



Disclaimer: unless otherwise agreed by the Council of UPOV, only documents that have been adopted by the Council of UPOV and that have not been superseded can represent UPOV policies or guidance.

This document has been scanned from a paper copy and may have some discrepancies from the original document.

Avertissement: sauf si le Conseil de l'UPOV en décide autrement, seuls les documents adoptés par le Conseil de l'UPOV n'ayant pas été remplacés peuvent représenter les principes ou les orientations de l'UPOV.

Ce document a été numérisé à partir d'une copie papier et peut contenir des différences avec le document original.

Allgemeiner Haftungsausschluß: Sofern nicht anders vom Rat der UPOV vereinbart, geben nur Dokumente, die vom Rat der UPOV angenommen und nicht ersetzt wurden, Grundsätze oder eine Anleitung der UPOV wieder.

Dieses Dokument wurde von einer Papierkopie gescannt und könnte Abweichungen vom Originaldokument aufweisen.

Descargo de responsabilidad: salvo que el Consejo de la UPOV decida de otro modo, solo se considerarán documentos de políticas u orientaciones de la UPOV los que hayan sido aprobados por el Consejo de la UPOV y no hayan sido reemplazados.

Este documento ha sido escaneado a partir de una copia en papel y puede que existan divergencias en relación con el documento original.



BMT/4/17

424

ORIGINAL: English

DATE: February 17, 1997

INTERNATIONAL UNION FOR THE PROTECTION OF NEW VARIETIES OF PLANTS

GENEVA

**WORKING GROUP ON BIOCHEMICAL AND MOLECULAR
TECHNIQUES AND DNA-PROFILING IN PARTICULAR**

Fourth Session

Cambridge, United Kingdom, March 11 to 13, 1997

CONCLUSIONS OF A MODEL STUDY ON ESSENTIAL DERIVATION USING
TOMATO AS A CROP

Document prepared by ASSINSEL

CONCLUSIONS OF A MODEL STUDY ON ESSENTIAL DERIVATION USING TOMATO AS A CROP

Preamble

This model study was undertaken to provide information that can be used in the development of guidelines for the interpretation of the concept of 'Essential Derivation', which was adopted in the 1991 Act of the International Union for the Protection of New varieties of Plants (UPOV).

Under the UPOV 1978 Act any protected variety may be freely used as an initial source of variation for the breeding of another variety and any such newly developed variety could be commercialized without an obligation towards the breeder of the initial variety, under the condition that the newly developed variety fulfills DUS criteria. Such rules did not prevent a person from finding a mutation or selecting a minor variant in a protected variety from claiming full protection for such a finding. Modern biotechnology greatly increased the likelihood of such 'abuse' by adding a new gene to the initial variety.

To discourage this practice, which was commonly felt as being unfair to the breeder of the initial variety, the concept of essential derivation was embodied in the 1991 UPOV Act. In Chapter 5, Article 14(5) of this Act the rights of the breeder are defined and extended to essentially derived varieties, which require the authorization of the breeder of the initial variety.

According to the 1991 Act a variety is essentially derived when it is predominantly derived from the initial variety, and when it can only be distinguished from it by differences resulting from the act of derivation. For the remainder of the genotype, the expression of essential characteristics conform the initial variety.

The model study in tomato was undertaken to provide background information that could be used in establishing the degree of genomic conformity between an initial and resulting variety that would result in essentially derived. When the project was started little was known about the usefulness of any given molecular marker technology to describe genetic variation in tomato. Nevertheless, molecular markers were thought to provide a potential new instrument to assist in the estimation of genomic conformity and therefore essential derivation.

Introduction

Tomato was chosen as a model crop for this study on essentially derived varieties. The study was financially supported by the American Seed Trade Association, Dutch Seed Trade Association, French Seed Trade Association, Japan Seed Trade Association and Israeli Seed Trade Association.

