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The application of discriminant analysis to identify *Cryptomyzus* aphids

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Abstract

Aphids of the species *Cryptomyzus galeopsidis* (Kaltenbach) and *Cryptomyzus maudamanti* Guldemon are very similar morphologically, although their summer host specificity is different. The host plants of *C. galeopsidis* are *Ribes rubrum* or *R. nigrum* and *Galeopsis* sp., while *C. maudamanti* feeds on *R. rubrum* and *Lamium galeobdolon*. Canonical discriminant functions are proposed for identification of these aphid species, especially in the cases when host plants are unknown. Canonical discriminant functions presented in the identification key to European species of the genus *Cryptomyzus* appeared to be not as effective as they were supposed to be. They allowed correct classification not of 90% of *C. galeopsidis* individuals with studied life cycle, but of 64.6% instead. Measurements, counts and ratios characterized by weak or very weak correlation (correlation coefficient $|r| < 0.5$) with body length were used for the forward stepwise discriminant analysis. Canonical discriminant functions for both apterous and alate viviparous females of *C. galeopsidis* and *C. maudamanti* enabling separation of 90–100% individuals of these species were obtained through the forward stepwise discriminant analysis of selected characters.

Key words: *Cryptomyzus galeopsidis*, *Cryptomyzus maudamanti*, aphids, morphology, discriminant analysis.

Introduction

Aphids (Hemiptera: Sternorrhyncha: Aphidoidea) are small-sized mostly sedentary colonial phytophagous insects, some of their species are well-known as pests of agriculture, horticulture and forestry. Complex life cycles of aphids are characterized by several different adult morphs emerging during the season and well-defined host specificity. Moreover, there are plenty of aphid species shifting host plants during the season. Genotype that in other groups of animals would be characteristic only of one individual considerably increases due to diploid parthenogenesis and fast rate of reproduction in aphids (Heie, 1987). Aphids not only damage the plants directly by feeding on phloem or parenchyma sap, but also transfer virus diseases (Minks, Harrewijn, 1987). For this reason precise aphid species identification is very important before decisions on measures of plant protection from pests can be made.

Aphid identification requires the complex of various characters: host plant species in the par-

ticular period of the season, the appearance of the colony and its location on plant, the colour of live aphids and the pattern of sclerotization, shapes of some structures and absolute and relative lengths of some parts of the body. Discriminant analysis is often used in aphid taxonomy, especially when species are difficult to distinguish (Guldemon, 1991; Tizado, Nieto Nafria, 1994; Rakauskas, 1998; Turčinavičienė, 2000; Barbagallo, Cocuzza, 2003). However, when dealing with the results of discriminant analysis to identify aphids, in some cases problems may emerge as canonical discriminant functions presented in identification keys may be of low effectiveness when applied to another data set than that they were based on.

There are about 4700 aphid species registered in the world (Remaudière, Remaudière, 1997), 18 of them belong to the genus *Cryptomyzus* (Remaudière, Remaudière, 1997; Holman, 2009). The representatives of this genus are important both

from practical as insects associated with agricultural plants, currants (*Ribes* spp.) and plants of mint (*Lamiaceae*) family, and theoretical point of view as the model of sympatric speciation in aphids (Guldemon, 1990; 1992; Guldemon, Dixon, 1994).

Cryptomyzus galeopsidis (Kaltenbach) and *Cryptomyzus maudamanti* Guldemon aphids are very similar morphologically, although their summer host specificity is different. The host plants of *C. galeopsidis* are *R. rubrum* or *R. nigrum* and *Galeopsis* sp., while *C. maudamanti* feeds on *R. rubrum* and *Lamiasrum galeobdolon*. In the case of unknown host plant or its questionable identification canonical discriminant functions are offered as additional tool (Guldemon, 1991; Blackman, Eastop, 2006). Nevertheless, the effectiveness of these functions from the identification key to European species of the genus *Cryptomyzus* (Guldemon, 1991) appeared to be markedly lower when applied to apterous viviparous females of *C. galeopsidis* collected from typical summer host plant, *Galeopsis* spp., in Lithuania (Ba ilova, Rakauskas, 2007). The aim of this study was to detect morphometric characters and their combinations suitable for the construction of canonical discriminant functions

enabling identification of apterous and alate viviparous females of *C. galeopsidis* and *C. maudamanti* and to evaluate the effectiveness of these functions.

