

**Thesis title : « Study of the domestication and adaptation of Yam (*Dioscorea spp*) in Africa using genomic approaches »**

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**Abstrat:**

Yam (*Dioscorea spp*) is a major staple for more than 100 million people in Africa. This species is vegetatively propagated from a relatively limited number of cultivated varieties. Several studies suggest that new varieties could be created using cultivated × wild hybrids or wild plants. However, this requires the characterization of the genetic resources available, as well as the identification of breeding targets for yam adaptation. The main objectives of the present PhD project were to understand the genetic and genomic bases of yam domestication in Africa, and to characterize the genomic determinism of its adaptation to different climatic zones. We investigated the genetic basis of yam domestication in a comparative genomic approach between the cultivated species *D. rotundata* and two wild close relatives *D. praehensilis* and *D. abyssinica*, by exploiting NGS sequencing data and the SNP variants identified. We demonstrated that the starch biosynthesis and storage pathway was selected during yam domestication, similarly to several cereals. More specifically to yam domestication, genes related to tuber morphology or phototropism ability, as well as genes of the NADH dehydrogenase complex were also under selection. With respect to an enrichment in photosynthesis-related functions, selection of the NADH DH complex suggests changes in adaptation with a transfer from shading environments of forest / savannah of wild yams to full sunlight environments in the field specific of cultivated yam. Interestingly, we also detected the same NADH-DH complex in the study that aimed at identifying significant associations between genetic variation and climate variability. Additional analyses are now necessary to confirm the possibility of studying adaptation during domestication through association studies between genes and environment. The study we performed on the repeat elements (REs) of the yam genome highlighted a strong correlation between the variability in relative abundances of numerous REs and climatic variability. We created a *de novo* database of yam transposable elements (TEs) and demonstrated quite similar TE contents for the three species. Nevertheless, we could identify some TEs with differential genomic abundances between the

180 genotypes surveyed, showing significant correlations with bioclimatic variables. Our study thus suggests the significant association of the repeat fraction of the yam genome, and eventually of the genome size, with adaptation to environment. Finally, we were able to make a first hypothesis on the origin of the cultivated yam *D. rotundata*, using the genomic data available to test for various domestication scenarios. Our hypothesis identifies the origin of yam in the forest areas, with the species *D. praehensilis* as the putative progenitor. Even if the precise geographical origin of yam domestication could not be established, our results question the generally admitted hypothesis of savannah origins for crops and agriculture in Africa.

**Keywords:** Adaptation – Association genetics – *Dioscorea* spp. – Demographic inferring – Domestication – Genes under selection – NGS – Population genomics – SNPs – Transposable elements – Yam