MORPHOLOGICAL AND KARYOLOGICAL RELATIONSHIPS
WITHIN ALPINE-DINARIC POPULATIONS
OF THE GENUS *IRIS* L., PALLIDAE SERIES (A. KERN.)
TRINAJSTIĆ (IRIDACEAE)

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ABSTRACT

The relationships within the Alpine-Dinaric and cultivated populations of the genus *Iris*, Pallidae series, have been analysed by methods of multivariate statistics (Cluster, PCA and MST analyses). The bases for multivariate analyses were seven morphological characteristics (stem length, length of largest leaf, greatest width of the largest leaf, length of smallest leaf, greatest width of the smallest leaf, the number of leaves and the number of flowers) and relative chromosome length for 12 chromosome pairs. In spite of two similar looking isolated populations (Stara Baška and Konavle), the presence of four groups within the series was established, to which a species status can be ascribed: *I. pallida* Lam. separated as a horticultural species, *I. cengialti* Ambr. – endemic in Alpine region, *I. illyrica* Tomm. – endemic to the northern Adriatic Littoral and *I. pseudopallida* Trinajstić – endemic to the southern Adriatic Littoral. To differentiate the established groups, in PCA analysis the most significant features turned out to be: relative chromosome length of eleventh and tenth chromosome pairs, the length of the smallest leaf, relative chromosome length of the seventh chromosome pair and length of the stem.

KEY WORDS: *Iris* L., Pallidae series (A. Kern.) Trinajstić, Alpine-Dinaric populations, morphological and karyological relationships.

INTRODUCTION

The cultivated species *Iris pallida* Lam. (Lamarck 1789) and its closely related Alpine-Dinaric populations are characterised in the first place by their dry-skinned spathe and pale blue or violet flowers (Ambrosi 1854; Kerner 1871; Tommasini 1875; Pampanini 1909; Trinajstić 1976; Scortegagna et al. 1996). Taxonomic problems of this complex are related to the varied understanding of specific or sub-specific status of individual population groups, that have resulted in descriptions of different numbers of taxa of the *I. pallida* s. l. complex: one variable species (Ascherson and Graebner 1906; Hegi and Dunzinger 1909; Randolph and Rechinger 1954; Ehrendorfer 1973; Webb and Chater 1980; Mathew 1981; Wraber 1998; 1999), two variable species (Pampanini 1909; Dykes 1913; Hayek 1933; Mayer 1952; Pignatti 1982), three species (Lawrence 1953; Köhlein 1981; Schulze 1988; Domac 1994; Scortegagna et al. 1996, Trpin and Vreš 1995), numerous endemic species (Rac and Lovrić 1990) etc. Trinajstić (1976; 1983) was the first to suggest that those Alpine-Dinaric populations and cultivated species of *I. pallida* can be put together into separate Pallidae series (A. Kern.)

Trinajstić, with four species: horticultural species *I. pallida* Lam. and three indigenous and endemic Alpine-Dinaric species: *I. cengialti* Ambr., *I. illyrica* Tomm. and *I. pseudopallida* Trinajstić.

Recently, we attempted to clarify the possible differentiation of the Pallidae series in the Alpine-Dinaric region with the help of morphological, anatomical and karyological characters using statistical methods (Mitić et al. 1999; Mitić and Pavletić 1999; Mitić et al. 2000). The to date results have tended to confirm the view that there are four species within the Pallidae series. Morphological analysis (Mitić and Pavletić 1999) has shown the stability of morphological characteristics, while analyses of leaf anatomical features have pointed to their phenotypic plasticity and lack of taxonomic usefulness (Mitić et al. 2000).

For further explanation of the relationships within the Alpine-Dinaric and cultivated populations of the Pallidae series, we used some of their karyological features (Mitić et al. 2001). Numerous data have borne out the importance of cytological data for the taxonomy of the Genus *Iris* and the Pallidae series (Simonet 1934; Mitra 1956; Mitra and Randolph 1959; Randolph and Mitra 1959; Lausi 1964; Ricci 1970/71; Maugini and Bini Maleci 1976; Bini Maleci

and Maugini 1977; Trinajstić and Lovašen-Eberhardt 1977; Sauer and Leep 1979; Trinajstić et al. 1980; Mitić 1991 etc.). Previous data about somatic chromosome numbers of the *I. pallida* s. l. complex show karyological uniformity with $2n=24$ (Simonet 1934; Darlington and Wylie 1955; Mitra 1956; Sušnik 1962; Lausi 1964; Bolkovskikh et al. 1969; Löve and Löve 1974; Mitić 1991; Scortegagna et al. 1996).

