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Enzyme Variability in Populations of Aphids

J. Tomiuk and K. Wöhrmann
Institut für Biologie II, Lehrstuhl für Populationsgenetik der Universität Tübingen (Federal Republic of Germany)

Summary. From 1976 to 1978 nine aphid species were investigated electrophoretically. A low degree of polymorphism was found. Only 5 of the species were polymorphic, and only at most in 3 enzyme systems out of 19.

Key words: Aphids – Parthenogenesis – Allozyme variation – Polymorphism

Introduction

In comparison with other subjects genetic investigations on aphid populations are rare, although aphids are of great importance as agricultural and horticultural pests. Furthermore aphids are an interesting subject for evolutionary and population genetic studies due to their use of parthenogenetic propagation, and their use of a multiplicity of host plants.

Recent publications have been mainly concerned with the interaction of esterase activity and resistance to organophosphorus insecticides in *Myzus persicae* (Sulzer) (Baker 1977; Beranek 1974; Beranek and Berry 1974; Beranek and Oppernoorth 1977; Needham and Sawacki 1971; Sudderuddin 1973). Blackmann and Takada (1977) and Blackmann et al. (1978) described a chromosomal polymorphism including a translocation between autosomes 1 and 3. Translocation heterozygotes were shown to occur in samples collected from all over the world.

Results of investigations considering evolutionary and population genetic aspects have been published by Baker (1977, 1978, 1979), Tomiuk et al. (1979), Wöhrmann et al. (1978) and Wool et al. (1978). Baker (1977) and Wool et al. (1978) reported of variations in electrophoretic mobility of two esterase loci in *Myzus persicae* and found also differences in the activity of these enzymes in the same species.

In this publication the degree of the enzyme polymorphism of nine species will be given. 19 enzyme systems were attempted with a maximum of 18 successes for one species, and a lesser number for other species. Staining of 14 other enzymes has been attempted, with success in only 4 cases: due to the small sample size these results are not included in this report.

Materials and Methods

The aphids investigated were collected in the South-West of Germany, mainly in the vicinity of Tübingen. From 1976 to 1978 samples from different hosts, localities and at different dates were collected at random in avoidance to take one sample from only one clone. Starch gel electrophoresis was used to determine enzyme mobility patterns, using a modified version of the method of Ayala et al. (1972). The following enzyme systems were investigated: malate dehydrogenase (MDH), phosphoglucomutase (PGM), α-glycerophosphate dehydrogenase (α-GPDH), malic enzyme (ME), glucose-phosphate isomerase (PGI), aldolase (ALD), hexokinase (HK), isocitrate dehydrogenase (IDH), 6-phosphogluconate dehydrogenase (6-PGDH), leucin amino peptidase (LAP), alkaline phosphatase (APH), catalase (KAT), glyceraldehyde-3-phosphate dehydrogenase (G-3-PDH), glucose-6-phosphate dehydrogenase (G-6-PDH), esterase (EST), sorbitol dehydrogenase (SDH), fructokinase (FK), acid phosphatase (ACPH) and fumarase (FUM).

Results and Discussion

Experimental results are listed in Tables 1 and 2. The number of individuals investigated ranged from 18 in the smallest to 5000 in the largest samples. The number of loci found in each system is shown, and those which are polymorphic are indicated. In contrast to the accepted definition, a locus is described as polymorphic only if more than one allele could be demonstrated. So far it has not been possible to carry out a genetic analysis by crossing individuals with different enzyme patterns. Therefore two groups of enzyme data are under consideration. First-

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ly, enzyme polymorphism could be detected by electrophoresis but without more genetic information the polymorphism could not be explained without doubt. This group involves *Aphis fabae* and *Acyrthosiphon pisum*. Thus, no genotype frequencies and average heterozygosity are calculated. Secondly, the genetic behaviour of loci can be determined by analogy with work on *Drosophila* and other species. There is no problem in a system involving 2 alleles where all 3 possible genotypes are found. Furthermore, if a pattern consists of two bands and these occur in all individuals, each band is probably determined by one locus: it is improbable that, in the case of holocyclic propagation, one or several populations consist exclusively of heterozygotes. The average data from 1976 to 1978 and from all localities of *Macrosiphum rosae, Aphis sambuci* and a third species are given in Table 3. The average heterozygosities of all three species agree and within these species only a value of 0,04 could be found approximately. However, *Acyrthosiphon pisum* is the most polymorphic of the species investigated, with 3 polymorphic loci out of a total of 6 loci. *Macrosiphum euphorbiae, Aphis pomi, Rhodobium porosum* and *Macrosiphum funestum* showed no polymorphism. In total 10 out of 111 loci (about 9%) are polymorphic. Even in the case of an overestimation of the number of loci, this is a very low percentage in comparison to most other subjects which have been investigated so far (Nevo 1978). This result is in agreement with those published by Wool et al. (1978), who found polymorphism only in the esterase system in *Myzus persicae*; they investigated 11 enzyme systems.

