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**WORKING GROUP ON BIOCHEMICAL AND MOLECULAR
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**ASSESSMENT OF ESSENTIAL DERIVATION USING MOLECULAR MARKERS:
A TOMATO PILOT STUDY**

Document prepared by ASSINSEL

Assessment of essential derivation using molecular markers A tomato pilot study

During the BMT meeting of March 11-13, 1997, the first conclusion of an ASSINSEL model study on tomato was briefly presented (BMT/4/17):

The purpose of this new presentation is to give further details on the California processing tomato cluster, composed of 18 varieties. Two replicates were also included: E6203 and UC204c.

As indicated in Fig. 1 some information was available on the pedigree relationship among those varieties.

A genetic distance matrix was constructed from 136 AFLP-EcoRI, AFPL-PstI, RAPD and microsatellite markers and the MDS procedure was used for visualization of the molecular distance matrix in two dimensions. (The same approach was also used for morphological data). (See Fig. 2). Distances between replicate samples of UC204c and E6203 are not zero, indicating that a source of variation contributes to the differences observed.

It was then decided to compare pairs of varieties according to their genetic background.

E.D.V. candidates:

- Diego = selection in UC204c
- 204Mi = 5 back-crosses of Mi (nematode resistance) into UC204c
- Far73-82 = 3 back-crosses of I2 (Fusarium wilt race 2 resistance) into 7879.

Possible E.D.V.'s:

- UC82b - H1916: UC82b is parent for H1916
- UC82b-Cannery Row: UC82b is parent for Cannery Row

Not E.D.V.'s:

- UC122-Lassen
- UC165-Yuba

The comparisons were made for the various markers and the results are given in Fig. 3

For these selected pairs, the rank order of estimated distances is in agreement with the pedigree information, so genetic distances based on molecular markers may be useful in assessing essential derivation.

- The distances between the replicates of E6203 and UC204c and between UC204c and Diego are lower than 10% and the distances between the replicates of UC204c and between UC204c and Diego are almost identical.
- The distances between varieties and one of their parents but without any known back-crossing process are comprised 15-30%.
- With one exception for AFLP- EcoRI for the pair UC65-Yuba, the distance between unrelated varieties is higher than 30% and up to 50% and more.

However, errors attached to genome sampling, genetic impurity and laboratory practices are, at this moment, of a magnitude that almost prevents the feasibility of using molecular markers to assess essential derivation in tomato.

The following is then recommended:

- A re-assessment of laboratory errors should be made, probably using AFLP-Eco, the marker with the highest precision. Especially the occurrence of laboratory errors should be registered with high

precision.

- For assessing more accurately the relation between genetic distance estimates and pedigree, a greater number of candidate EDV pairs should be studied, together with cultivars known to be unrelated to the EDV pairs. It is crucial to define the population within which comparisons are to be made.
- For optimizing the size and informativeness of the marker set and for reducing genomic sampling errors, mapped markers should be investigated.
- The earliest procedure for EDV would be: use markers to estimate genetic distances between pairs of known relationship, where these pairs constitute the "threshold relationship" above which EDV would apply. The standard deviation of the genetic pairs can be used to construct confidence intervals.

That ASSINSEL document is based on:

- the publication "Comparison of molecular markers and morphological data to determine genetic distance among processing tomato varieties", by Julie Villand *et al.* (to be published by the end of 1998)
- the presentation "Feasibility of an EDV concept based on molecular markers in tomato - a pilot study", made by Fred van Eeuwijk at the ASSINSEL Congress in June 1998.

Fig. 1: Available pedigree relationships among California processing tomato varieties used to understand the ability morphological and molecular markers estimated genetic relationships

