Population structure, phenotypic information and association studies in long-generation crops

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POTATO

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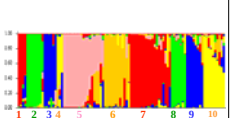
Level of structure of S. phureja population (Bayesian Clustering Method)

K	Ln P(X/P)	P(K/X)
1	-6614	~0.00
2	-6149	~0.00
3	-5846	~0.00
4	-5664	~0.00
5	-5493	~0.00
6	-5437	~0.00
7	-5276	~0.00
8	-5171	~0.00
9	-5101	~0.00
10	-5071	1.00
11	-5141	~0.00



Distribution of 96 landraces in the 10 suggested subpopulations

- 98 landraces
- 48 SSR

Gap-filling genotyping by SSRs and phenotyping for morphological descriptors, agronomic, resistance and quality traits are being conducted for two potato populations: the *S. phureja* germplasm collection (2x) and the *Solanum tuberosum* subsp. andigena advanced bred population B1C5 (4x) were selected for this study.

Thirteen of the 116 accessions comprising the S. phureja population and the entire 105 bred lines comprising the B1C5 population are currently being genotyped with SSRs. To date, DNA has been prepared for all of this material and 18 of the 45 SSR markers planned have been run. Complementary molecular data sets (S. phureja SP1 CGS) have been compiled for complementation with this new data, and GCP data formats downloaded.

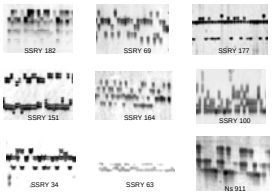
Both populations underwent propagation from healthy in-vitro plantlets and clean tubers were obtained to initiate standard trials with the complete set of each population. At present the S. phureja population is planted in replicated trials in two locations. Filling gaps on morphological descriptors and phenotypic evaluations is ongoing.

A preliminary analysis to evaluate conditions and opportunities for LD mapping of QTLs in this population was performed with a sample of 96 landraces of S. phureja and 48 mapped SSRs. Results showed few significant pairwise LD values within chromosomes Population Structure based on Bayesian model provided evidence of a real population structure and suggested the presence of 10 subpopulations. Relationship among individuals from recent co-ancestry was also observed within subpopulations. More markers are needed to get a meaningful estimation of LD decay.

The research assistant responsible for the project received three weeks of individual training on statistical analysis for association mapping at the Institute of Genomic Diversity during June 2006.

CASSAVA

Martin Fregene, Paula Hurtado and Amparo Rosero, CIAT



Molecular patterns of 9 SSR markers out of the group of 100 selected for association studies in cassava

Overall progress summary: A sub-set of 200 cassava accessions was selected out of 800 lines generated by the breeding program in the last 15 years. Phenotypic information includes dry matter content, yield, harvest index, cyanide content, commercial number of roots and traits related with farmer's interest (branching number, plant height and root length). To estimate LD as a preliminary step towards association studies with the 200 accessions, 100 closely linked SSR markers were selected, based on their distribution in the 18 linkage groups of the cassava genetic map (between 2-10 SSR per LG).

Tangible outputs: 1) Compilation of phenotypic data for 200 varieties from cassava databases, 2) Genotyping of 185 cassava accessions with 85 SSR markers and 3) Scoring and database development for 138 accessions evaluated with 20 SSR markers.

YAM

Jean Louis Noyer (CIRAD), Vincent Lebot (VARTC) and Roger Malapa (VARTC)

An unexpected mixture of tubers of an unknown number of accessions disrupted the collection of phenotypic data in 2004 and 2005. A collection of 200 accessions was re-assembled, and the identification of clones is close to complete. Phenotypic data for the Vanuatu National Collection will be available for tuber descriptors and for resistance to anthracnose for the two last years.

Plant material for the present study comprises a sexual progeny of 124 C2 individuals. This material has been obtained through clonal propagation of mixed tubers from an initial set of 88 distinct F1 clones (C1) with no individual identification. Information regarding the genitors as well as the genitors themselves is not available.

Accessions used as genitors are usually described as 4x. However, in our study, it looks like the result of an open pollination between heterozygous diploids sharing some alleles. Ploidy level of cultitivated yams needs confirmation.

In spite of the difficulties, genotyping of the Vanuatu collection will be achieved in due time. Three-hundred polymorphic loci will be analyzed with both AFLP and SSR markers. The collection has already been characterized with IPGRI morpho-agronomic descriptors. The re-assembled collection has been characterized for the underground organs (yield, number of tubers, shape of tubers, outer and inner skin tuber color, tuber flesh color and presence of nematodes).

MUSA

Kodjo Tomepke (CARBAP), Nicolas Roux (IPGRI/INIBAP), M Carmen de Vicente (IPGRI)

The experimental layout is a one block model (as for field germplasm collection) with 4-5 mats per hybrid without replication. In dry season, the plants are submitted to a light supplementary watering. The hybrids were slightly treated against nematodes and black weevil but not against the Black Sigatoka. Parental clones were also involved in the experiment. Almost all the plants were grown for two consecutive crop cycles in the three locations (stations at Nyombe, Mbouroukou and Ekona). The following traits are recorded: number of functional leaves at flowering, number of leaves at harvest, height of the mother plant, circumference of the mother plant, bunch weight, number of hands, humber of fingers, length of finger, circumference of finger. Means and standard deviations will be calculated.

Two types of plant material are under evaluation, 1) 132 cultivars of plantain (AAB) representing the whole plantain germplasm and 2) four 4x/2x populations (AAAB x AA) totalizing 181 triploid hybrids. The results of using 9 SSR and AFLP markers to assess the genetic diversity of 30 plantains landraces confirmed a very narrow genetic base of this cultivar group.

Activities for the following months are as follows: 1) Extract the DNA from the four hybrid populations established at a location at CARBAP, 2) Send the DNA to DArT P/L in Australia for analysis with the Musa DArT, 3) Compile the agronomical data and calculate means and standard deviations for each trait and each clone, 4) Analysis of agronomic traits and DArT markers to examine association mapping.

COCONUT

Luc Baudouin (CIRAD)

A mission to Vanuatu in June 2005 allowed the collection of leaf samples from 219 individuals representing 4 breeding generations of the Vanuatu Tall cultivar. The first three generations were represented by 22 individuals each and the most advanced by 153 individuals whose pedigrees are partly known (the grand-parents are identified). Samples were analyzied with 347 DArT and 30 SSR markers. Phenotypic observations (fruit yield and composition + vegetative observations) are being performed at VARTC (Vanuatu).

A Bayesian method was used for calculating haplotype frequencies and various linkage disequilibrium parameters in Mendelian populations. The results indicate that LD is more likely to be observed and more intense in paired loci than between independent loci.

The next steps will be: 1) Splitting the populations into subsets and perform LD analyses on the subsets in order to minimize the effects of population structure, and 2) Adapting the Bayesian method to dominant markers in order to use it with DArT markers and to apply it to the above 219 individuals from Vanuatu.