MATERIALS AND METHODS

Twenty-five populations were sampled by collecting 2-20 specimens (depending on the extent of populations) from each population (Table 1). In total, 418 specimens from 21 populations collected from all over the Alpine-Dinaric area were analysed, as well as four control populations of the species *I. pallida* of horticultural origin (Ble, Sam, Zdu and ZZr – for abbreviations see Table 1). The samples were collected in 1992-1997, during the flowering time (between April and June).

For morphological analyses the plants were prepared by pressing and drying in a steriliser at 47°C. Morphological features for morphometry were used according to Melkó (1976) and taken from Mitić et al. (1999). They included: stem length (without flowers) (cm), length of largest leaf (cm), greatest width of the largest leaf (cm), length of

smallest leaf (cm), greatest width of the smallest leaf (cm), the number of leaves and the number of flowers.

A study of somatic chromosomes was made using the root-tip squash technique and aceto-carmin staining, after pre-treatment with p-dichlorobenzen. The most satisfactory procedure was found to be 3 hours pre-treatment in the p-dichlorobenzen at 4°C. Slides were made permanent by first removing the cover glass with the freezing technique (CO₂) and mounting the material in Canada balsam. Karyotype analysis was based on five to ten metaphase plates (according to Rafinski and Passakas 1976; Sauer and Leep 1979). Description of the karyological features of the populations analysed, except the relative chromosome lengths, has been presented in Mitić et al. (2001).

For multivariate analyses, we used 19 variables: seven morphological features (see below) and 12 variables containing the arithmetical means of relative chromosome length (%) for each of 12 chromosome pairs.

The row data matrix with 25 OTU-s (populations) and 19 variables was standardised by variables. The means of each variable were subtracted. The differences were then divided by the standard deviation. A standardised data matrix was the input matrix for cluster and principal component analyses (PCA).

Cluster analysis was done by calculating the average taxonomic distance. The clustering method was UPGMA (Unweighted pair-group method, arithmetic average). The results were presented as a dendrogram. The cophenetic correlation (r_c) was used to test the fit of a cluster analysis by comparing the original dissimilarity matrix with cophenetic value matrix.

PCA was carried out by computing eigenvalues and eigenvectors from the variables correlation matrix. The three dimensions were retained. The eigenvectors matrix and the eigenvalues, their percentages, and their cumulative percentages are listed. The results, spatial relationships between populations, are presented in the form of a 3D scatter diagram, each axis according to three principal components. Minimum spanning tree (MST) was used to detect local distortion – pairs of points which look close together in a plot, but actually are apart if other dimensions – MST tree – are superimposed on 3D PCA scatter diagram.

All calculations were done by the NtSys-pc 1.6 package (Rohlf 1990).

RESULTS

Morphometry of analysed seven morphological features was taken from Mitić et al. (1999). Results of the calculations of relative chromosome length (%) for each of 12 chromosome pairs are shown in Table 2.

The results of the hierarchical cluster analysis UPGMA were obtained on the basis of 19 variables: seven quantitative morphological and 12 variables containing the arithmetical means of relative chromosome length (%) for each of 12 chromosome pairs. Drawing matrix of the average taxonomic distance were shown by a dendrogram (Fig. 1). Cophenetic correlation was $r_c = 0.9069$ and could be interpreted subjectively as a very good fit (Rohlf 1990). Their grouping effect showed up four main groups of the populations (marks A-D) and two populations – Konavle (Kon) and Stara Baška (Stb), separated from the whole sample at

TABLE 1. The populations sampled: name of locality; co-ordinates: Latitude (N) and Longitude (E); no. mo. – number of specimens morphologically analysed; no. ka. – number of specimens karyologically analysed; Cult. – cultivated populations; Alp. – Alpine populations; N. Litt. – northern Littoral populations; C. and S. Litt. – central and southern Littoral populations.