Materials and methods

Life cycle studies of *C. galeopsidis* and *C. maudamanti* collected in Lithuania were carried out in Pakalniškės, Vilnius distr. (Lithuania), during 2007–2009 (Table 1). Isolated aphid colonies were kept under outdoor conditions and checked twice a week, every 3–4 days, to evaluate the state of both host plants and aphid colonies. Herbaceous hosts of the family Lamiaceae were collected in the field and then grown potted and isolated. Branch tip aphid exclusion cages (Rakauskas, 1993) were put on currant shoots after their thorough examination. When host plants were infested with aphids, groups of 5–10 individuals were transferred into new cage depending on the size of aphids and plants. When alate viviparous females were emerging, the migration was simulated by transferring groups of 5–15 individuals onto new host plants. For the preparation of microscope slides aphids were collected and preserved in 70% ethanol.

Table 1. Aphids used for life cycle studies and their collection sites.

Line code	Season of rearing	Collection site of aphids used for rearing	Coordinates of collection sites	
			Latitude N	Longitude E
<i>Cryptomyzus galeopsidis</i>				
A1, A2, A3, A4	2007	Skaidiškės, Vilnius distr.	54°36'15"	25°23'29"
F1, F2, F3, F4	2007	Pakalniškės, Vilnius distr.	54°38'42"	25°22'5"
A5, A11B	2007–2008	Pakalniškės, Vilnius distr.	54°38'39"	25°22'10"
A3, A12A	2008–2009	Pakalniškės, Vilnius distr.	54°38'42"	25°22'8"
<i>Cryptomyzus maudamanti</i>				
J1	2007	Vingis park, Vilnius	54°41'11"	25°14'4"
J2	2007–2008	Skaidiškės, Vilnius distr.	54°36'7"	25°23'20"

Microscope slides in Canada balsam were prepared following the protocol of Blackman and Eastop (2000). The identification of *C. galeopsidis* and *C. maudamanti* was based on host plant specificity of reared aphids. Microscope slides are stored at the Department of Zoology, Vilnius University (Vilnius, Lithuania). Characters for morphometric analysis (Table 2) were selected from three identification keys (Hille Ris Lambers, 1953; Guldemon, 1991; Heie, 1994) with morph description. Measurements were performed using "Olympus BX40" microscope with an interactive measurement system *MicroImage*.

Measurements, counts and ratios were used for the discriminant analysis of apterous and alate viviparous females of *C. galeopsidis* and *C. maudamanti* with studied life cycles. Characters and their abbreviations are given in Table 2. After Pearson correlation coefficients (r) were calculated for the whole data set of each studied morph, the correlation of characters with body length was evaluated and characters with statistically significant ($p < 0.05$) correlation coefficient $|r| \geq 0.5$ were removed from the further analysis. The data set was then divided into two subsets, as one of them was used to construct canonical discriminant function and the other

one to evaluate its effectiveness. When performing forward stepwise discriminant analysis, the data-set containing selected measurements, counts and ratios was used. Then the procedure was repeated

with measurements and counts only. From these two types of functions obtained, the most effective ones were chosen and their values were visualised as scatter plots.

