Recombination and clonality in taro (*C. esculenta*):

implications for the evolution of cultivar diversity

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the distribution of allelic diversity in taro:

- how this diversity is distributed geographically within and between regions ?

- within and between cultivated and wild forms ?

- how did farmers create, identify and use, so many different morphotypes while true seeds are unknown to them ?

- what part of the variation is due to fixed somatic mutations accumulated during clonal evolution, and what part results from sexual recombinations ?

Exemples of morphological variability

to answer these questions :

(1) comparative data, covering a range of spatial and temporal scales, on both the genetic diversity of cultivars and the factors that can affect it;
(2) indicators of diversity that are relatively insensitive to sampling effects and adapted to a range of spatial and temporal scales;
(3) appropriate tools for analysis; and
(4) models for the evolution of diversity.

Lebot & Aradhya (1991) and Lebot *et al.* (1994) used isozymes on 1417 and 2081 accessions (cvs and wild)

Kreike *et al.* (2004) used AFLPs on 217 cultivars

SSR markers are highly reliable, co-dominant, and polymorphic for :

- evaluation of levels of heterozygosity within individuals and genetic distances between individuals.
- examination of the genetic relationships between accessions from different geographic origins.
- discussion of the respective roles of clonality and sexual recombination in the genetic diversity

Materials and Methods:

- 141 acc.: 102 acc. TANSAO core (previously analysed by Kreike et al. (2004)) & 39 acc. used as parents in the Vanuatu breeding program
- from a microsatellite-enriched library 49 sequences were identified, 35 primer pairs were designed using the software Primer3.
- 6 SSR markers revealing more than 10 alleles each were used to survey the 141 acc.
- an additional set of 16 loci was used to survey 39 acc. used as parents.

Traditional distinction between Asian and Pacific taros

Eddoe taros

Dasheen taros

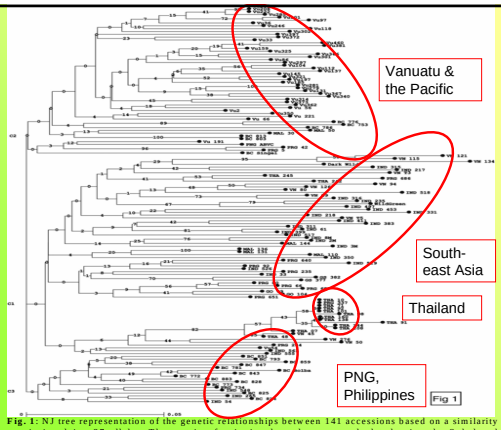

Fig. 1: NJ tree representation of the genetic relationships between 141 accessions based on a similarity matrix involving 87 alleles. The matrix of pairwise d_{i-j} values was calculated using the Sokal and Michener index.

Name	Island	Location	Ind. H°	Name	Island	Location	Ind.H°
VU 002	Pentecost	Martelli	0.68	VU 279	Santo	n.a.	0.68
VU 033	Pentecost	Martelli	0.55	VU 281	Santo	Matantas	0.73
VU 036	Pentecost	Martelli	0.64	VU 285	Santo	Matantas	0.64
VU 054	Pentecost	Martelli	0.55	VU 297	Tanna	Middle bush	0.59
VU 086	Santo	n.a.	**0.77**	VU 301	Tanna	Middle bush	0.59
VU 097	Santo	Najara	0.64	VU 302	Tanna	Middle bush	0.59
VU 101	Santo	Najara	0.64	VU 314	Tanna	Imaki	0.55
VU 104	Santo	Najara	0.59	VU 321	Santo	Pessena	0.77
VU 112	Santo	n.a.	0.64	VU 325	Santo	Pessena	0.59
VU 118	Santo	Jarakoru	0.55	VU 340	Santo	Pessena	0.77
VU 131	Santo	Jarakoru	0.77	VU 350	Santo	Pessena	0.59
VU 137	Santo	Malovira	0.64	VU 362	Santo	Pessena	0.59
VU 145	Santo	Ngoru	0.68	VU 366	Santo	Pessena	0.77
VU 159	Santo	Wusiroro	0.64	VU 367	Santo	Pessena	0.59
VU 185	Santo	Tjarahat	0.55	VU 372	Santo	Pessena	0.59
VU 197	Santo	Fanafo	0.64	VU 373	Santo	Pessena	0.68
VU 208	Malekula	Lamap	0.59	VU 381	Santo	Pessena	0.59
VU 219	Malekula	Lamap	0.59	VU 397	Banks	Qanqap	0.59
VU 222	Malekula	n.a.	0.59	VU 460	Tanna	Lowiakimak	**0.50**
VU 246	Santo	Valeteruru	0.55				