Locality (mark)	Latitude (N)	Longitude (E)	no. mo.	no. ka.
Cult.				
Bled (cult.) (Ble)	46° 21' 00"	14° 06' 55"	2	1
Samobor (cult.) (Sam)	45° 48' 05"	15° 43' 30"	20	5
Zagreb-Dubrava (cult.) (ZDu)	45° 49' 55"	16° 03' 30"	20	5
Zagreb-Zrinjevac (cult.) (ZZr)	45° 53' 42"	16° 03' 00"	20	5
Alp.				
Kobarid (Kob)	46° 16' 30"	13° 33' 05"	15	5
Komarča (Kom)	46° 17' 47"	13° 47' 40"	10	4
Rovereto (Rov)	45° 45' 30"	11° 40' 00"	2	3
N. Litt.				
Čičarija (Cic)	45° 27' 12"	14° 01' 00"	5	3
Grobničko polje (Gro)	45° 22' 13"	14° 28' 48"	10	5
Matulji (Mat)	45° 21' 50"	14° 20' 05"	7	3
Meja (Mej)	45° 17' 40"	14° 36' 38"	5	2
Plomin (Plo)	45° 08' 22"	14° 10' 50"	5	2
Ribarica (Rib)	44° 33' 06"	15° 03' 07"	20	5
Senj (Sen)	44° 49' 00"	14° 44' 59"	16	5
Stara Baška (Stb)	44° 57' 26"	14° 41' 37"	20	9
Starigrad (Stg)	44° 46' 07"	14° 54' 00"	20	5
Žrnovnica (Zrn)	45° 06' 35"	14° 51' 00"	20	5
C. and S. Litt.				
Biokovo (Bio)	43° 17' 18"	17° 03' 22"	20	5
Dubrovnik (Dub)	42° 38' 13"	18° 08' 20"	20	5
Konavle (Kon)	42° 32' 18"	18° 17' 32"	10	2
Marušići (Mar)	43° 24' 50"	16° 46' 42"	9	3
Omiš (Omi)	43° 27' 03"	16° 42' 00"	5	2
Trstenik (Trs)	42° 55' 03"	17° 24' 58"	10	2
Velika Paklenica (Vpa)	44° 18' 08"	15° 28' 47"	15	5
Vrulje (Vru)	43° 24' 10"	16° 53' 12"	12	4

TABLE 2. The arithmetical means of relative chromosome length (%) for 12 chromosome pairs in 25 populations of the *Pallidae* series: A – central and southern Littoral populations; B – cultivated populations; C – northern Littoral populations; D – Alpine populations.

Chromosome pair no.	1	2	3	4	5	6	7	8	9	10	11	12
Population												
A												
Biokovo (Bio)	9.80	7.52	7.00	6.96	6.42	6.48	6.30	5.74	5.90	5.54	4.88	4.32
Dubrovnik (Dub)	9.68	7.34	6.92	6.50	5.90	6.24	6.00	5.90	5.82	5.50	4.80	3.88
Marušići (Mar)	9.95	7.65	6.78	7.40	6.50	6.33	6.45	6.45	6.08	5.48	4.90	4.03
Omiš (Omi)	9.90	7.50	6.90	7.10	6.60	6.90	6.60	6.10	6.00	5.40	5.00	3.90
Trstenik (Trs)	9.86	7.72	6.84	7.08	6.44	6.62	6.48	6.30	6.18	5.60	5.08	4.26
Vrulje (Vru)	9.60	7.70	7.10	7.35	6.38	6.43	6.53	6.30	6.28	5.53	4.70	4.20
B												
Bled (Ble)	9.70	6.90	6.90	6.70	6.20	6.70	6.20	5.50	5.20	4.90	4.90	3.80
Samobor (Sam)	9.80	6.56	6.82	6.44	6.48	6.90	6.28	5.54	5.18	5.04	4.56	4.02
Zagreb-Dubrava (ZDu)	9.90	6.70	6.86	6.48	6.52	6.26	5.94	5.54	5.18	4.92	4.52	3.96
Zagreb-Zrinjevac (ZZr)	9.92	6.68	6.54	6.34	6.02	6.02	5.76	5.28	5.10	4.80	4.64	4.08
C												
Čićarija (Cic)	9.63	6.33	5.70	5.80	5.60	5.50	5.20	5.17	4.67	4.33	3.97	3.63
Grobničko polje (Gro)	9.88	7.18	6.56	6.44	5.80	5.56	5.00	4.80	4.58	4.32	4.02	4.02
Matulji (Mat)	9.67	7.07	6.53	6.37	5.87	5.60	5.40	4.87	4.80	4.40	4.20	3.97
Meja (Mej)	9.65	6.65	6.25	6.10	5.50	5.20	4.65	4.75	4.50	3.95	3.85	3.65
Plomin (Plo)	9.35	6.65	5.85	5.95	6.05	5.45	5.20	5.15	4.50	4.55	4.05	3.90
Ribarica (Rib)	9.36	6.12	6.10	6.02	6.04	5.50	5.28	5.12	4.56	4.14	4.14	4.02
Senj (Sen)	9.68	6.74	6.42	6.26	5.84	5.44	5.14	4.64	4.40	4.16	3.98	3.70
Starigrad (Stg)	9.92	7.12	6.64	6.42	5.70	5.40	4.84	4.52	4.42	4.18	4.00	3.60
Velika Paklenica (Vpa)	9.48	6.50	6.16	6.28	5.96	5.60	5.44	5.26	4.56	4.46	4.18	3.80
Žrnovnica (Zrn)	9.60	6.90	6.44	5.98	5.68	5.28	5.10	4.42	4.20	4.24	4.06	4.00
D												
Kobarid (Kob)	9.94	7.12	6.56	6.16	6.38	6.40	6.06	5.64	5.16	4.62	4.08	3.86
Komarča (Kom)	9.83	7.08	6.60	6.23	6.05	6.55	6.13	5.75	5.08	4.55	4.08	3.80
Rovereto (Rov)	9.96	6.38	7.4	6.55	6.3	6.03	5.75	5.45	5.08	4.5	4.1	3.88
Isolated populations												
Konavle (Kon)	9.87	7.94	6.77	6.59	4.39	4.50	5.60	5.00	5.82	5.60	4.80	4.86
Stara Baška (Stb)	11.2	7.72	6.66	6.34	5.84	5.22	5.04	2.20	4.67	4.07	3.87	3.34