Table 2. Characters used for morphometric analysis and their abbreviations

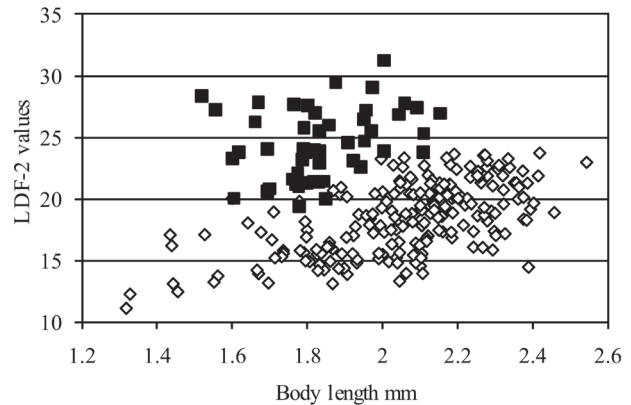
Character name	Abbreviation
Measurements	
Body length, excluding cauda, mm	body
Hind tibia length, mm	htibia
Length of antennal segment 3, mm	ant3
Length of antennal segment 4, mm	ant4
Length of basal part of antennal segment 5, mm	ant5a
Length of processus terminalis, mm	pt
Length of distal part of antennal segment 5, mm	ant5b
Length of the base of antennal segment 6, mm	bant6
Length of cauda, mm	cauda
Length of siphunculus, mm	siphon
Minimal width of the proximal part of siphunculus, mm	miwsi
Maximal width of the distal part of siphunculus, mm	mawsi
Length of the last rostral segment, mm	lrs
Length of segment 2 of hind tarsus, mm	tars2
Diameter of the base of antennal segment 3, mm	dbant3
Length of the longest hair on antennal segment 1, mm	hant1
Length of the longest hair on antennal segment 3, mm	hant3
Length of the longest hair on abdominal tergites 2–4, mm	abhair
Counts	
Number of dorsal hairs on abdominal segments 1–4	dhas1–4
Number of secondary rhinaria on antennal segment 3–5	srhin3–5
Number of additional hairs on the last rostral segment	hlrs
Ratios	
Minimal width of siphunculus / Maximal width of siphunculus	miwsi/mawsi
Length of the last rostral segment / Length of segment 2 of hind tarsus	lrs/tars2
Processus terminalis / Length of antennal segment 3	pt/ant3
Processus terminalis / Length of the base of antennal segment 6	pt/bant6
Length of the longest hair on antennal segment 3 / Diameter of the base of antennal segment 3	hant3/dbant3
Length of the longest hair on antennal segment 1 / Length of the longest hair on antennal segment 3	hant1/hant3
Length of the longest hair on abdominal tergites 2–4 / Diameter of the base of antennal segment 3	abhair/dbant3
Length of the longest hair on abdominal tergites 2–4 / Length of the base of antennal segment 6	abhair/bant6
Length of siphunculus / Body length, excluding cauda	siphon/body
Length of siphunculus / Length of cauda	siphon/cauda
Length of cauda / Length of siphunculus	cauda/siphon

When performing discriminant analysis with morphometric data of apterous viviparous females the following characters were removed from the whole dataset (the values of correlation coefficient (r) are given in parenthesis): length of segment 2 of hind tarsus ($r = 0.60$), length of processus terminalis ($r = 0.65$), diameter of the base of antennal segment 3 ($r = 0.67$), length of cauda ($r = 0.68$), length of the base of antennal segment 6 ($r = 0.69$), length of antennal segment 3 ($r = 0.75$), hind tibia length ($r = 0.87$), body length, excluding cauda ($r = 1$). When performing discriminant analysis with morphometric data of alate viviparous females the following characters were removed from the whole dataset (the values of correlation coefficient (r) are given in parenthesis): length of the base of antennal segment 6 ($r = 0.55$), length of processus terminalis ($r = 0.58$), length of basal part of antennal segment 5 ($r = 0.61$), length of cauda ($r = 0.64$), length of antennal segment 4 ($r = 0.66$), diameter of the base of antennal segment 3 ($r = 0.72$), length of antennal segment 3 ($r = 0.77$), hind tibia length ($r = 0.82$), body length, excluding cauda ($r = 1$). Initial data analysis was done with *Excel 2003*, for other calculations *Statistica* (version 5.5) was used.

