

## TE-GWAS in rice

**Unlocking rice genetic diversity to secure food production in the context of global change : deciphering the functional impact of transposable elements using genome-wide association studies.**

### ABSTRACT

We propose a new strategy, hereafter referred to as TE-GWAS, that endeavours to identify agronomic traits controlled by TEs through association studies of TEASVs with phenotypes. One major advantage of this new strategy is that it should allow one to directly identify the genetic factor that control the trait of interest as the TE insertions used as marker are expected to modify gene expression and thus be causative of the phenotypic change. Rice is a major crop species worldwide and is a staple food for the lowest income populations. Recently, the availability of the genome sequence of 3000 rice varieties has opened new perspectives in large scale genomic studies for this crop, such as the one we propose in this post-doctoral project.

This project should deliver new genetic factors enabling rice cultivation in poor soils, a particularly important challenge for securing food production in poorest areas.

**Year :** 2017

**Project number :** 1502-505

**Type of funding :** AAP

**Project type :** AAP MOBILITE

**Research units in the network :**

**Start date :** 2018-06-01

**End date :** 2019-12-31

**Flagship project :** no

**Project leader :** Olivier Panaud

**Project leader's institution :** UPVD

**Project leader's RU :** LGDP

**Budget allocated :** 76660 €

**Total budget allocated ( including co-financing ) :** 76660 €

**Funding :** Labex