

# Striga resistance

## Integrating genomic and phenotypic approaches to enhance Striga hermonthica resistance in Pearl millet

### ABSTRACT

The project aims to uncover the genetic basis of resistance to an important pest, Striga in an African cereal, pearl millet. Striga is recognized as a major pest in West Africa both for sorghum and pearl millet (Ejeta 2007). Heritability of Striga resistance in pearl millet is high (Kountche et al. 2013) and consequently have a strong genetic basis. But the exact genes associated with this resistance are still unknown. One of the originality of the project is to use a genetic approach to identify different mechanisms leading to this resistance. We describe here the whole project, but the scientific mobility will focus on the genome wide association study of Striga resistance.

□ During the mobility, the analysis will first focus on already available phenotypic dataset.

The objectives are to perform genome-wide association study and to identify single nucleotide polymorphism (SNP) significantly associated with Striga resistance.

[Le projet comporte 3 grandes activités (Cf. Gantt chart). Les activités de phénotypage au champ et de quantification des strigonolactones (et essai en gel) sont réalisées en amont ou en parallèle de l'activité 3]

Activité 3 du projet faisant l'objet des recherches lors du séjour en France : « Association analysis »  
Total genomic DNA of each of the 200 inbred lines will be isolated from 2 weeks old seedlings. All DNA samples will be genotyped at IRD-Montpellier. We recently develop a hybridization technique allowing sequencing 32000 genes of the pearl millet genomes. We will use this approach to obtain a genome wide datasets of single nucleotide polymorphism (SNP). All phenotypic data collected in above sections will be analyzed and combined with the SNP data to conduct the genome wide association studies. We will perform the GWAS analysis by correction for relatedness and/or population structure (Saïdou et al. 2009). All bioinformatics tools and R pipeline are already available at the host laboratory in Montpellier. The PhD student will modify them to fit this new dataset, learn how to do these analyses and identify the markers and the genes linked to the studied phenotypes.

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**Project type :** AAP MOBILITE

**Research units in the network :**

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**Flagship project :** no

**Project leader :** VIGOUROUX Yves

**Project leader's institution :** IRD

**Project leader's RU :** DIADE

**Budget allocated :** 15644 €

**Total budget allocated ( including co-financing) :** 15644 €

**Funding :** Labex