

# Study of the evolution of reproductive development in the genus *Oryza* for the improvement of modern cultivated rice

## OBJECTIFS

The broad aim of this project was to identify the evolutionary determinants of panicle architecture in African and Asian rice and of the reproductive barriers that exist between these species. The first objective was to characterize the cellular events underlying panicle development and reproductive barriers between Asian and African species. The second objective was to identify the molecular mechanisms leading to inter- and intra-specific variations of panicle architecture and to female sterility of F1 interspecific hybrids between *O. glaberrima* and *O. sativa*.

## RESULTATS

- Diversity of panicle structure complexity between domesticated and wild-relatives is associated with differences in rachis meristem size and differential rates of axillary meristem establishment rather than heterochronic effects (ie. timing of acquisition of floral fate).
- A marked switch in expression profile is observed in the panicle between apical and axillary meristem types followed by more gradual changes during transitions in axillary meristem identity. Moreover, differential gene expression patterns were observed between crop and wild relatives with convergences and divergences between the Asian and African domestications.
- F1 interspecific hybrids between *O. glaberrima* and *O. sativa* are characterised by a defect in embryo sac differentiation and an alteration of expression of certain genes from the S1 locus.
- Several putative targets of the OsMADS13 protein controlling ovule development in rice were identified and functionally characterised.
- Genetic approaches using interspecific population (CSSL) and Genome-wide association studies (GWAS) on Asian and African populations allowed the identification of several QTLs associated with panicle morphological traits.

## PERSPECTIVES

Beyond this project, the activities of the partnership will focus on the functional characterisation of the candidate genes identified via transcriptomic and genetic approaches and on the modelling of morphology and Gene Regulatory Networks governing panicle development and its diversity in order to identify the determinants of this vital plant structure.

**Responsable :**

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