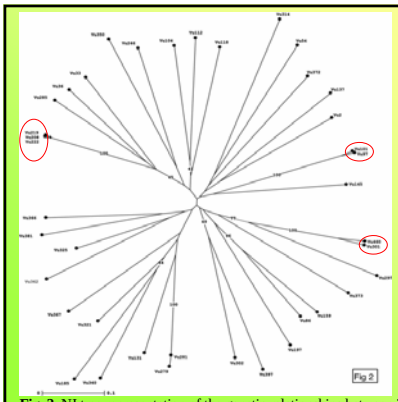

Fig. 2: NJ tree representation of the genetic relationships between 39 Vanuatu accessions based on a similarity matrix involving 134 alleles. The matrix of pairwise d_{i-j} values was calculated using the Dice index. Bootstrap values >40 are indicated.

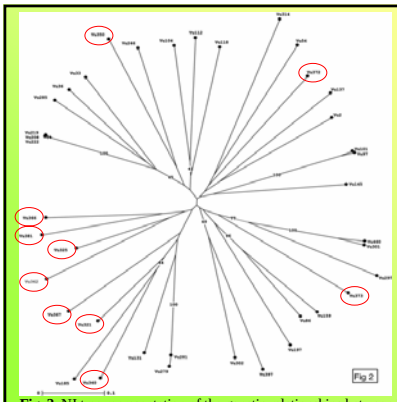

Fig. 2: NJ tree representation of the genetic relationships between 39 Vanuatu accessions based on a similarity matrix involving 134 alleles. The matrix of pairwise d_{i-j} values was calculated using the Dice index. Bootstrap values >40 are indicated.

Conclusions:

i) as expected, the microsatellite markers used in this study are locus-specific and locus duplication, if it occurs, is not sufficiently frequent to disrupt the analysis.

ii) despite some differences, the NJ tree based on microsatellite loci (fig. 1) and the UPGMA dendrogram based on AFLP data (Kreike *et al.* 2004) gave consistent results. An explanation for this qualitative agreement could be linked to the sampling itself:

The analysis of allelic frequencies gave unexpected information:

-with a high average of **14.5** alleles/locus, we observed a few (**1 to 4**) very common alleles and many rare ones at each locus.

-Even the Indonesian sample that was considered to be the most diverse showed the same distribution without covering the whole allelic diversity of the sample.

⇨ these observations suggest that the entire sample is issued from a **narrow genetic base** and future studies should include more wild populations including areas such as India or Yunnan.

iii) High diversity of Vanuatu parents unexpected: **2 to 18** alleles with mean of **6.1**

The accumulation of somatic mutations cannot solely explain this result:

☞ Role of **sexual reproduction**: high levels of heterozygosity and quasi-equal branch length between accessions (NJTree)

☞ Role of **clonality** (Meselson effect): multiplication of initially infrequent heterozygous genotypes (more vigourous). However, this leads to rare alleles.

iv) Results from SSR markers also confirmed those using AFLPs (Quero *et al*.,2004) regarding the absence of clear structure within the Vanuatu germplasm, with no correspondence between geographical origin and morpho-agronomical variation.

Many thanks for your attention!!