Dataset Report

Work Package 3
High-Throughput Phenotyping Protocols (HTPP)
Report Template: Existing Nirs Databases

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Work Package 3

High-throughput phenotyping protocols (HTPP)

REPORT TEMPLATE: EXISTING NIRS DATABASES

General identification

Institute/Partner	CIRAD/INRA
Country	Guadeloupe (FWI)
Project(s)[1]	CavalBio (40%), RTBfoods (60%)
Product	Yam
Presentation	Dried flour

Sampling and measurement protocols

Sampling

At INRA, harvest took place at maturity (full senescence) between November and March depending on genotype while at Cirad a single harvest was carried on whatever the maturity. At harvest, three tubers by genotype were used. Tubers were peeled with a knife, and washed. At Cirad, the head and the tail were removed while at INRA the whole tuber was kept. Then tuber was cut longitudinally. Half of the tuber was used for fresh analysis (*i.e.* color, oxidation, texture) and the other half was processed into flour. Flour was obtain from 5/10mm tuber pieces oven dried at 60 and 70°C for Cirad and INRA respectively, during 3 days that were milled and sieved successively at 2 and 0.2mm.

Near infrared measurement.

Measurements were made on subsamples of dried flour. All samples were scanned in a NIRSystems 6500 spectrometer (FOSS NIRSystems Inc., Silver Spring, MD) using an autocup sampler. Spectra were acquired in reflectance mode at 2 nm intervals over a wavelength range from 400 to 2498 nm (visible and NIR regions) and reported as log(1/R) , where R is reflectance. Each reflectance spectrum was time-averaged from 32 scans and compared against the 32 average ceramic reference measurements. Three tubers per genotype were analyzed and each tuber samples was measured twice.

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[1] Names of projects in which the databases were established

Database description

Product	Fresh yam
Product presentation	Dried peeled tuber flour
Instrument Brand	FOSS
Instrument model	6500
Instrument measurement device	Auto cup and ring cups
Acquisition software	Isiscan
Type of spectra	Diffuse reflectance (log(1/R)
Scanning range	400 nm – 2500 nm
Acquisition step	2 nm
Number of data point per spectrum	1050
Number of sub samples	3
Number of spectra	570
Years of acquisitions	2 years (2016 – 2017)
Outliers identification	Yes
Type of outliers identification	Spectral and chemical
Available spectra files formats	Winisi (.nir) / Excel (.xls)
Name of the data base	ZIYANM
Meta data available	- Genotype identification - Genotype growing location - Growth cycle length - Year of harvest - Weight of sample tuber - Wet chemistry : Dry matter, sugar, starch, protein, amylose, amylopectin - Texture profiles - …
Database published in scientific papers (DOI + Reference)	no
Observation	

Database summary

The yam data base was built over 2 years (2016-2017) and 3 sites and is still under completion. The number of samples per year and site is reported in table 1. Two spectra were done per sample. The average spectra of the 2 subsamples was computed and kept in the final database.

Table 1: Number of samples per year and site.

	Duclos (INRA)	Godet (INRA)	Roujol (CIRAD)
2016	0	0	95
2017	64	36	90

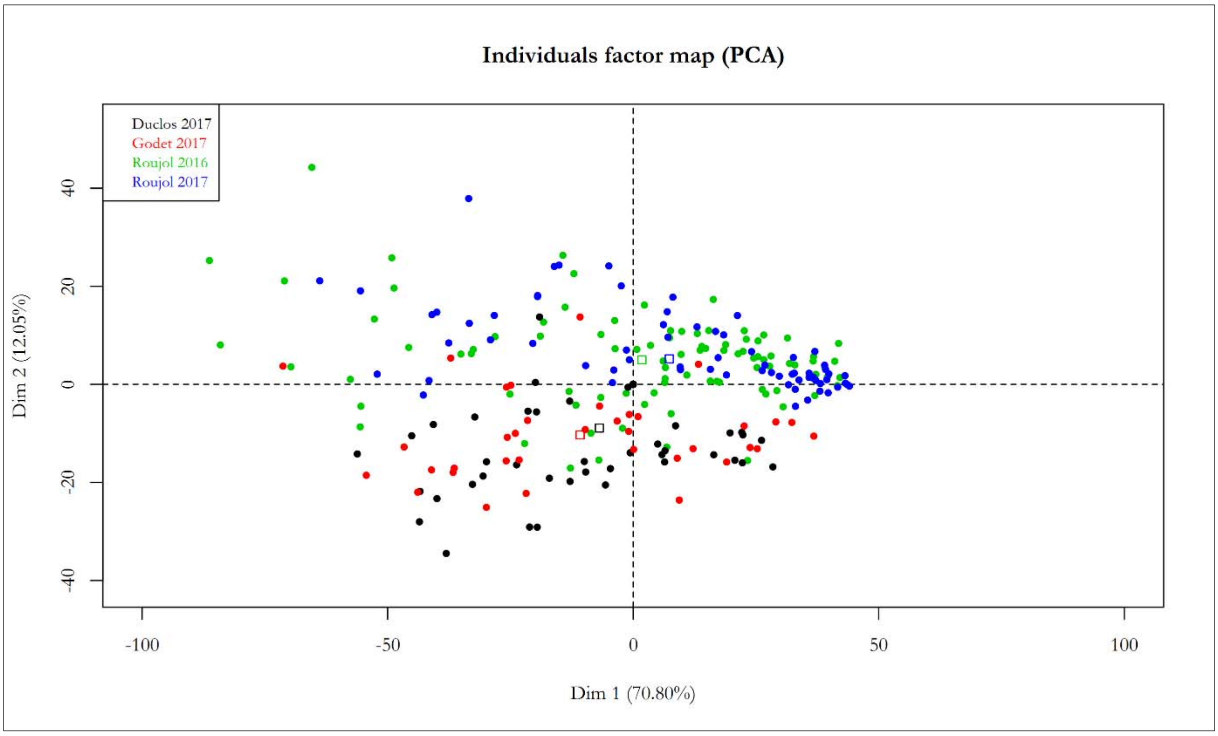

Figure 1: Scatter plot of samples scores for PC1 and PC2

A Principal Component Analysis (PCA) was done on the raw spectra. The first three PCs explained respectively 70.8%, 12.0% and 9.2% of the total inertia. The calculated generalized Mahalanobis distances (GH) identified no sample with GH higher than 3. So all the samples are kept in the database. The dispersion of the samples according to PC1 and PC2 scores showed that there might be an effect of the site or the sample preparation between INRA (Duclos and Godet) and Cirad (Roujol) on spectral signature.

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