Tomato was selected as it presented a special challenge for the use of molecular markers in estimating genomic conformity between varieties. At the time the project started very little polymorphisms were found for RFLP loci among cultivated varieties. It was however known that other marker technologies, notably RAPD, micro-satellites and AFLP showed higher levels of polymorphisms between closely related lines. Additionally, tomato had a number of assets which made it attractive for this study. The crop is well characterized genetically for mutants and traits of agronomic interest, it is economically of great importance, and, amongst horticultural species, tomato had been developed most as a model crop for molecular studies.

For this study three clusters of genotypes were selected, each composed of 15 different genotypes. The three variety clusters were based on the Moneymaker and Montfavet fresh market ideotypes (respectively for protected and open field cultivation) and on the California processing ideotype.

Phenotypic data were collected on the California cluster. Molecular analyses on the three clusters were conducted by Keygene, the Netherlands and the Department of Plant Breeding, Cornell University, USA using AFLP, RAPD and microsatellite technology. All molecular data were analyzed independently by the Department of Horticulture, University of Wisconsin and the Center for Plant Breeding and Reproduction Research, the Netherlands Department of Agricultural Research (CPRO-DLO).

Pedigree information was available for the variety cluster of California processing tomatoes. No such information could be made available for the other two clusters.

Objectives

The main objectives of this study are:

- to establish the suitability of different molecular marker techniques for determining genomic conformity between varieties;
- to verify the reliability and effectiveness of the before-mentioned methods in establishing a relationship between genomic conformity and variety relatedness, independent of the sample of tomato genotypes chosen;
- to establish the number and genomic distribution of molecular markers required for a reliable estimate of the genomic conformity between varieties;
- to establish methods for the assessment of thresholds for determining the level of derivation between varieties, taking into account experimental error and within-variety genetic variation.

Conclusions

- Assignment of individual varieties to one of the three variety ideotype clusters (Moneymaker, Montfavet and California processing) was possible with either phenotypic or molecular data. The same variety clusters were discerned using each of the three molecular techniques.
- For the California cluster, where phenotypical data was available, it was shown that discriminatory power between phenotypic data and molecular technologies were comparable.
- Within the obtained data sets from different molecular technologies the information content and error variance were similar.
- Between 150-200 bands of discriminatory molecular marker data will be required to achieve a satisfactory and reliable difference between varieties (confidence interval of $\pm 5\%$).
- Varieties in the California cluster showed higher intra-variety banding variation than the varieties in the Moneymaker and Montfavet clusters. This is due to the fact that at least some of the varieties in the California cluster were developed using mass selection. Phenotypic uniformity is less crucial in the latter type.
- All duplicate variety samples showed some degree of heterogeneity in marker pattern, resulting in estimates of mean between-plant-within-variety distance from 0.6% (Montfavet) to 6.3% (UC204b). It is obvious that none of the selected varieties is fixed for its molecular banding pattern.
- For the American cluster a clear link existed between deduced marker pattern and relatedness based on the known genealogy.
- The precise assessment of threshold levels for essential derivation is hampered by the design of this study and remaining statistical problems.

Recommendations

- The solving of the issue of essential derivation, as established by the UPOV 1991 Act needs ample attention. It is an important concept to the prevention of abuse of protected varieties.
- A proposal for an action plan for further studies should be developed which contains the issues identified in the current project. The goal should be resolution of the issue of how to establish threshold levels for essential derivation.

- In such a proposal special attention needs to be given to i) the handling of redundancy of bands and avoidance of over-/undersampling of certain parts of the genome, ii) the constitution of the reference population to assess relation between genomic conformity, genealogy and breeding history.
- In addition to further study on tomato, a project on self-pollinated species such as lettuce, beans or peas could be considered.
- The follow-up study should take into account the principles adopted in the ASSINSEL position paper on the use of DNA profiling for assessing genomic conformity (see document BMT/4/6).

[End of document]