**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 knowledge about the genetic control of characters that determine the quality
2/ to identify the genomic regions involved in different 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.

<table>
<thead>
<tr>
<th>Genitors</th>
<th>Tuber shape</th>
<th>Flesh colour</th>
<th>Oxidation of flesh</th>
<th>Starch content</th>
<th>Dry matter</th>
<th>Sugar content</th>
</tr>
</thead>
<tbody>
<tr>
<td>74F</td>
<td>long and cylindrical</td>
<td>yellow</td>
<td>yes</td>
<td>71.25±0.5</td>
<td>23.87±0.0</td>
<td>7.23±0.1</td>
</tr>
<tr>
<td>Kabusa</td>
<td>compact and oval</td>
<td>white</td>
<td>yes</td>
<td>80.05±0.2</td>
<td>29.39±0.1</td>
<td>5.35±0.0</td>
</tr>
<tr>
<td>14M</td>
<td>compact and oval</td>
<td>white-cream</td>
<td>non</td>
<td>79.15±0.1</td>
<td>25.97±0.1</td>
<td>3.25±0.1</td>
</tr>
</tbody>
</table>

Table 1. Mean ± standard deviation.

**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 flesh) 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.

**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 progeny correspond to the QTLs identified in another population.

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