Table 1. The total number of loci (a) and the number of polymorphic loci (b) of enzyme systems found in the samples of size n of *Macrosiphum rosae* and *Aphis fabae*

Enzyme	*M. rosae*			*A. fabae*		
	a	b	n	a	b	n
MDH	2	1	5000	2	–	541
PGM	2	1	5000	2	–	189
α-GPDH	1	–	5000	1	–	541
ME	1	–	5000	1	–	541
PGI	1	–	5000	1	–	189
ALD	1	–	1000	1	–	352
HK	2	–	150	2	1	126
FK	1	–	150	1	–	126
IDH	2	–	200	2	–	88
6-PDGH	1	–	120	1	–	88
LAP	–	–	–	2	–	88
APH	1	–	120	1	–	352
KAT	1	–	80	1	–	66
G-3-PDH	1	–	200	1	–	40
G-6-PDH	1	–	200	1	–	40
Est	–	–	–	3	1	402
ACPH	1	–	160	1	–	88
FUM	1	–	120	1	–	88

It may be argued that parthenogenesis leads to monomorphism caused by selection. However, Suomolainen et al. (1976) published data from investigations on some exclusively parthenogenetic insects, which demonstrate a very high degree of polymorphism within and between populations. In the case of *Otiorrhynchus scaber* the authors found 11 out of a total of 20, and in *Adoxus obscurus* 5 out of 16 loci to be polymorphic. This genetic variability is explained as being established by mutations and being stored during the evolution of the parthenogenetic species. Hebert (1974) found polymorphism in *Daphnia magna* in esterase, malic enzyme and alkaline phosphatase. The proportion of polymorphic loci in 3 natural populations of the cyclically parthenogenetic species *Simocephalus serrulatus* was described by Smith and Frazer (1976) to be between 33 and 60%; they investigated 16 loci.

Most of the aphid species considered in this paper are holocyclic. A parthenogenetic phase, with the chance of strong differential selection of certain genotypes, is fol-

Table 2. The total number of loci (a) and the number of polymorphic loci (b) of enzyme systems found in samples of size n in *Macrosiphum euphorbiae*, *Macrosiphum funestum*, *Aphis pomi*, *Aphis sambuci*, *Acyrthosiphon pisum* and a species on rosa which is probably *Wahlgreniella nervata* (tentative identification)

Enzyme	*M. euphorbiae*			*M. funestum*			*A. pomi*			*A. sambuci*			*A. pisum*			*R. porosum*			*W. nervata*		
	a	b	n	a	b	n	a	b	n	a	b	n	a	b	n	a	b	n	a	b	n
MDH	2	–	432	2	–	20	2	–	2228	2	–	61	2	1	43	2	–	50	2	1	274
PGM	2	–	432	2	–	20	2	–	1852	2	1	61	2	–	46	2	–	51	2	1	274
α-GPDH	1	–	432	1	–	20	1	–	2228	1	–	39	1	1	24	1	–	47	1	–	274
ME	1	–	432	1	–	20	1	–	2228	1	–	41	1	–	35	1	–	57	1	–	221
PGI	1	–	432	1	–	20	1	–	100	1	–	61	1	1	46	1	–	41	1	–	221
ALD	1	–	432				1	–	100	1	–	18				1	–	41	1	–	221
HK							2	–	438	–	–	–				–	–	–	–	–	–
IDH							2	–	2228	–	–	–				2	–	39	2	–	53
6-PGDH										1	–	20				1	–	44			
LAP																2	–	36			

Table 3. The allele frequencies of MDH (slow (s) and fast (f)) and of PGM (slow (s), intermediate (i) and fast (f) and the average heterozygosities of the samples of *Macrosiphum rosae*, *Aphis sambuci* and probably *Wahlgreniella nervata* from 1976 to 1978. The number of all investigated loci is listed

Species	MDH		PGM			Loci	Average heterozygosity
	s	f	s	i	f		
M. rosae	0.432	0.567	0.02	0.77	0.21	20	0.044
A. sambuci	–	–	0.367	–	0.633	9	0.037
W. nervata	0.351	0.649	0.340	0.437	0.223	10	0.037

lowed by sexual reproduction with the possibility of rearrangement of the genetic material. *Macrosiphum euphorbiae*, and the other species in favorable natural conditions, show anholocyclic reproduction. There is no obvious difference, however, between the degree of polymorphism in these 2 groups. It therefore seems that parthenogenesis per se cannot be solely responsible for the low degree of enzyme polymorphism in aphid populations.

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J. Tomiuk
Prof. Dr. K. Wöhrmann
Institut für Biologie II
Lehrstuhl für Populationsgenetik
Auf der Morgenstelle 28
D–7400 Tübingen (Federal Republic of Germany)