Modeling the morphodynamics of inflorescence development in rice

Hélène Adam / EDI Team

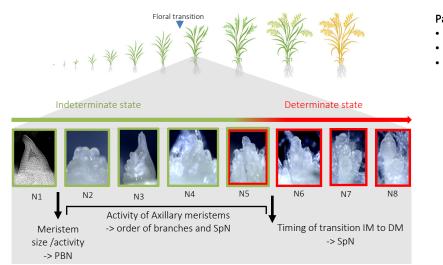
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EDI team context

The inflorescence (panicle) architecture of rice is one of the key components of yield potential and displays high inter- and intra-specific variability. The architecture of the rice inflorescence is mainly determined by the length and number of primary branches (PBL, PBN) and number of secondary branches (SBN) which can influence spikelet number (SpN). The diversity of rice panicle architecture seems to be related to changes in the pattern and timing of branching and conversion of meristem fate/identity. **The cellular and molecular mechanisms underlying the diversity of panicle complexity between and within rice species** are still limited.

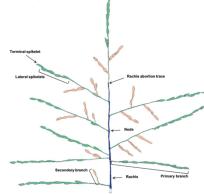




Panicle Architecture variation:

- Number of branches (axillary meristems)
- Number of orders of branches

Axis elongation



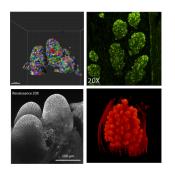
How can we model the events controlling the panicle structure diversity?

Multiscale Analysis in EDI team:

Imaging the cellular events during early development of panicle

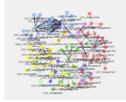
M1 training:

- Meristem morphometry
- Cellular localization of Tagged lines (Membrane & Nuclear/Actin/Auxin reporters)
- 3D *In situ* hybridization of landmark genes of meristem fate and activity



Construct of GRN Gene Regulatory Network using RNA-seq analysis -> panicle gene network

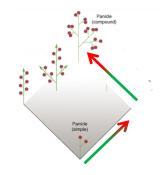
In progress in EDI team:



Evolution of GRN depending of branching complexity (species and/or environmental conditions)

M2 training:

Integration of molecular and cellular data: Molecular Regulatory Network controlling panicle development and branching complexity



References

Ta et al., 2017; doi: 10.1186/s13227-017-0065-y; Harrop et al., 2016; doi: 10.1111/tpj.13147; Harrop et al., 2019; doi: 10.1093/jxb/erz340; Tanaka et al., 2023; doi: 10.1270/jsbbs.22088

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