Results and discussion

Identification key to European species of the genus *Cryptomyzus* (Guldmond, 1991) provides one character to distinguish between apterous viviparous females of *C. galeopsidis* and *C. maudamanti* – number of dorsal hairs on abdominal segment 3. The values of this character are referred to as 4–11 for *C. galeopsidis* and 8–14 for *C. maudamanti* and appear partly overlapping. To ensure more precise identification of *C. galeopsidis* and *C. maudamanti* Guldmond (1991) offered canonical discriminant function LDF-2: $181.1 \times (\text{abhair}) + 113.0 \times (\text{bant6}) + 1.3 \times (\text{dhas3}) - 327.6 \times (\text{hant1})$; *C. galeopsidis*, if LDF-2 < 20.0, *C. maudamanti*, if LDF-2 > 20.0. When this function was applied to the measurements of cloned apterous viviparous females of *C. galeopsidis* and *C. maudamanti* (Figure 1) 64.6% individuals of *C. galeopsidis* (137 from 212) and 98.0% individuals of *C. maudamanti* (48 from 49) were classified correctly. Although, as it was noted in the identification key, about 90% of individuals belonging to both species were supposed to be identified correctly when canonical function LDF-2 was applied.

In this study, canonical discriminant function, called GM-Apt (G – *C. galeopsidis*, M – *C. maudamanti*, Apt – apterous viviparous fe-



Notes. LDF-2: $181.8 \times (\text{abhair}) + 113.0 \times (\text{bant 6}) + 1.3 \times (\text{dhas 3}) - 327.6 \times (\text{hant 1})$; *C. galeopsidis*, if LDF-2 < 20.0, *C. maudamanti*, if LDF-2 > 20.0. Character abbreviations as given in Table 2.

Figure 1. The application of canonical discriminant function LDF-2 (Guldmond, 1991) to the measurements of *Cryptomyzus galeopsidis* (\diamond) and *Cryptomyzus maudamanti* (\blacksquare) apterous viviparous females from clonal samples

males), was constructed to distinguish between apterous viviparous females of *C. galeopsidis* and *C. maudamanti* from clonal samples: $13.230 \times (\text{cauda/siphon}) + 6.935 \times (\text{siphon/cauda}) - 0.924 \times (\text{dhas1-4}) - 7.170 \times (\text{siphon}) + 58.009 \times (\text{siphon/body}) + 1.909 \times (\text{abhair/bant6}) - 135.983 \times (\text{mi-wsi}) - 32.505$; *C. maudamanti*, if GM-Apt > 2, *C. galeopsidis*, if GM-Apt < 2; character abbreviations as given in Table 2. This function discriminates between all individuals of *C. galeopsidis* ($n = 106$) and *C. maudamanti* ($n = 25$) (100% effectiveness) from the data set used for function construction (Figure 2, left graph). When function GM-Apt was applied to the data set for evaluation of its effectiveness (Figure 2, right graph), all individuals of *C. maudamanti* ($n = 24$, 100% effectiveness) and 104 individuals of 106 *C. galeopsidis* (98.1% effectiveness) were classified correctly. Mean values of characters used in canonical discriminant function GM-Apt, their standard deviation together with minimum and maximum are given in Table 3.