Two varieties, UC204c and E6203, were replicated in the study

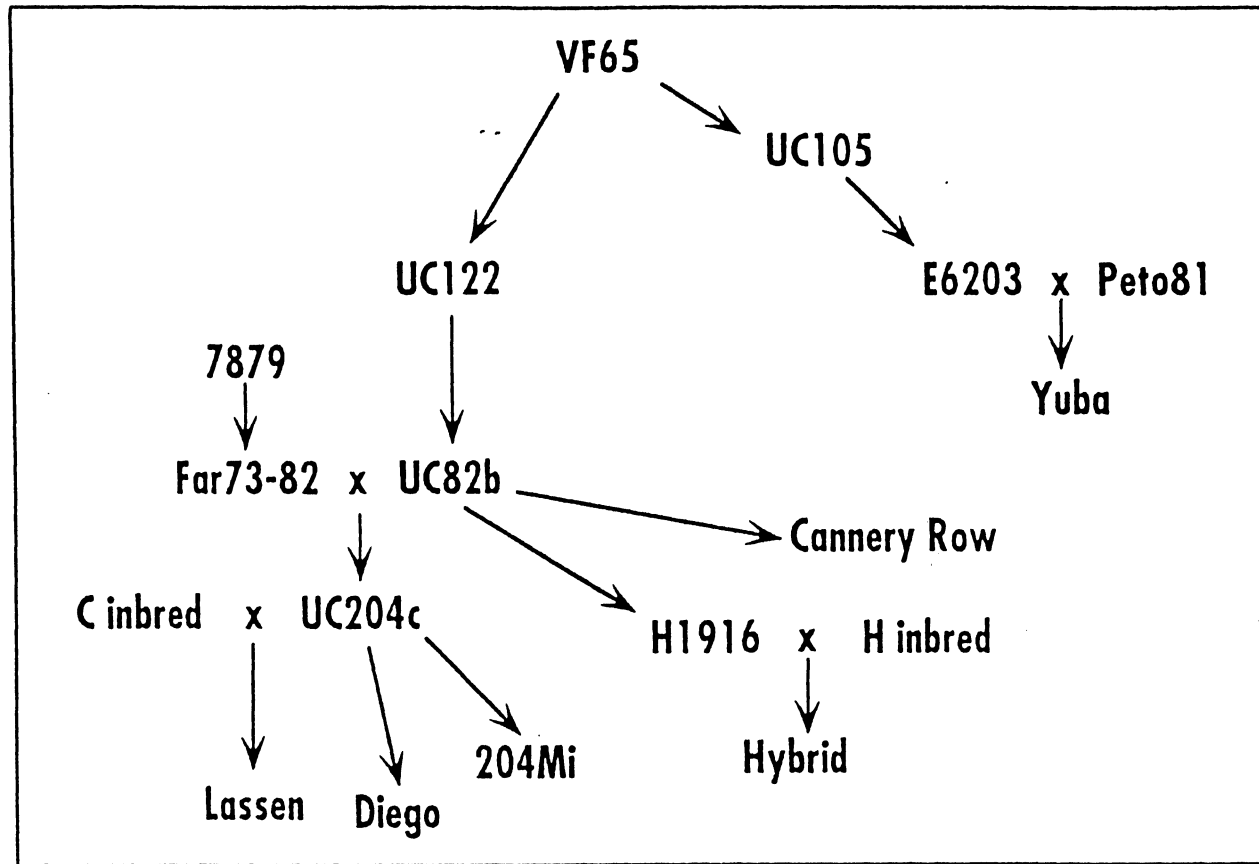


Fig. 2: MDS plots of genetic distances among 20 California processing tomato varieties analyzed using either morphological traits or a combined set of AFLP - EcoRI, AFLP - PstI, RAPD and microsatellite molecular markers (Replicated varieties are indicated with a filled circle)

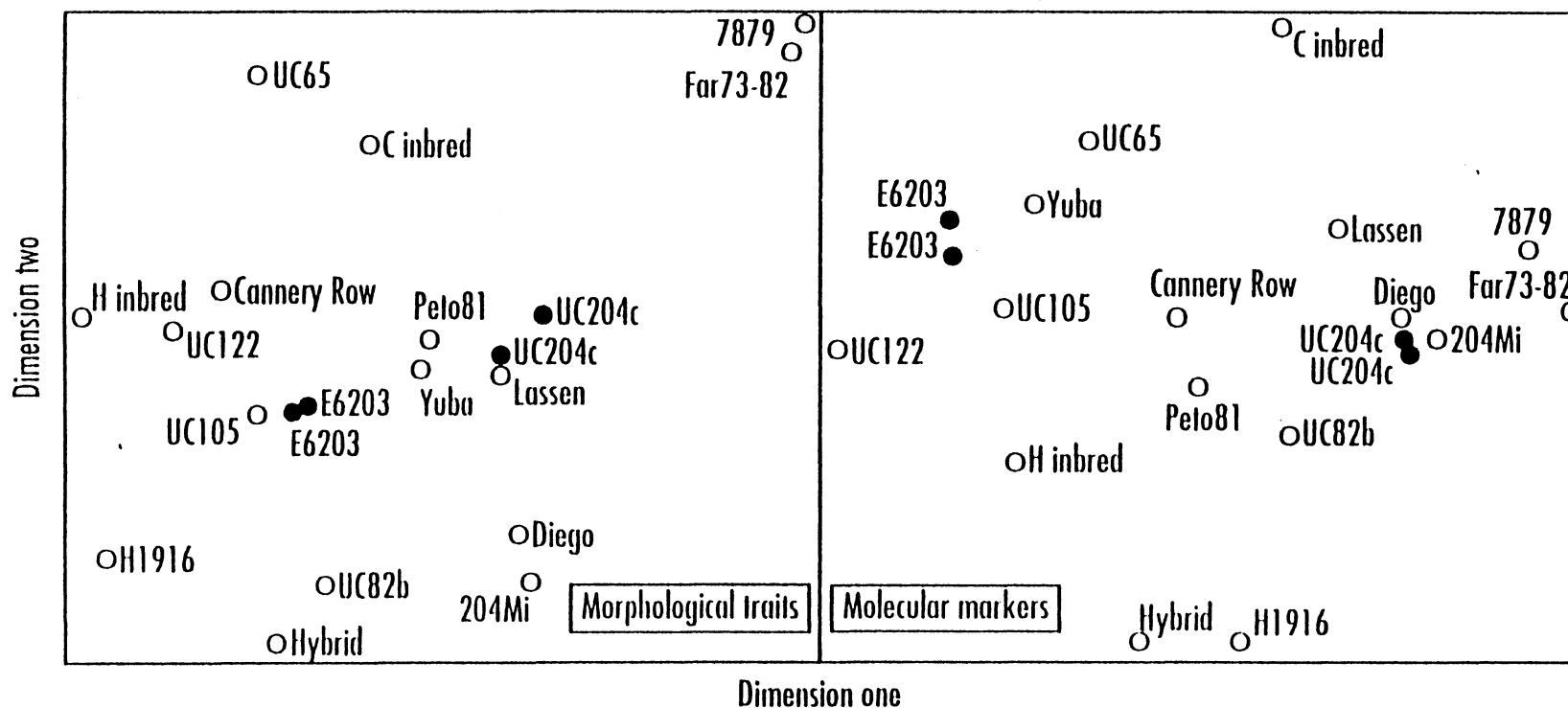


Fig. 3 Distance estimates among key comparisons of California processing tomato varieties using molecular and morphological data

