GENETIC VARIATION IN *TETRANYCHUS URTICAE*: EVIDENCE FOR HOST-RACE FORMATION?

R. Geerts, T. van Opijnen & J.A.J. Breeuwer

University of Amsterdam, Institute for Systematics and Population Biology
Kruislaan 320, 1098 SM, Amsterdam

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Summary
Based on genetic variation, host-race formation on two host plant species within a small area (0.064 km^2) in the two-spotted spider mite *Tetranychus urticae* was shown. Crossing relationships between mites collected from different host plants did not result into significant differences in sex-ratio and number of hatched eggs. The populations were not reproductively isolated.

INTRODUCTION

The two-spotted spider mite *Tetranychus urticae* Koch (Acari: Tetranychidae) is found on several host plant species throughout the world. It is not clear if populations of *T. urticae* consist of true polyphagous arthropods or if they are formed by a mixture of oligophagous populations. Genetic variation between populations from different host plant species may provide information about host-race formation in sympatry. Crossing relationships were tested between populations that were also used in the AFLP-analysis.

MATERIALS & METHODS

Originally, the mite populations used in the RAPD analysis were collected from two different host plant species in Geversduin (0.064 km^2), the Netherlands in 1997. The mites used in the AFLP-analysis were collected from two different host plant species in the same area in 1998. The mites were reared on bean leaves (t=23°C, RH=60-70%, L:D=16:8).
DNA of female mites was isolated using the CTAB method (Philips & Simon, 1995). RAPD-PCR was done as described by Edwards *et al.* (1997). Four primers were used (OPC2, OPC5, OPD20, OPF4, Operon Technologies Inc.). The amplification products were separated by electrophoresis on a 2% agarose gel. After staining with ethidium bromide, the DNA bands were visualised under UV-light.
AFLP was done following a modification of the procedure by Vos *et al.* (1995) with the primers EcoRI+AC and MseI+CTT, extended resp. with two and three selective nucleotides.
For both RAPD and AFLP individual loci were scored as band present (1) or absent (0). In both studies bands of similar size were assumed to represent the same locus with two alleles. The RAPD data consisted of 22 polymorphic loci, the AFLP-data of 30 polymorphic loci out of 53. The data were analysed with Popgene Version 1.21 (Yeh *et al.*, 1997) by bootstrapping the data matrix. UPGMA diagrams were based on simple matching with unbiased genetic identity and genetic distance (Nei, 1978).
From three populations used in the AFLP-analysis intra- and interstrain isofemale lines were produced by crossing single pairs of females and males to test crossing relationships. Differences in sex ratio and eggs hatched were tested with a Mann-Whitney U test.

RESULTS & DISCUSSION

In both analyses, genetic variation was present. Especially the AFLP data analysis clearly showed two spider mite strains each linked to their own host plant species (figure b). The dendrogram obtained with RAPD data showed a mixture of both plant types (figure a) which may be due to the interpretation difficulties of the presence/absence of some bands on the gel as well as the small number of loci.

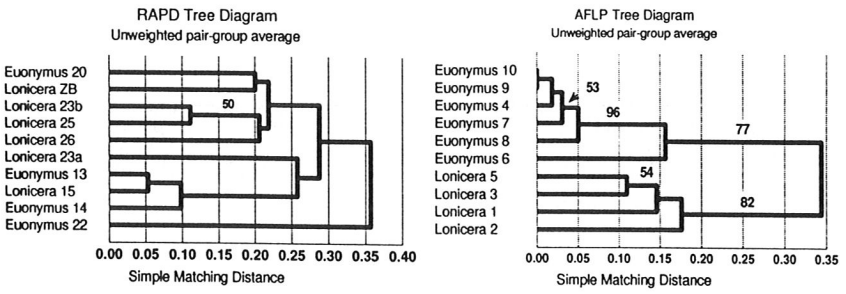

figure a figure b

The UPGMA diagrams obtained with the RAPD data (a) and the AFLP data (b). Bootstrap values of more than 50% are shown above the branches.

Mites from different host plants produced viable progeny. The mites were not reproductively isolated, since there were no significant differences in sex-ratio as well as hatched eggs. The host races may be isolated rather recently.

CONCLUSIONS

AFLP-analysis demonstrated host-race formation of *T. urticae* on two host plant species within a small area. The resolution depends on the molecular technique and the number of markers used. Mites from different host plant species were not reproductively isolated.

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