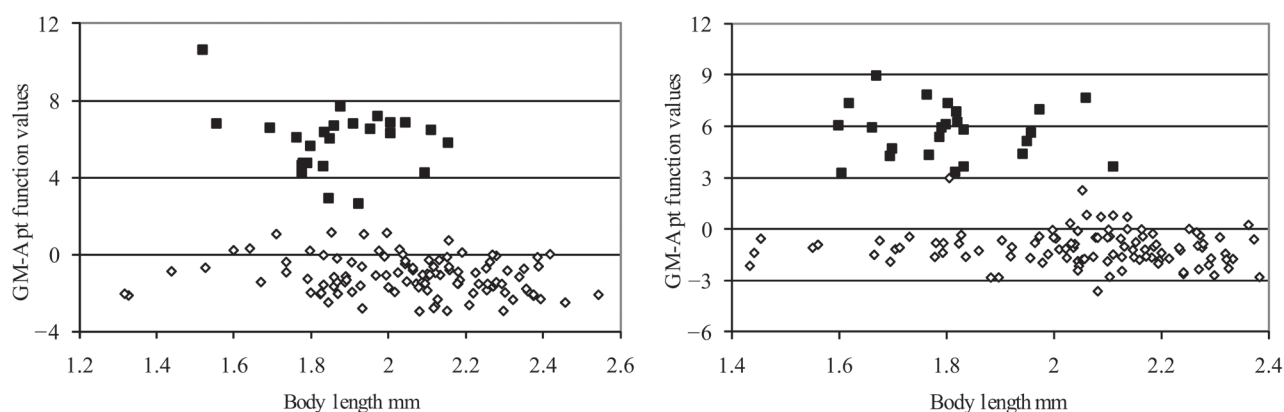
Two characters are offered in the identification key to European species of the genus *Cryptomyzus* for discrimination between alate viviparous females of *C. galeopsidis* and *C. maudamanti*: number of dorsal hairs on abdominal segment 3, which ranges from 7 to 11 in *C. galeopsidis* and from 9 to 14 in *C. maudamanti*; and number of secondary rhinaria on antennal segment 3, which varies

from 25 to 64 in *C. galeopsidis* and from 26 to 42 in *C. maudamanti*. The morphometric analysis of alate viviparous females from clonal samples showed that the values of these characters were overlapping. The

number of dorsal hairs on abdominal segment 3 and number of secondary rhinaria on antennal segment 3 were respectively 3–10 and 26–68 for *C. galeopsidis* and 6–14 and 28–54 for *C. maudamanti*.

Table 3. Values of characters (mean \pm standard deviation, min-max in parentheses) used in canonical discriminant function GM-Apt for apterous viviparous females of *C. galeopsidis* and *C. maudamanti* from different host plants

Character abbreviation	<i>C. galeopsidis</i> apterous viviparous female from <i>Lamium purpureum</i> <i>n</i> = 42	<i>C. galeopsidis</i> apterous viviparous female from <i>Galeopsis tetrahit</i> <i>n</i> = 95	<i>C. galeopsidis</i> apterous viviparous female from <i>Ribes nigrum</i> <i>n</i> = 75	<i>C. maudamanti</i> apterous viviparous female from <i>Lamiaestrum galeobdolon</i> <i>n</i> = 49
siphon	0.307 \pm 0.037 (0.250 – 0.386)	0.341 \pm 0.034 (0.265 – 0.424)	0.285 \pm 0.038 (0.179 – 0.367)	0.314 \pm 0.030 (0.208 – 0.382)
miwsi	0.026 \pm 0.003 (0.020 – 0.033)	0.028 \pm 0.002 (0.022 – 0.032)	0.026 \pm 0.003 (0.019 – 0.031)	0.029 \pm 0.003 (0.022 – 0.034)
dhas4	7.1 \pm 0.9 (5–9)	6.7 \pm 1.0 (4–9)	5.9 \pm 0.7 (4–8)	10.2 \pm 1.5 (8–16)
dhas3	6.9 \pm 0.9 (5–8)	7.0 \pm 1.0 (5–10)	5.7 \pm 1.0 (3–8)	10.9 \pm 1.7 (8–17)
dhas2	7.1 \pm 1.2 (4–9)	7.0 \pm 1.1 (5–10)	5.9 \pm 0.9 (4–8)	10.5 \pm 1.7 (7–17)
dhas1	6.5 \pm 1.8 (2–10)	6.0 \pm 1.2 (3–9)	5.0 \pm 1.4 (2–9)	8.1 \pm 1.3 (6–13)
abhair/bant6	0.49 \pm 0.06 (0.33 – 0.63)	0.45 \pm 0.06 (0.30 – 0.69)	0.46 \pm 0.05 (0.34 – 0.60)	0.56 \pm 0.06 (0.45 – 0.76)
siphon/body	0.15 \pm 0.02 (0.12 – 0.19)	0.15 \pm 0.01 (0.12 – 0.19)	0.15 \pm 0.01 (0.13 – 0.18)	0.17 \pm 0.01 (0.11 – 0.21)
siphon/cauda	1.93 \pm 0.27 (1.46 – 2.56)	2.02 \pm 0.19 (1.51 – 2.49)	1.90 \pm 0.17 (1.61 – 2.72)	2.40 \pm 0.23 (1.71 – 2.97)
cauda/siphon	0.53 \pm 0.07 (0.39 – 0.69)	0.50 \pm 0.05 (0.40 – 0.66)	0.53 \pm 0.04 (0.37 – 0.62)	0.42 \pm 0.04 (0.33 – 0.58)



