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**Introduction**

Improving the quality of yams (*Dioscorea* sp.) is an ongoing challenge for yam breeders. The acceptability of newly developed varieties depends on several tuber traits that are routinely measured in breeding programs (e.g., shape, colour flesh) and on several physico-chemical characteristics that determine its organoleptic properties (e.g., starch content, dry matter). Breeding for the quality (boiled and pounded yam) is essentially carried out on the basis of phenotypic observations and it's a difficult and long process. However, the genetic basis of characteristics that determine tuber quality is not known, which limits the efficiency of genetic improvement programs.

**Objectives**

The objectives are (1) to test the feasibility of use NIRS for predicting different textural and chemical quality attributes, (2) to acquire knowledge about the genetic control of characters that determine the quality, and (3) to identify the genomic regions involved in different quality traits via a meta-QTL analysis in two biparental *D. alata* populations.

**Materials and methods**

Two populations were generated by hand pollinations between contrasted diploid genitors. Parents and progenies were genotyped by GBS. A consensus genetic map was constructed using JoinMap 4.1. Phenotyping of progenies (314 hybrids x 2 blocks x 9 replicates x 2 years) is in process. The measured traits are: flesh color and browning, tuber size (length and width), regularity of shape, hairiness (scored to 0 to 2), skin rough (scored 0-1) and yield.

Twenty seven varieties were used for NIRS calibration. The following characteristics were analyzed: starch content, D.M., amylose, proteins, sugars, hardness, adhesiveness, cohesiveness, springiness and extensibility. Textural evaluation was conducted on pounded samples using texture profile analyses (TPA).

**Results**

First results of NIRS calibration and validation are presented. This work shows that it is possible to use this technology for predicting starch content, protein and sugars. We intend to use it to characterize the progenies. The distribution of tuber shape was close to bimodal. QTL detection identified a locus involved in tuber shape on linkage group LG16 on both populations.

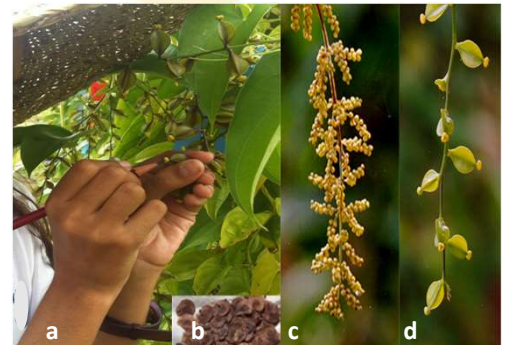


Figure 1. Hand pollinations (a), seeds (b), male flowers (c) and female flowers (d).

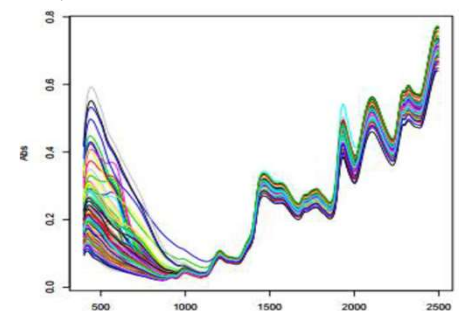


Figure 2. NIRS spectra corresponding to 94 flour samples over 400-2500 nm wavelength (absorbance).

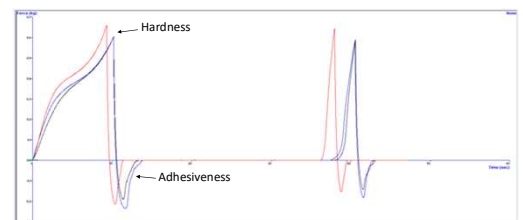


Figure 3. Example of double-compression texture profile for pounded yam.

| Parameters | Calibration |      |        |        | Validation |        |                |
|------------|-------------|------|--------|--------|------------|--------|----------------|
|            | M           | SD   | SEC/SD | SD/SEC | SEP        | SD/SEP | R <sup>2</sup> |
| Protein    | 5.06        | 0.82 | 0.31   | 2.47   | 0.271      | 2.66   | 0.865          |
| Starch     | 79.69       | 2.75 | 0.44   | 1.90   | 1.144      | 2.41   | 0.828          |
| Sugars     | 3.56        | 1.72 | 0.16   | 4.56   | 0.478      | 3.79   | 0.929          |
| Amylose    | 60.7        | 6.17 | 0.62   | 1.44   | 4.338      | 3.26   | 0.441          |

Table 1. Statistical parameters of the calibration and validation sets.

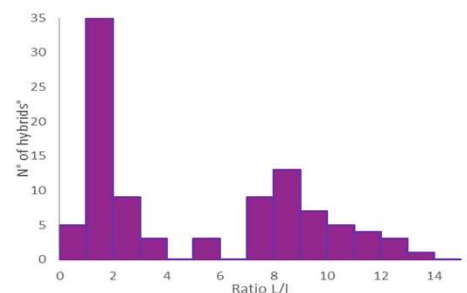


Figure 4. Distribution of tuber shape for the individuals of population B.