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**Meta-QTL analysis of the genetic control of quality related traits in Yam (*Dioscorea alata* L.)**

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Improving the food quality of yams (*Dioscorea* spp) is an ongoing challenge for yam breeders. The acceptability of newly developed varieties depends on several characteristics that are routinely measured in breeding programmes (colour of tuber flesh, tuber shape, etc.) and on several physico-chemical characteristics of the tuber as well that determine its organoleptic properties, the most important of which are starch content, dry matter and sugars.

The genetic basis of characteristics that determine tuber quality is not known, which limits the efficacy of genetic improvement programmes. A joint partnership is ongoing between CIRAD and IITA, within the framework of the project, "AFRICA YAM", funded by the Bill Gates Foundation, which aims to acquire knowledge about the genetic control of characteristics that determine tuber quality and to identify the genomic regions involved in the determination of different quality traits.

To do this, four diploid full-sib families of *D. alata* were produced by the CIRAD and IITA (two each) by crossing contrasting diploid progenitors. The genotyping of parents and progeny clones is in progress using GBS (Genotyping by Sequencing) and microsatellites. Phenotyping of progenies will focus on the characteristics commonly evaluated in selection schemes, as well as several physico-chemical characteristics. By using the same type of markers in all populations, it will be possible to generate a consensus genetic map to identify possible QTL clusters and to check if the QTLs detected in one particular progeny for a given trait correspond to the QTLs identified in another population for the same or a related trait.