Notes. GM-Apt: $13.230 \times (\text{cauda/siphon}) + 6.935 \times (\text{siphon/cauda}) - 0.924 \times (\text{dhas1-4}) - 7.170 \times (\text{siphon}) + 58.009 \times (\text{siphon/body}) + 1.909 \times (\text{abhair/bant6}) - 135.983 \times (\text{miwsi}) - 32.505$; *C. maudamanti*, if GM-Apt > 2 , *C. galeopsidis*, if GM-Apt < 2 . Character abbreviations as given in Table 2.

Figure 2. The application of canonical discriminant function GM-Apt to the morphometric data of *Cryptomyzus galeopsidis* (\diamond) and *Cryptomyzus maudamanti* (\blacksquare) apterous viviparous females used for its construction (left graph) and evaluation of its effectiveness (right graph)

Canonical discriminant function, called GM-AI (G – *C. galeopsidis*, M – *C. maudamanti*, AI – alate viviparous females), was obtained to separate alate viviparous females of *C. galeopsidis* and *C. maudamanti*: $0.940 \times (\text{dhas1-4}) - 0.040 \times (\text{srhin3}) + 147.389 \times (\text{miwsi}) - 158.074 \times (\text{hant1}) + 0.525 \times (\text{hlrs}) - 8.373$; *C. maudamanti*, if GM-AI > 3.5, *C. galeopsidis*, if GM-AI < 3.5; character abbreviations as given in Table 2. It distinguishes all individuals of *C. galeopsidis* ($n = 61$) from all individuals of *C. maudamanti* ($n = 26$) (100% ef-

fectiveness) from the data set used for function construction (Figure 3, left graph). When function GM-AI was applied to the data set for evaluation of its effectiveness (Figure 3, right graph), 26 of 29 individuals of *C. maudamanti* (89.7% effectiveness) were separated from 61 of 62 individuals of *C. galeopsidis* (98.4% effectiveness). Mean values of characters used in canonical discriminant function GM-AI, their standard deviation together with minimum and maximum are given in Table 4.

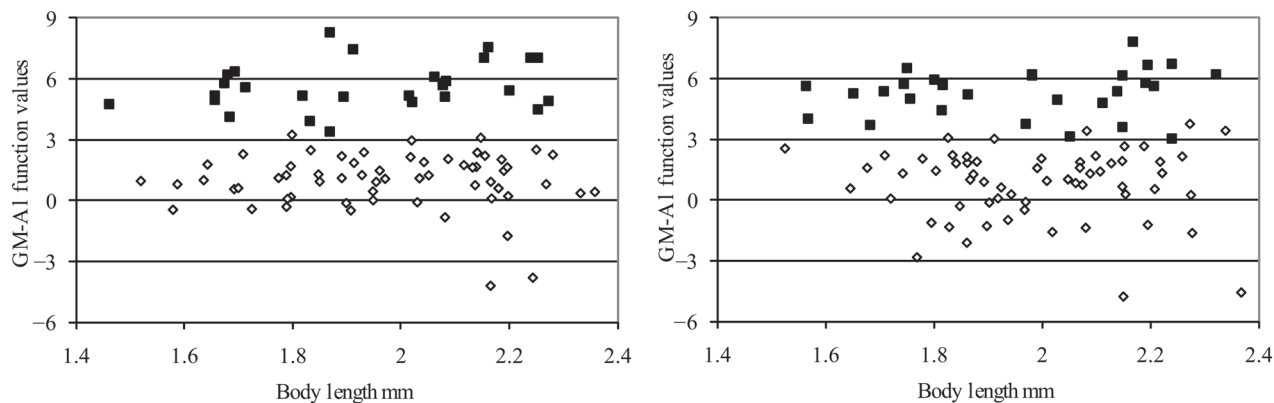
Table 4. Values of characters (mean \pm standard deviation, min-max in parentheses) used in canonical discriminant function GM-AI for alate viviparous females of *C. galeopsidis* and *C. maudamanti* from different host plants

