agriculture and Health, Cornell University, Ithaca, NY, 14853, USA; <sup>4</sup>Department of Plant Breeding and Genetics, 240 Emerson Hall, Cornell University, Ithaca, NY, 14853, USA ; <sup>5</sup>Dept of Botany and Plant Pathology, 3082 Cordley Hall, Oregon State University, Corvallis, OR, 97331, USA

*Gramene is used by plant biologists to conduct basic and applied research in genomics. Its power comes from the integration of functional, genetic & comparative information.*

# Gramene Provides Multiple Entry Points into Genomic Data

### Genome Browsers for 15 Species

Maize, sorghum, domesticated and wild rice, *Brachypodium* and *Physcomitrella*. Eudicots *Arabidopsis thaliana*, *A. lyrata*, soybean, poplar, and grape. Algae, moss and spikemoss.

The image displays a screenshot of the Phylo-P browser interface, showing genomic tracks for 15 species. The tracks are organized into a grid with columns representing genomic regions (100,000 to 1,000,000 bp) and rows representing different genomic features. The tracks include Chromosome (Mb), EST Cluster (Hs), EST Cluster (Mus), EST Cluster (Dros), EST Cluster (Ank), Gene (Hs), Gene (Mus), Gene (Dros), Gene (Ank), EST Cluster (Hs), EST Cluster (Mus), EST Cluster (Dros), EST Cluster (Ank), and EST Cluster (Hs). The tracks are color-coded by species: Hs (red), Mus (green), Dros (blue), Ank (purple), and others. The tracks show gene models, EST clusters, and other genomic features across a genomic region from 100,000 to 1,000,000 bp.

[illegible]

Automated ortholog and paralog calls made by reconciliation of gene trees with species tree. Orthologs used to detect synteny between genomes.

[illegible][illegible]

## Selected Publications

**Youns-Clark K, et al.** (2010) Genome database in 2010: updates and extensions. *Nucleic Acid Research*, 39 (suppl 1): D1085-D1094.

**Jaiswal P, et al.** (2006) Genome: a bird's-eye view of cereal genomes. *Nucleic Acids Research*.

**Wamazaki Y, et al.** (2005) *Plant Cell Physiol* 46: 63-68.

**Ware D, et al.** (2006) Genome: a resource for comparative grass genomics. *Nucleic Acids Research*, 30, 103-105.


**Ware D, et al.** (2002) Genome: a tool for grass genomics. *Plant Physiol* 130: 1606-1613.

**Jaiswal P, et al.** (2002) Genome: development and integration of trait and gene ontologies for rice. *Comparative and Functional Genomics* 3: 132-136.

[illegible]

**Funding**

This work was initially supported (2001-2004) by the USDA initiative for Future Agriculture and Food Systems (IFAFS) (grant no. 00-52100-9622) and a Cooperative State Research and Education Service (CSREES) agreement through the USDA Agricultural Research Service (grant no. 58-1907-0-0-41). For the years 2004-2008, this work was supported by the National Science Foundation (NSF) PGI grant award #0321665. Current work is being supported by the NSF Plant Genome Research Resource grant award IOS-0703908. Genome works alongside with EMBL-EBI funded Ensembl Genomes.



[illegible]