

# Florimaize

## FLORIMAIZE - Role of florigen proteins in maize developmental reprogramming under drought stress

### ABSTRACT

The objective of FLORIMAIZE is to identify the role of a florigen gene (ZCN8) in the genetic variability of growth maintenance in maize (parent lines) to identify and develop novel maize phenotype. The project is closely related with DROPS project which analyzes same factors on F1 hybrids.

**Keywords :** Developing the plant of the future, Plant, Genomics, Ecophysio/architecture/phenotyping, Operation/adaptation, Drought, Flowering, Phenotyping, Protein/proteomic, Corn

**Year :** 2013

**Project number :** 1301-006

**Type of funding :** AAP CARIPO

**Project type :** AAP

**Research units in the network :**

**Start date :** 2014-09-01

**End date :** 2017-08-31

**Flagship project :** no

**Project leader :** François Tardieu

**Project leader's institution :** INRA-INRAE

**Project leader's RU :** LEPSE

**Budget allocated :** 169000 €

**Total budget allocated ( including co-financing) :** 423072 €

**Funding :** Labex

### GOAL

The project has three objectives :

- Objective 1
  - Evaluating the variability in Florigen expression within a panel of Maize lines, temperate and tropical.
  - Detailing the mode(s) of florigen regulation under different watering conditions.
- Objective 2
  - Identifying QTLs affecting growth, flowering, transpiration and water use efficiency.
- Objective 3
  - Identifying ZCN8 eQTLs. What is the basis for ZCN8 expression variations?
- Objective 4
  - Relating individual eQTLs to physiological QTLs via: comparison with the two platform experiments (co-locations of eQTLs of ZCN8 with QTLs of flowering time, leaf growth, biomass, control of transpiration and water use efficiency).
  - Relate ZCN8 expression to phenotypes in the Maize tropical Tropical panel.

The project has this time line :

- Year 1 :
  - Phenotypic analysis of the temperate maize panel (X2)
  - Set up RNA extraction and transcript quantification methods
  - Variability of expression of ZCN8 and related genes in a subset of lines
- Year 2
  - List of QTLs affecting growth, transpiration and water use efficiency

- Variability of expression of ZCN8 and related genes in all lines
  - Year 3
- Identification of eQTLs of ZCN8 and related genes
- Phenotypic and gene expression analyses of the Maize tropical panel
- eQTLs X QTLs association studies

## RESULTS

Overall the Florimaize project was extremely successful. While the initial goals were very ambitious and the experimental design technically complex I believe we managed to complete most of the tasks. Key achievements include (i) the extraction of gene expression data on such a big scale (ii) the successful modelling of gene expression data from individual plants to genotypes and (iii) the setting up of a robust GWAS pipeline for QTL discovery. The study of the interaction between drought stress and gene expression was admittedly not exhaustive. However, our experiment in Kenya was successful in terms of providing information as to the effects of early drought stress on flowering time and the possible genotypic variability in this trait. The Dakar meeting prompted us to explore the allelic composition of tropical germplasm (for the early maturity QTLs that we have discovered), and test transgenic material (in preparation) to accelerate maturity in Maize. Overall, these results and ideas could form the basis for a joint grant application on the topic of Sustainable Intensification in Africa planned at the end of this year. Thus, because of the constructive attitude of all the partners, we expect to continue collaborating on these specific aspects in the future.