Character abbreviation	<i>C. galeopsidis</i> alate viviparous female from <i>Ribes nigrum</i> $n = 46$	<i>C. galeopsidis</i> alate viviparous female from <i>Lamium purpureum</i> $n = 42$	<i>C. galeopsidis</i> alate viviparous female from <i>Galeopsis tetrahit</i> $n = 35$	<i>C. maudamanti</i> alate viviparous female from <i>Ribes rubrum</i> $n = 20$	<i>C. maudamanti</i> alate viviparous female from <i>Lamium galeobdolon</i> $n = 39$
miwsi	0.022 \pm 0.003 (0.017 – 0.028)	0.020 \pm 0.002 (0.016 – 0.023)	0.022 \pm 0.002 (0.019 – 0.027)	0.026 \pm 0.002 (0.022 – 0.028)	0.023 \pm 0.002 (0.018 – 0.029)
hant1	0.019 \pm 0.003 (0.011 – 0.029)	0.020 \pm 0.004 (0.015 – 0.032)	0.021 \pm 0.003 (0.017 – 0.027)	0.014 \pm 0.002 (0.010 – 0.019)	0.016 \pm 0.002 (0.011 – 0.021)
dhas4	6.3 \pm 1.1 (4–9)	6.4 \pm 1.4 (3–9)	7.3 \pm 1.1 (4–9)	10.8 \pm 1.5 (8–13)	10.4 \pm 1.3 (8–13)
dhas3	6.4 \pm 1.3 (4–9)	6.3 \pm 1.6 (4–10)	7.5 \pm 1.1 (4–10)	10.8 \pm 1.3 (9–13)	9.8 \pm 2.1 (3–13)
dhas2	6.5 \pm 1.3 (4–9)	6.2 \pm 1.6 (2–10)	6.7 \pm 1.8 (4–10)	10.6 \pm 1.7 (6–13)	10.2 \pm 1.8 (6–14)
dhas1	4.6 \pm 1.4 (2–7)	5.3 \pm 1.4 (2–8)	5.5 \pm 1.4 (3–8)	7.2 \pm 1.5 (4–9)	6.4 \pm 1.5 (3–10)
srhin3	45.7 \pm 8.2 (32–64) 45.4 \pm 8.0 (33–68)	42.0 \pm 7.0 (27–54) 43.1 \pm 7.2 (26–54)	48.4 \pm 5.1 (41–61) 47.8 \pm 5.4 (38–63)	46.9 \pm 3.2 (41–52) 47.3 \pm 4.3 (39–54)	39.0 \pm 4.2 (28–48) 38.3 \pm 4.3 (31–48)
hlrs	4.2 \pm 1.3 (2–6)	3.9 \pm 0.8 (2–6)	3.5 \pm 1.0 (2–5)	4.0 \pm 0.9 (2–5)	3.9 \pm 0.8 (2–5)

There was an attempt to find characters enabling more reliable and precise identification of *C. galeopsidis* and *C. maudamanti* (Guldemond, 1991). Canonical discriminant functions are also offered in other identification keys to the genus *Cryptomyzus* (Heie, 1994; Blackman, Eastop, 2006) based on those compiled by Guldemond (1991). If one compared characters (dhas3, abhair, bant6, hant1) used in the function LDF-2 (Guldemond, 1991) with those from the function GM-AI, one would easily note that they share some of these characters (dhas1-4 and abhair/bant6) together with other two characters (siphon/body and dhas3) from the identification key (Guldemond, 1991). Furthermore, through the discriminant analysis performed

in the present study ratios cauda/siphon and siphon/cauda proved to be important for the identification of apterous viviparous females of *C. galeopsidis* and *C. maudamanti*. Characters suitable for discrimination between alate viviparous females of these two species were also detected.