the first two steps (outlayers). The population of Stara Baška (Stb) diverged at the coefficient of distance $D =$

1.94, and the population of Konavle (Kon) diverged at the coefficient of distance $D = 1.77$.

With coefficient of distance $D = 1.57$, analyses showed up two distinct clusters. The populations of the central and southern Adriatic Littoral (mark A) and all the populations of cultivated irises (mark B) formed the first one. The second cluster was made by the northern Croatian Littoral (mark C) and Alpine populations (mark D).

In the first cluster, the populations of cultivated irises (mark B) split off ($D = 1.39$) from the remaining populations (mark A); inside the central Dalmatian (Mar, Omi, Vru) diverged from the southern populations (Bio, Trs, Dub) at coefficient of distance $D = 0.75$.

The second cluster comprised the populations of the northern Croatian Littoral (mark C) and the Alpine populations (mark D). They made up two clearly separated groups at the coefficient of distance $D = 0.97$.

The results of PCA analysis on the whole confirm the results of cluster analysis (Table 3, Fig. 2). The total variability of the first PC axis contributes as much as 49.30% of the total inter-species variability, and the first three PC axes contribute 80.20% of the cumulative variabilities, which indicates a good representation of the relationships among the populations, that is, the reliability of PC analysis. Other dimensions explain very little additional variation and probably can be ignored. The distribution along

Fig. 1. UPGMA dendrogram based on seven quantitative morphological and 12 karyological variables in 25 populations (OTUs) of *Pallidae* series (A-D populations groups; A – central and southern Adriatic Littoral, B – cultivated irises, C – northern Adriatic Littoral and D – Alpine populations).

Fig. 2. PCA scatter diagram based on the correlation of seven quantitative morphological and 12 karyological variables in 25 populations of the Pallidae series (A – central and southern Adriatic Littoral, B – cultivated irises, C – northern Adriatic Littoral and D – Alpine populations).

the first PC axis is in a large measure contributed to by the relative chromosome length of the eleventh and tenth chromosome pairs, and the length of the smallest leaf. The relative chromosome length of the second and fourth chromosome pairs is most correlated on the second PC axis, and the relative chromosome length of the fifth chromosome pair on the third.

The scatter diagram of the first three PC axes (Fig. 2) shows the presence of four groups and two more or less

TABLE 3. Eigenvectors of the characteristics observed for the first three PC axes for 25 populations of the series Pallidae and eigen values, their percentages and cumulative percentages for first three PC axes.

