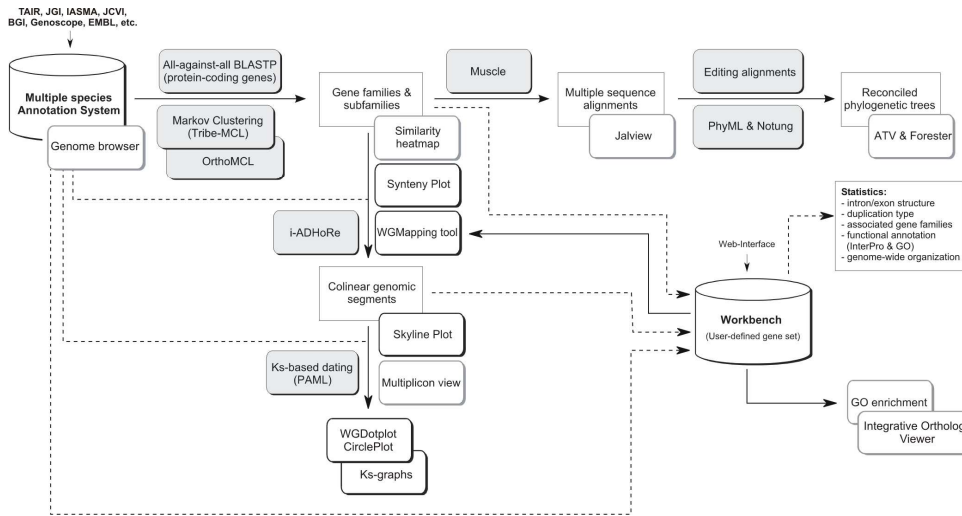


Structure of the PLAZA platform

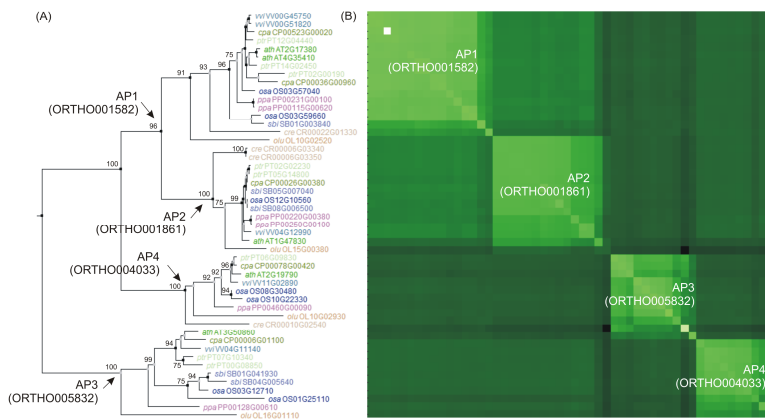


Features

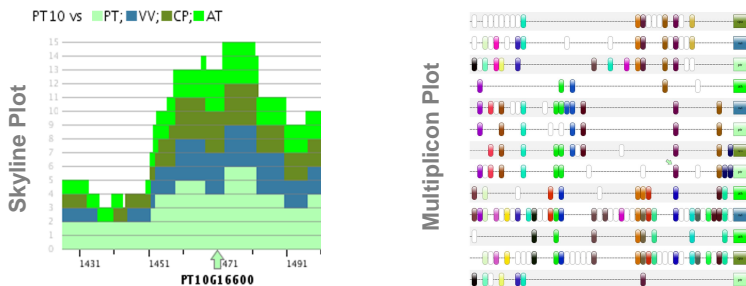
- Includes pre-computed **gene families, multiple sequence alignments & phylogenetic trees**
- Contains intra- and inter-species **gene colinearity** identified using i-ADHoRe
- **Interactive workbench** allows users to perform analyses on their genes. Currently PLAZA hosts **18 different tools**
- Includes **>20 genomes from flowering plants, (club-)mosses and several green algae**
- All data can be **downloaded** for further study

