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MORPHOMETRIC DISCRIMINATION OF HOST-ADAPTED POPULATIONS OF *BRACHYCAUDUS HELICHRYSI* (KALTENBACH) (HEMIPTERA APHIDIDAE)

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Madjdzadeh S.M., Mehrparvar M., Abolhasanzadeh F. – Morphometric discrimination of host-adapted populations of *Brachycaudus helichrysi* (Kaltenbach) (Hemiptera Aphididae).

Brachycaudus helichrysi is a world-wide polyphagous pest which has economic importance. The study was based on field samples of *B. helichrysi* collected from different host plants. Twenty two morphological characters were measured. The aphid populations were separated using discriminant function analysis. Based on this analysis the aphid individuals associated with *Pulicaria dysenterica* (Asteraceae) were completely separated from other populations. In addition, individuals associated with *Crepis sancta* (Asteraceae) showed considerable morphological divergence and were separated from other populations. The results demonstrated that the morphology of *B. helichrysi* has been affected by its host plants. A stepwise canonical variates analysis selected four morphological characters from which two showed the highest contribution to the separation of host-adapted populations, and 84.8% of individuals were reclassified correctly into their original populations. The results demonstrated that three host adapted biotypes exist within *B. helichrysi*. The overall conclusion is that morphological divergence has been occurred in *B. helichrysi* populations associated with different host plants.

KEY WORDS: *Brachycaudus helichrysi*, Aphididae, Morphometric, Host-adapted biotypes, Morphological variation.

INTRODUCTION

Aphids are a group of herbivorous insects which have been considered as pests of agriculture, horticulture and forestry (BLACKMAN and EASTOP, 2007). They have achieved some adaptations in relation to host plants. Many aphid taxa have a biological complexity in their life cycle (MARTIN and BROWN, 2008). This has led to the occurrence of several distinct morphs in most aphid taxa which make their identification difficult.

Among different groups of aphids many cryptic species have been recognised (BLACKMAN and EASTOP, 2007; DRES and MALLET, 2002). Most aphid species comprise a set of closely related populations which may have diverged genetically so that they could be considered as host races, incipient or sibling species (or subspecies) (LOZIER *et al.*, 2008; FEDER *et al.*, 1998). The recognition of these divergent populations can help to understand their ecology and evolution and thereby to devise effective biological control programmes. Aphids have undergone morphological and physiological changes in order to live on different host plant species. In other word they show a very high degree of host-specific behavioural adaptations.

The members of different species within the genus *Brachycaudus* are difficult to identify because of reduced morphology and also their association with host plants. *B. helichrysi* is associated with many host plants in the Asteraceae and also in other plant families (BLACKMAN and EASTOP, 2006). There has been little work on intraspecific variation in this species.

So far no morphometric studies of morphological variations in *B. helichrysi* associated with various host plants have yet been carried out. Multivariate morphometric techniques could help to discriminate between populations and/or species of aphids from a taxonomic point of view (DALY, 1985). Several morphometric studies have been carried out on aphids (e.g. BLACKMAN and SPENCE, 1994; BLACKMAN, 1987; MARGARITOPOULOS *et al.*, 2006). The purpose of the present study was to find out the relative effects of host plant species on morphological characters of the *B. helichrysi*.

MATERIALS AND METHODS

Sampling was carried out in Kerman province which is located in south-eastern Iran. The study was based on field samples of *B. helichrysi* collected from different host plant species: *Crepis sancta* (Asteraceae), *Calendula* sp. (Asteraceae), *Pulicaria dysenterica* (Asteraceae), *Nonnea* sp. (Boraginaceae) and *Anchusa capensis* (Boraginaceae). Since environmental conditions can affect the morphology of aphids, all of the studied samples were collected from an area which has similar climatic conditions. Sampling data such as host plant name, feeding site, color of the live specimens, locality, date, biological information and GPS data were recorded at the time of collection. Specimens were preserved in ethanol 80% just after they were collected in the field. Adult apterous viviparous specimens of *B. helichrysi* were cleared and mounted in Canada balsam on microscopic slides. Twenty two morphological characters were scored (Tab. 1). All morphological measurements were made using a phase contrast microscope (ZEISS, Axiostar, Germany) fitted with a calibrated micrometer eyepiece. Multivariate morphometric analysis (discriminant function analysis or canonical variates analysis) was performed using the statistical package SPSS Software, version 12.

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Table 1 – Morphological characters used for morphometric analysis of populations of *Brachycaudus helichrysi*.