PCA axes	1	2	3
Features			
relative chromosome length (pair 1)	-0.07	-0.27	-0.51
relative chromosome length (pair 2)	0.34	-0.66	-0.58
relative chromosome length (pair 3)	0.62	-0.40	-0.19
relative chromosome length (pair 4)	0.67	-0.64	-0.07
relative chromosome length (pair 5)	0.40	-0.29	0.71
relative chromosome length (pair 6)	0.68	-0.26	0.56
relative chromosome length (pair 7)	0.84	-0.41	0.24
relative chromosome length (pair 8)	0.68	-0.24	0.50
relative chromosome length (pair 9)	0.80	-0.54	-0.10
relative chromosome length (pair 10)	0.86	-0.38	-0.14
relative chromosome length (pair 11)	0.90	-0.26	-0.08
relative chromosome length (pair 12)	0.59	-0.07	-0.35
stem length	0.82	0.51	-0.16
number of leaves	0.61	0.50	0.13
length of the biggest leaf	0.73	0.61	-0.03
greatest width of the biggest leaf	0.79	0.51	-0.01
length of the smallest leaf	0.86	0.36	-0.20
greatest width of the smallest leaf	0.73	0.58	-0.16
number of flowers	0.78	0.51	-0.05
Var. (%)	49.30	20.17	10.73
Cum. var. (%)	49.30	69.47	80.20
Eigen values	9.37	3.83	2.04

Fig. 3. PCA scatter diagram based on the correlation of seven quantitative morphological and 12 karyological variables in 25 populations of the Pallidae series with superimposed MST diagram (same scatter but different angle of view than in Fig. 2) (A – *I. pseudopallida*, B – *I. pallida*, C – *I. illyrica*, D – *I. cengialti*).

isolated populations within the Pallidae series, of the same qualitative composition as in the group manifested in the cluster analysis (Fig. 1). Group A includes the central and southern Dalmatian populations, group B all populations of cultivated irises, group C the populations of the northern Littoral and group D the Alpine populations. The populations of Stara Baška (Stb) and Konavle (Kon) have isolated positions, as in the cluster analysis.

Groups A-D (Figs 1, 2) of the pertinent populations established on the whole coincide with the limits of the ranges and species diagnoses proposed by Trinajstić (1976): group A being *I. pseudopallida*, group B *I. pallida*, group C *I. illyrica* and group D *I. cengialti*.

The relationships of two isolated populations (Stb, Kon) with the established groups were analysed by MST superimposed on PCA scatter diagram (Fig. 3). The population from Konavle was joined to species *I. pseudopallida* (group A), (to the population Dub, distance 1.35) and the population from Stara Baška was joined to the species *I. illyrica* (group C), (to the population Stg, distance 1.25). Also, some local distortion could be detected: for example, the populations from Ribarica (Rib) and Plomin (Plo) seem to be closest together, but actually both are connected with the population from Velika Paklenica (Vpa).

DISCUSSION

Multivariate analysis, on the basis of seven quantitative morphological and 12 karyological variables (Table 3, Figs 1-3), confirmed the presence of four groups within the "*I. pallida* s. l. complex", to which a separate taxonomic status can be ascribed. To differentiate the groups established, in PCA analysis the most significant features turned out to be: the relative chromosome length of the eleventh and tenth chromosome pairs, the length of the smallest leaf, the relative chromosome length of the seventh chromosome pair and length of stem.

The relative chromosome length of the eleventh and tenth chromosome pairs, the longest length of the smallest leaf and the relative chromosome length of the seventh chromosome pair caused the formation of three groups: the first containing the populations from the central and southern Croatian Littoral (mark A) and the horticultural populations (mark B), the second with the northern Croatian Littoral populations (mark C) and the third with the Alpine populations (mark D), (Table 3, Figs 1-3). The relative chromosome length of the eleventh, tenth and seventh chromosome pairs was the greatest in the first group (mark A and B) and the smallest in the populations of the northern Croatian Littoral (mark C), (Table 2). The same relations obtained for the longest length of the smallest leaf (cf. Mitić et al. 1999).

The features which contributed most to the separation of group B (mark B on Figs 1-3) were the relative chromosome length of the second and fourth chromosome pairs (with lower values for cultivated than for south Dalmatian populations, Table 2) and the greatest length of the biggest leaf (with the highest values for the cultivated populations, cf. Mitić et al. 1999).

The isolation of the populations of Stara Baška (Stb) and Konavle (Kon), (Fig. 2) was mostly caused by relatively high values for the relative chromosome length of the fifth, second and sixth chromosome pairs (Tables 2, 3). In spite of these isolated positions, the MST superimposed on the PCA scatter diagram (Fig. 3) shows that the population of Stara Baška (Stb) is connected with the population from the northern Croatian Littoral (Stg), and the population of Konavle (Kon) is connected with the south Dalmatian population (Dub). Thus, both isolated populations (Stb and Kon) dovetail into groups related closely ecologically and geographically (groups C and A).