Gene Family & Genome Evolution

- Pre-computed gene families can be browsed using **similarity heatmaps** and **multiple sequence alignments** (viewable with JalView)
- **Reconciled phylogenetic trees** can be viewed online (using Archaeopteryx)

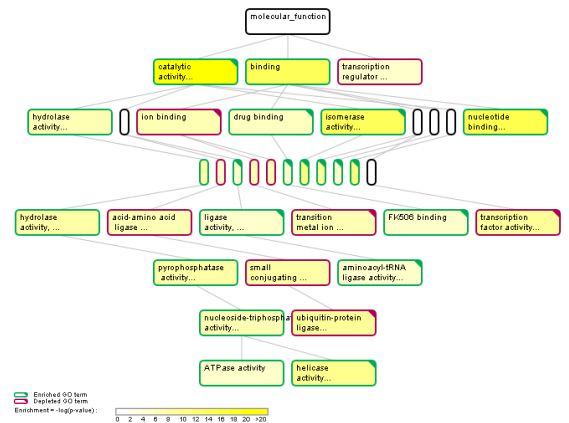


- **i-ADHoRe** was used to identify colinear regions within and between genomes, **K_s-based dating** was applied on retained homologs.

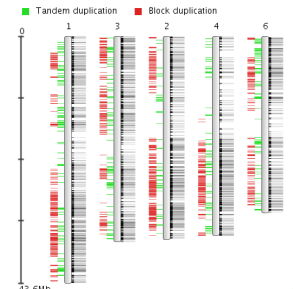


Workbench

- **Personal workbench** where max. 30 experiments (~custom gene sets) can be stored and analyzed
- Compare **intron-exon structure & InterPro domains**
- **BLAST interface** to map data from non-model species onto reference organisms included in PLAZA
- **GO enrichment** to find overrepresented functional annotations



- Gene sets can be **visualized on the genome** using **WGMapping** including information about block and tandem gene duplicates