Generally, the application of discriminant analysis to the morphologically similar aphid species can be very useful. When characters are being selected for these procedures, those without strong correlation with body length ($|r| < 0.5$) should be chosen. If the effectiveness of obtained functions were evaluated with another dataset than that used for its construction, the identification of closely related aphid species would become more precise.



Note. GM-AI: $0.940 \times (\text{dhas1-4}) - 0.040 \times (\text{srhin3}) + 147.389 \times (\text{miwsi}) - 158.074 \times (\text{hant1}) + 0.525 \times (\text{hlrs}) - 8.373$; *C. maudamanti*, if GM-AI > 3.5, *C. galeopsidis*, if GM-AI < 3.5. Character abbreviations as given in Table 2.

Figure 3. The application of canonical discriminant function GM-AI to the morphometric data of *Cryptomyzus galeopsidis* (◇) and *Cryptomyzus maudamanti* (■) alate viviparous females used for its construction (left graph) and evaluation of its effectiveness (right graph)

Conclusions

1. Canonical discriminant functions constructed for *C. galeopsidis* and *C. maudamanti* apterous (GM-Apt) and alate (GM-AI) viviparous females exhibited the effectiveness of 98.1–100% and 89.7–98.4%, respectively.

2. Ratios cauda/siphon and siphon/cauda proved to be important for the identification of apterous viviparous females of *C. galeopsidis* and *C. maudamanti*.

3. Canonical discriminant functions are a useful tool to distinguish between morphologically close aphid species, especially in the cases when host plants are unknown.

4. When characters for discriminant analysis are selected, it is important to evaluate their correlation with body length.

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Diskriminantinės analizės taikymas *Cryptomyzus* amarų rūšims atpažinti

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Santrauka

Cryptomyzus galeopsidis (Kaltenbach) ir *Cryptomyzus maudamanti* Guldemonid rūšių amarai yra labai panašūs morfologiškai, bet skiriasi jų mitybos specializacija. *C. galeopsidis* mitybiniai augalai yra *Ribes rubrum* arba *R. nigrum* ir *Galeopsis* sp., o *C. maudamanti* maitinasi ant *R. rubrum* bei *Lamiaeastrum galeobdolon*. Šioms rūšims atpažinti taikomos kanoninės diskriminantinės funkcijos, ypač tais atvejais, kai augalo rūšis yra nežinoma. Tačiau europinių *Cryptomyzus* genties rūšių atpažinimo raktuose pateikiamos kanoninės diskriminantinės funkcijos nėra tokios efektyvios, kaip nurodoma. Jos leidžia klasifikuoti ne 90, o tik 64,6 % *C. galeopsidis* individų, kurių gyvenimo ciklas yra ištirtas. Taikant diskriminantinę analizę, naudoti matuojamieji bei skaičiuojamieji požymiai ir požymių santykiai, pasižymintys silpnu ar labai silpnu ryšiu su kūno ilgiu (koreliacijos koeficientas $|r| < 0,5$). Atlikus pasirinktų požymių analizę, *C. galeopsidis* bei *C. maudamanti* rūšių amarų besparnėms ir sparnuotoms partenogenetinėms patelėms sudarytos kanoninės diskriminantinės funkcijos, leidžiančios atskirti nuo 90 iki 100 % šių rūšių individų.

Reikšminiai žodžiai: *Cryptomyzus galeopsidis*, *Cryptomyzus maudamanti*, amarai, morfologija, diskriminantinė analizė.