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**Chrystian Camilo Sosa**

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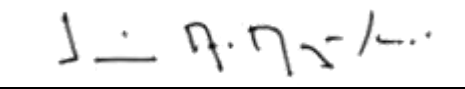
*Multi-layer reconstruction of the abiotic stress (Drought, Heat, HMR, and ROS) response network in rice* at the **Virtual Symposium in Plant Omics Science**

Held between November 23rd - 27th, 2020 at Santiago de Cali, Colombia



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Andrés Jaramillo Botero  
Scientific Director



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Institutional Strengthening Sub-director

Support:





Multi-layer reconstruction of the abiotic stress (Drought, Heat, HMR and ROS) response network in rice

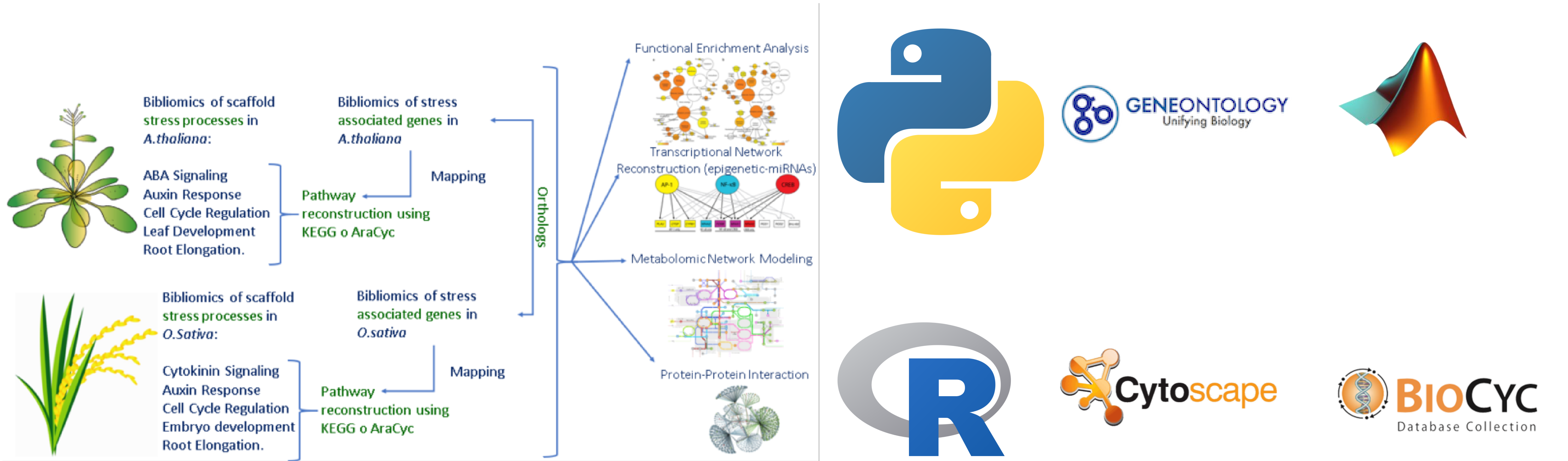
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Introduction

- Rice is one of the main staple crops in the world and a main player to ensure the food security worldwide.
- Rice is tolerant to heavy metals and is cropped in acid soils (30% of world soils).
- Rice is one the main crops in Colombia .
- Colombia will be one of the most affected countries by the climate change increasing abiotic stress on plants.
- Even with mathematical models that describe how rice can adapt to abiotic stresses, a systemic description of rice tolerance to abiotic stresses is lacking
- OMICAS project pretends contribute alternatives and solutions to agricultural problems in Colombia where rice and sugarcane are vital crops for present and future.

Aim

- To evaluate the biological processes to explain four abiotic stresses(Drought, Heat, HMR and ROS) in *O. sativa* and *A. thaliana* through functional enrichment analysis.
- To build a regulation network using transcriptional and epigenomics information to find regulatory genes in four abiotic stresses(Drought, Heat, HMR and ROS) in *O. sativa*.
- To evaluate *in-silico* the protein - protein interaction network in order to find candidate genes involved in for four abiotic stresses (Drought, Heat, HMR and ROS) in *O. sativa*.
- To reconstruct and modelling the genome scale metabolic network associated with four abiotic stress features in *O. sativa* under the FBA approach to understand the influence of four abiotic stresses on metabolic phenotypes.



Expected results:

- A list of orthologues genes of *A. thaliana* (plant model by reference) in *O. sativa* using to find possible no reported candidate genes in the four abiotic stress in rice.
- A transcriptional regulatory network that might control four abiotic stresses in rice.
- A list of candidate genes involved in abiotic stress features in rice derived from protein-protein interactive network
- A metabolic reconstruction of rice for four abiotic stress using either a previous version of GSM or WGS resequencing data annotated from the OMICAS project.
- Obtain probable metabolic phenotype resulting from the GSM of the variation in genes involved in abiotic stress in rice.
- Outcomes: Three articles peer reviewed (Frontiers in plant science, PlosOne, Heliyon)

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