<http://bioinformatics.psb.ugent.be/plaza>

Tool Navigation Table

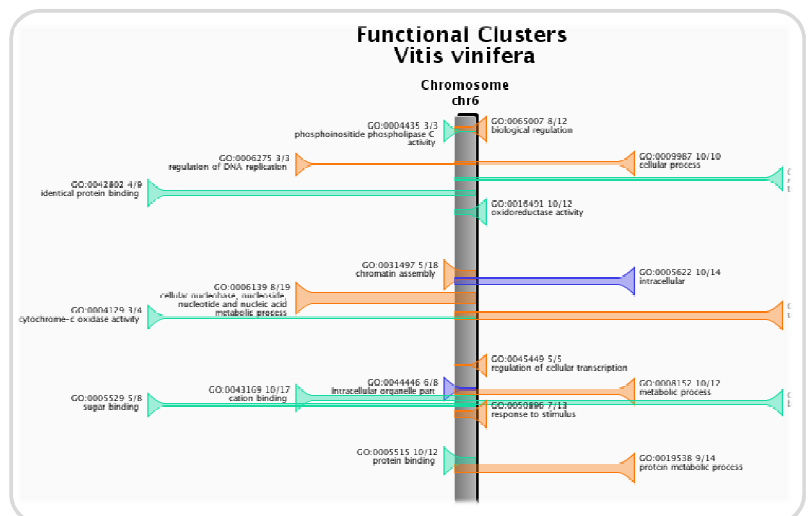
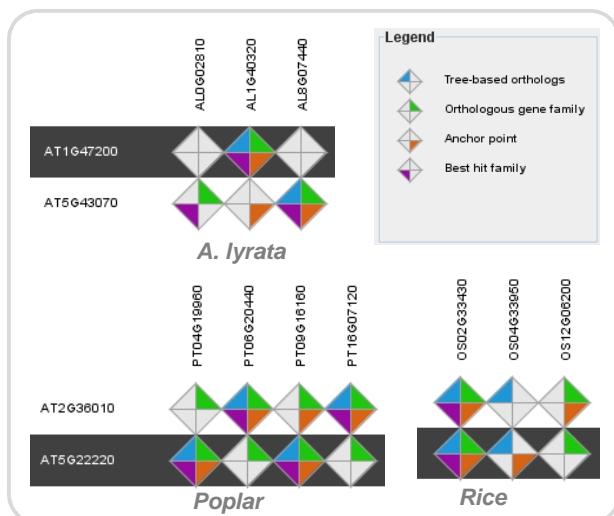
| Tool | Usage | How to get there |
|-------------------------------------|---|--|
| AnnoJ | Genome browser | Organism page → View organism in genome browser. or Gene page → Toolbox → View the gene in the Genome Browser. |
| BLAST | BLAST interface | Menubar → Analyze → BLAST |
| CirclePlot | Genome evolution / Colinearity research | Menubar → Analyze → WGDotplot (2) |
| Conversion tool | Gene identifier conversion | Menubar → Archive → Conversion tool |
| Functional Clustering | Functional clustering gene annotations | Menubar → Analyze → Functional clusters |
| Gene Family Finder | Select families based on phylogenetic profile | Data → Find gene families |
| Genomeview | Genome browser | Organism page → View organism in genome browser. or Gene page → Toolbox → View the gene in the Genome Browser |
| Integrative Orthology Viewer | Overview orthologous genes | Gene page → Toolbox → Explore the orthologous genes in other species. |
| Julview | Gene family evolution / Explore multiple sequence alignment | Gene family page → Toolbox → View the multiple sequence alignment or Gene page → Toolbox → Explore the multiple sequence alignment of the homologous gene family |
| Ks-dating Tool | Genome evolution / Colinearity research | Menubar → Analyze → Ks-dating tool |
| Multiplicon View | Genome evolution / Colinearity research | From chromosome view in WGDotplot, click on a colinear region or Workbench experiment overview → Toolbox → View the orthologous genes |
| Similarity heatmap | Gene family evolution / Explore gene similarity | Gene family page → Toolbox → View the similarity heatmap |
| Skyline Plot | Genome evolution / Colinearity research | Menubar → Analyze → Skyline plot or Gene page → Toolbox → Explore the colinearity of this gene with other genomes |
| Synteny Plot | Genome evolution / Colinearity research | Menubar → Analyze → Synteny plot or Gene page → Toolbox → Explore the local gene organization for homologous genes. or Gene family page → Toolbox → Explore the local gene organization for homologous genes |
| Tree Explorer | Gene family evolution / Phylogenetic tree representation | Gene family page → Toolbox → Explore the phylogenetic trees |
| WGDotplot | Genome evolution / Colinearity research | or Gene page → Toolbox → Explore the phylogenetic tree of the homologous gene family Menubar → Analyze → WGDotplot |
| WGMapping | Mapping of gene sets on chromosomes | or Gene page → Block Duplicate (1) Menubar → Analyze → WGMapping or Gene family page → Toolbox → View the genome wide organization of this gene family or Workbench experiment overview → Toolbox → View the genome-wide organization |
| Workbench | Analyze custom gene set | Menubar → Analyze → Workbench |

(1) Only available for genes with paralogs in a duplicated region (block duplicates)
(2) Only for intra-species comparisons

More info? Check **PLAZA Documentation & Tutorials**

New features PLAZA release 2.5

- Includes >900,000 genes from **25 plants** covering 13 dicots, 5 monocots, 2 (club-)mosses and 5 algae
- Integrative **Orthology detection** tool to explore cross-species orthologs incorporating information from phylogenetic tree construction, protein clustering, simple Best-Blast hit scoring and conserved genome organization
- Functional clustering tool** to explore genome-wide clustering of genes annotated with a specific Gene Ontology, InterPro, Gene family or Workbench term



<http://bioinformatics.psb.ugent.be/plaza>