The group of the central and southern Littoral populations (mark A on Figs 1-3), including the remote population of Konavle (Kon), (Fig. 3), coincides with the description of the endemic taxon *I. pseudopallida* Trinajstić (Trinajstić 1976), often neglected in taxonomic and floristic works (Hayek 1933; Webb and Chater 1980; Hećimović 1981; Köhlein 1981; Mathew 1981; Hećimović 1982; Hećimović and Hećimović 1989; Domac 1994; Volarić-Mršić 1994 etc.).

Cultivated irises of the Croatian and Slovenian populations (mark B on Figs 1-3) appeared in a separate group of plants determinable as *I. pallida* Lam. (Lamarck 1789). The Slovene population (Ble) is to some extent more isolated, which is probably caused by ecological modification in the morphological structure (cf. Mitić et al. 1999).

All the populations of low irises from the northern Croatian Littoral (mark C on Figs 1-3) were separated out into group, which have characteristics that correspond to the description of the endemic species *I. illyrica* Tomm. (Tommasini 1875). In this group included was also the isolated population of Stara Baška (Stb), (Fig. 3), although it seems to be an interesting case for future research, with its special morphological (cf. Mitić et al. 1999; Mitić and Pavletić 1999) and karyological features (two specimens with mitotic chromosome number $2n=22$, cf. Mitić et al. 2001).

The Alpine populations from Slovenia and Italy, separated by Cluster and PCA analysis into group (mark D on Figs 1-3) correspond in their distribution and in morpho-

logical and karyological feature diagnosis to the species *I. cengialti* Ambr. (Ambrosi 1854). Interpopulation variability is manifested in the existence of two sub-groups. The first is composed of the population from Italy (Rovereto), already described as *I. cengialti* Ambr. subsp. *cengialti* (Trinajstić 1976). This subgroup coincides with the descriptions of the Italian populations of the species *I. cengialti* as a relatively low iris with dryskinned spathes (Ambrosi 1854; Kerner 1871; Pampanini 1909, Lasén 1977). In the other group there are plants of the Slovene populations (Komarča and Kobarid), also noticed earlier as well (Paulin 1917; Mayer 1952; Sušnik 1984), described as *I. cengialti* Ambr. subsp. *vochinensis* (Paulin) Trinajstić (Trinajstić 1976).

The results show that the same taxonomic ranks have to be adopted for all four groups of Alpine-Dinaric populations of the Pallidae series and confirm our earlier conclusions from morphological and karyological analyses (Mitić et al. 1999; Mitić and Pavletić 1999, Mitić et al. 2001). For this reason, irrespective of the interpopulation variability present, the taxonomic status of the established groups should be treated in the same way, which tends to confirm the opinion about the existence of four species in the "*I. pallida*" complex, grouped in the Pallidae series (Trinajstić 1976): horticultural *I. pallida* Lam., *I. cengialti* Ambr. – endemic in Alpine region, *I. illyrica* Tomm. – endemic to the northern Adriatic Coast and *I. pseudopallida* Trinajstić – endemic to the southern Adriatic Coast.

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MORFOLOGICZNE I KARIOLOGICZNE ZALEŻNOŚCI
MIĘDZY ALPEJSKO-DYNARSKIMI POPULACJAMI Z RODZAJU *IRIS* L.,
SERIA PALLIAE (A. KERN) TRINAJSTIĆ (IRIDACEAE)

STRESZCZENIE

Powiązania między hodowanymi alpejsko-dynarskimi populacjami z rodzaju *Iris* analizowano metodami statystyki wielocechowej (skupiska, PCA i MST). Podstawę analizy wielocechowej stanowiło siedem cech morfologicznych oraz względna długość chromosomów dla 12 par chromosomów. Pomimo wyizolowania dwóch podobnych populacji (Stara Baška i Konavle), stwierdzono występowanie czterech grup w ramach serii Pallidae, którym można przypisać status gatunku: *I. pallida* Lam. wydzielonego jako gatunek hodowlany, *I. cengialti* Ambr. – endemiczny w regionie alpejskim, *I. illyrica* Tomm. – endemiczny w północnym litoralu adriatyckim, oraz *I. pseudopallida* Trinajstić – endemiczny w południowym litoralu adriatyckim. Najważniejszymi cechami wyróżniającymi analizowane grupy okazały się według analizy PCA: względna długość jedenastej i dziesiątej pary chromosomów, długość najmniejszego liścia, względna długość siódmej pary chromosomów i długość łodygi.

SŁOWA KLUCZOWE: *Iris* L., seria Pallidae (A. Kern.) Trinajstić, populacje alpejsko-dynarskie, związki morfologiczne i kariologiczne.