PLAZA workshop

Advanced orthology, synteny, and expression analysis in cereals using the Workbench

October 21-22, 2019

# Topics Covered

In this series of exercises, you will learn how to study the evolution of genes and genome organization between different plant species with varying levels of gene complexity using the PLAZA Workbench. Furthermore, you will combine orthology information with gene expression data available to identify genes with conserved/diverged gene expression profiles.

* ePlant maize - <http://bar.utoronto.ca/eplant_maize/> - will be used to browse maize gene expression data.
* Wheat Expression Browser - <http://www.wheat-expression.com/> - will be used to browse wheat gene expression data.

# Data Content

In this series of exercises we will make use of an existing data set from a publication.

Title: Genome‐wide atlas of transcription during maize development (PubMed ID: 21299659)  
Data: Supplemental Table S4 contains 863 organ-specific genes for 8 different organs/tissues.   
Download: Download the data from the PLAZA FTP:

* Location : ftp://ftp.psb.ugent.be/pub/plaza/workshop/ELIXIR/2019/
* Name: tpj\_4527\_sm\_tables4.xls

# Exercises

## Part 1: Comparative analysis of marker genes in maize

1. Starting from Table S4, create a Workbench experiment called *Zma\_embryo* and upload all maize B73 genes showing *embryo* specific expression.

[PLAZA **Monocot 4.5** PLAZA: Workbench 🡪 Create Experiment 🡪 Import using gene identifiers]

1. How many of your input genes only have homologs in one/more maize genomes?

[View associated gene families 🡪 Use header Species to sort gene families]

1. For the maize B73 gene present in only two species, confirm the gene indeed is a marker for embryo [ePlant maize 🡪 Tissue and Experiment viewer using gene Zm00001d011345]
2. For this gene, how many copies are present in the B73 genome? Is their expression profile identical?

[PLAZA Gene page 🡪 Gene family page] + [ePlant maize 🡪 Tissue and Experiment viewer]

1. Starting from the maize embryo specific gene Zm00001d029446, select all orthologs in wheat (*T. aestivum*) using the Integrative Orthology Viewer and check the expression levels of these genes in wheat. To avoid doing copy-paste for all wheat genes, use this protocol:
   1. Go to Experiment Zma\_embryo
   2. View the orthologous genes using the PLAZA integrative method.
   3. Select as Target species *Triticum aestivum*
   4. Set Required number of evidence types = 2 + hit Find orthologs
   5. At the bottom of the table, select Download results
   6. Open this file in Excel or a text editor, search for Zm00001d029446
2. For the wheat genes orthologous to Zm00001d043323, perform an expression analysis to prioritize and identify embryo markers.

[Wheat Expression Viewer 🡪 Enter genes 🡪 Select Developmental time-course of Chinese Spring + Developmental time-course of Azhurnaya]

1. Are any if the best hit orthologs (BHIF) showing conserved expression in wheat? [use result of step 5.6 or check Integrative Orthology Viewer for Zm00001d043323]

## Part 2: The complex relationship between gene function, orthology, collinearity and expression

1. Starting from the maize embryo marker Zm00001d005322, identify orthologs in wheat and determine if the ortholog showing conserved collinearity between wheat and maize shows the highest expression in embryo.

[use result of step 5.6 or check Integrative Orthology Viewer]

1. For maize gene Zm00001d022089,
   1. which wheat ortholog is clearly (not) a conserved marker gene. Do the number of supporting evidence types correlate with the limited expression breadth expected for a marker gene?
   2. Explore the phylogenetic tree and verify if the wheat gene showing organ-specific expression is clustering closest together with the maize gene.
2. Starting from the experiment *Zma\_embryo*, how many genes are encoding transcription factors? For the LEC1 transcription factor, verify if you find conserved embryo-specific orthologous regulators in wheat.

[Workbench 🡪 view InterPro domains] + [Integrative Orthology Viewer OR result step 5.6] + [Wheat Expression Viewer 🡪 Enter genes 🡪 Select Developmental time-course of Chinese Spring + Developmental time-course of Azhurnaya]