Character No.	Character	Character No.	Character
1	Body length	12	2nd segment of hind tarsus length
2	Antennal segment I length	13	Siphunculus length
3	Antennal segment II length	14	Basal diameter of siphunculus
4	Antennal segment III length	15	Cauda length
5	Antennal segment IV length	16	Basal diameter of cauda
6	Antennal segment V length	17	Hind femora length
7	Basal part of antennal segment VI length	18	Hind tibia length
8	Processus terminalis length	19	Proportion of character No. 13 to 14
9	Antennal flagellum length	20	Proportion of character No. 15 to 16
10	Ultimate rostral segment length	21	Proportion of character No. 8 to 7
11	Basal diameter of ultimate rostral segment	22	Proportion of character No. 10 to 12

RESULTS AND DISCUSSION

A summary of canonical discriminant functions considering 22 morphological characters for *B. helichrysi* populations associated with host plant species is given in Table 2, including the levels of variance and the significance for three functions. Low values of Wilks' Lambda test and statistically significant chi-square values show that, in particular the first two functions are significant predictors. The first function accounted for 85.2% and the second function for 12.1% of the total variation in the data.

Table 3 shows the standardised canonical discriminant function coefficients that determine the relative importance of the characters in discriminating the populations. The characters processus terminalis length and siphunculi length show the highest magnitudes at function 1. The first two functions contribute most to the separation between populations. As a whole 84.8% of *B. helichrysi* individuals were reclassified correctly into their original groups. A plot of the first two functions (Fig. I) showing the degree of inter-population differences. The population associated with *Pulicaria dysenterica* is separated from other populations without overlaps on function 1.

The observed morphological differences among aphid individuals associated with *P. dysenterica* is possibly due to the fact that the plant has secondary metabolites, that can change the chemical components of the plant. So that this could change the composition of plant sap which is the diet of aphids. This different diet can affect indirectly the morphological characters of related aphids. CVA has proved to be a powerful technique that helps to resolve taxonomic difficulties in closely related taxa (MARGARITOPOULOS *et al.*, 2007; LOZIER *et al.*, 2008; BARBAGALLO and COCUZZA, 2003). The morphological separation in this study is mostly due to host-related differences, although the contribution of environmental factors might be considered (MARGARITOPOULOS *et al.*, 2000). However it must be mentioned that morphological variation alone is not adequate for resolving taxonomic relationships among aphids.

Table 3 – Standardized canonical discriminant function coefficients for the first three functions on the basis of *Brachycaudus helichrysi* populations.

Character	Function		
	1	2	3
Antennal segment I	0.513	0.910	-0.204
Processus terminalis	1.041	-0.440	0.112
Siphunculi length	-0.824	-0.557	0.337
Cauda /basal width of cauda	-0.042	0.615	0.879

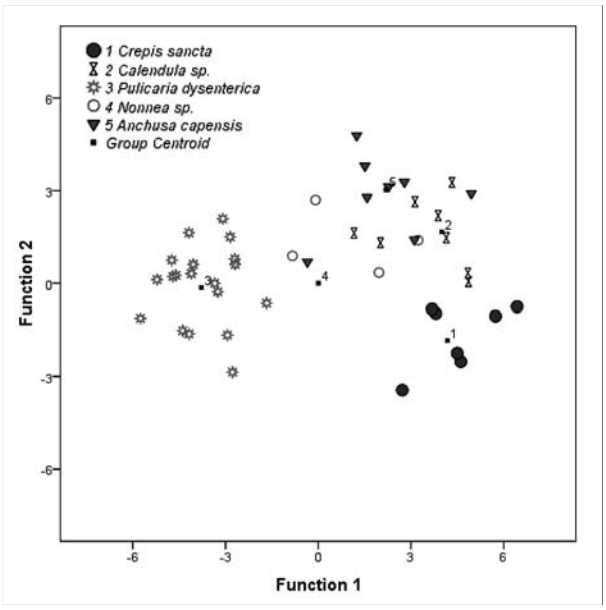

Fig. I – Scatter-plot of the scores of the first two canonical variates for populations of *Brachycaudus helichrysi* associated with different host plants.

Generally, there is no previous study of host-associated genetic variation and reproductive isolation within samples under study to support our view. So, more investigations are needed, especially involving DNA techniques, before exact conclusions are drawn.

Table 2 – Canonical discriminant functions of *Brachycaudus helichrysi* populations associated with different host plants.

Function	Eigenvalue	% of Variance	Wilks' Lambda	Chi-square	df	Sig.
1	17.488	85.2	0.010	87.417	12	.000
2	2.493	12.1	0.186	31.992	6	.000
3	0.542	2.6	0.649	8.228	2	.016

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