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

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INTRODUCTION

Improving the food quality of yams (*Dioscorea* sp.) 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 (including starch content, dry matter and sugars..). However, the genetic basis of characteristics that determine tuber quality is not known, which limits the efficacy of genetic improvement programmes.

OBJECTIVES

1/ to acquire kowledge about the genetic control of characters that determine the quality

2/ to identify the genomic regions involved in diffèrent quality traits, via a Meta-QTL approach in four *D.alata* diploid mapping populations

MATERIALS AND METHODS

MATERIALS: Four bi-parental populations (with 150 individuals each) have been generated by CIRAD and IITA (two each) by manual fertilization between contrasted genotypes. Table 1 and Figure 1 shows the tuber characteristics of genitors 74F, Kabusa and 14M.

Genitors	Tuber shape	Flesh colour	Oxydation of flesh	Starch content	Dry matter	Sugar content
I 74F	long and cylindrical	yellow	yes	71.25±0 .5	23.87±0.0	7.23±0.1
II Kabusa	compact and oval	white	non	80.05±0.2	29.39±0.1	5.35±0.0
II 14M	compact and oval	white-cream	non	79.15±0.1	25.97±0.1	3.25±0.1

Table 1. Mean ± standart deviation.

Fig. 1 Photograph showing the tubers of genitors 74F, Kabusa and 14M.

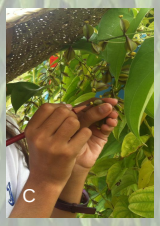
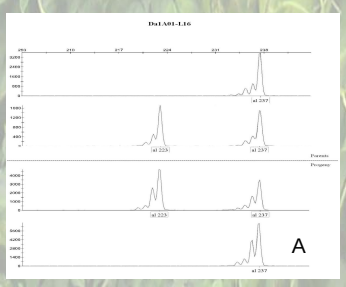


Fig. 2 Photographs showing flowers of genitor male14M (A), flowers of female 74F (B), manual fertilization by the pencil method C), fruits (D), some capsules and seeds (E), and hybrids of progeny 74F x Kabusa (F), that were introduced in vitro to rapidly multiply them by *in vitro culture*.

GENOTYPING and PHENOTYPING : The genotyping of four progenies is in progress by using GBS (Genotyping by Sequencing) and microsatellites markers (Figure 3). The Phenotyping will be initiated early and will be focus both on characters evaluated in selection schemas (oxydation of the fleshé)and several physico-chemical characteristics (sugar content, starch content, dry matter) to be able to identify a maximum number of genomic regions involved in the determination of the quality.



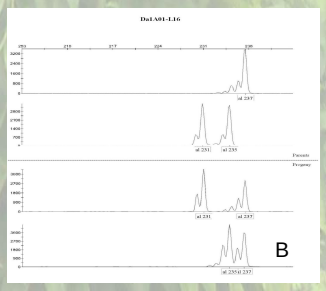


Fig.3 Segregation analysis. Example of electrophoregram obtained for microsatellite loci Da1A01. The parent and one example of each genotype obtained in progenies 74Fx Kabusa (A) and 74F x 14M (B) are represented.

PROSPECTS: 1/ The genetic basis of quality traits understood and utilized in breeding 2/The genomic regions involved in the variability of traits that determine the tuber quality identified 3/ Markers associated with genomic regions that determine the tuber quality identified 4/ A consensus genetic map generated and useful to identify possible QTL clusters and check if the QTLs detected in one particular progreny correspond to the QTLs identified in another population.

Acknowledgements - The authors acknowledge the financial support by the Bill and Melinda Gates Foundation for undertaking the nternational project ñAfrica Yamò.