



# Webinar Oct 2015: BLAST

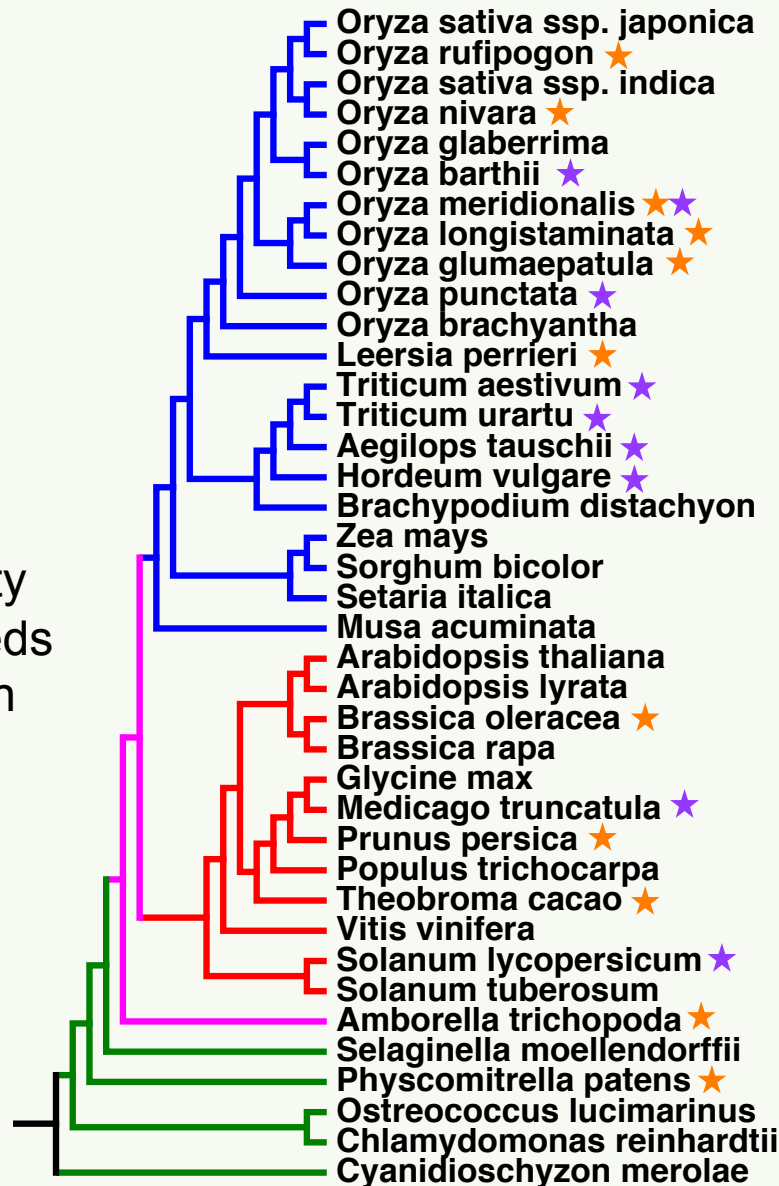
Sharon Wei



★ = New (11)  
★ = Updated (9)

### Gramene Release 46

- 39 complete reference genomes
- 21 Monocots
- 12 Eudicots
- 1 basal angiosperm
- 5 Lower plants



Driven by:

- Assembly quality
- Community needs
- Depth & breadth
- Project Support
- INSDC

# Data served by Gramene browser



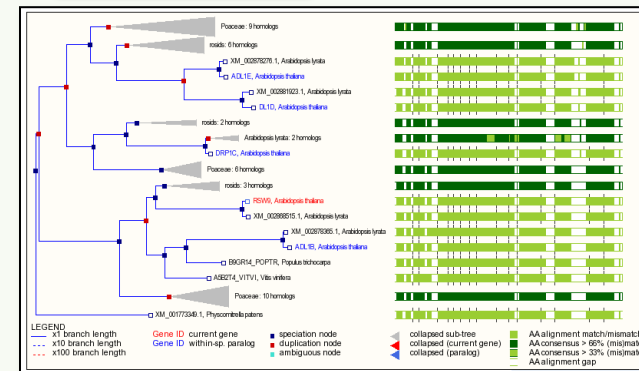
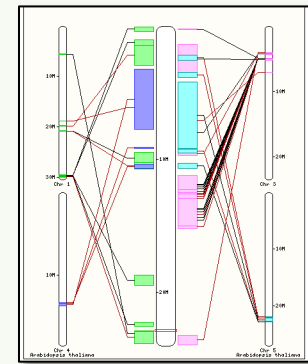
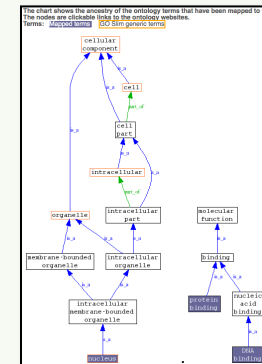
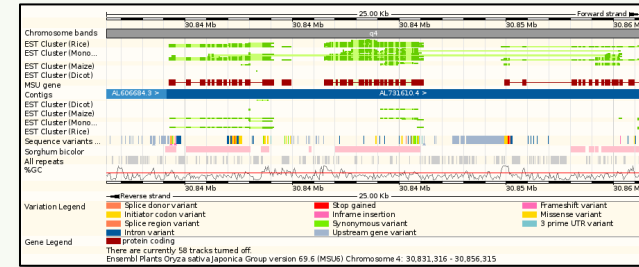
- ✓ Accessioned Genomes
- ✓ Community Annotation
- ✓ Expression
- ✓ Variation
- ✓ Epigenomics

- Repeats/TE's
- Genes
- EST/cDNA features
- InterPro domain
- Gene Ontology (GO)
- Variants (Effect Predicted)

- ftp
- Public mysql server
- Ensembl API & RESTFUL interface
- Genome Browser

- Whole Genome Alignment
- Phylogenetic Gene Trees
- Ortholog/Paralog
- Synteny mapping

## Browser Displays



# Where to start



- Species + Genomic Location

Location:



[http://ensembl.gramene.org/Arabidopsis\\_thaliana/Location/View?r=1:8001-18000](http://ensembl.gramene.org/Arabidopsis_thaliana/Location/View?r=1:8001-18000)

- Terms and IDs (Gene, Interpro, Variation, GO)

Search all species...



- Sequences (Protein, DNA)



# Background on Basic Local Alignment Search Tool



Database Type Query Type	DNA databases	Protein databases
DNA	<b>blastn</b> , tblastx	blastx
Protein	tblastn	<b>blastp</b>

## Basic BLAST

Choose a BLAST program to run.

### [nucleotide blast](#)

Search a **nucleotide** database using a **nucleotide** query  
*Algorithms: blastn, megablast, discontinuous megablast*

### [protein blast](#)

Search **protein** database using a **protein** query  
*Algorithms: blastp, psi-blast, phi-blast*

### [blastx](#)

Search **protein** database using a **translated nucleotide** query

### [tblastn](#)

Search **translated nucleotide** database using a **protein** query

### [tblastx](#)

Search **translated nucleotide** database using a **translated nucleotide** query



# Why Gramene Blast

- Gramene Blast is integrated with Gramene genome browser.
- Serve as entry point for Genome browsing
- Position a sequence to the genome
- Identify orthologs and paralogs, gene trees

# Highlights

- Improved drastically since release 45 April 2015. Better user interface and better efficiency.
- EBI NCBI-blast web services.
- Taxonomic tree of the target genomes
- Ticketing system. Automatic refreshing.
- Karyotype view of result hits
- Results can be downloaded and saved
- Hits lead to the location view of target region



Please see the Demo video at  
[ftp://ftp.gramene.org/pub/gramene/outreach/  
webinars/DemoFinal.zip](ftp://ftp.gramene.org/pub/gramene/outreach/webinars/DemoFinal.zip)