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MORPHOLOGICAL VARIATION OF THE ROUGH SMALL-REED (*CALAMAGROSTIS ARUNDINACEA* L.) POPULATIONS FROM NORTHERN AND CENTRAL POLAND

Maria Drapikowska, Zbigniew Celka, Katarzyna Buczkowska, Ewa Kaszkowiak

M. Drapikowska, Department of Ecology and Environment Protection, August Cieszkowski Agricultural University, Piątkowska 94c, 60-649 Poznań, Poland, e-mail: mariadra@au.poznan.pl
Z. Celka, Department of Plant Taxonomy, Adam Mickiewicz University, Umultowska 89, 61-614 Poznań, Poland, e-mail: zcelka@amu.edu.pl
K. Buczkowska, Department of Genetics, Adam Mickiewicz University, Umultowska 89, 61-614 Poznań, Poland, e-mail: androsac@amu.edu.pl
E. Kaszkowiak, Department of Detailed Plant Cultivation, Technical-Agricultural University, Kordeckiego 20c, 85-225 Bydgoszcz, Poland, e-mail: ekasz@utp.edu.pl

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ABSTRACT. Eleven populations of *Calamagrostis arundinacea* in northern and central Poland were studied with respect to 10 morphological panicle traits. The data were analysed by multivariate analysis of variance, principal component analysis (PCA), and cluster analysis. We found that the considered populations were significantly different in respect of the morphological traits under study. Intrapopulation units which have been distinguished on the basis of used morphological characters do not have systematic significance. The differences did not seem to be correlated with habitat differences.

KEY WORDS: *Calamagrostis arundinacea*, panicle, morphological variation

INTRODUCTION

Calamagrostis arundinacea (L.) Roth is a grass species widely distributed in lowlands, uplands and low mountains of Central, Northern and Eastern Europe. In Poland it is less frequent only in Silesia (Atlas... 2001). This is a forest species, strongly associated with open forests, but found also in thickets along dry forest edges, and in logging areas. *Calamagrostis arundinacea* is a characteristic species of the alliance *Calamagrostion* and the association *Bupleuro-Calamagrostietum arundinaceae* (Matuszkiewicz 2001). It usually grows in partly shaded habitats, both in moderately cold and moderately warm areas of both: the more Atlantic (western) and continental (eastern) regions of Poland. It is found on moderately humid, mesotrophic (moderately fertile), acidic and moderately acidic soils, on heavy loams, clay soils, and on mineral-humus soils (Zarzycki et al. 2002).

The rough small-reed is a polymorphic species. *Calamagrostis arundinacea* produces hybrids with *C. canescens*, *C. epigejos*, *C. pseudophragmites*, *C. stricta*, *C. **varia***, and *C. villosa* (Clarke 1980, Trawy polskie 1982, Pogan 1983, Greene 1984).

The aim of the present study was to examine variation among 11 *Calamagrostis arundinacea* populations situated in northern and central Poland (Table 1). It must be mentioned that the morphological variation of *Calamagrostis **arundinacea*** was described earlier by other investigators (Frey and Paszko 1999, Paszko 2001, 2003, Paszko and Krawczyk 2005), whose study deal with distribution, taxonomy, anatomy, and karyology of *Calamagrostis* species and based on a detailed morphological analysis of the entire plant. The present study is an attempt to estimate variation of populations situated in different parts of Poland and different habitats, on the basis of morphological panicle traits. Generative parts in grasses can display advanced variation and for this reason they are chosen for analyses of morphological variation and for taxonomic classification (**Polska księga traw 2002**).

MATERIAL AND METHODS

Material for the study was collected from 11 populations located near Koło, Krotoszyn and Poznań (central Poland), Augustów and Olsztyn (north-east Poland), as well as Szczecinek (north-west Poland). The rough small-reed was there a dominant species in the herb layer of acidophilous oak forests - *Calamagrostio arundinaceae-Quercetum petraeae*, situated in one of the largest complexes of this forest type in Europe (Brzeg et al. 2001), thermophilous oak forests, acidophilous beech forests or mixed forests (Table 1). **Hybridization between** *C. arundinacea* and *C. epigejos* can occur in all examined sites due to wide distribution of *C. epigejos* populations in

Table 1. Location of studied populations of *Calamagrostis arundinacea* and dates of sample collection

Population no.	Forest district, range, site, and region	Geographical coordinates	Habitat type
1	Koło, Kiejsze, site 1, Wielkopolska region	N 52°19'30.1" E 18°44'55.6"	thermophilous oak forest
2	Augustów, Białobrzegi, site 2, Podlaskie region	N 53°46'47.1" E 22°57'49.7"	mixed forest
3	Koło, Kiejsze, site 2, Wielkopolska region	N 52°19'28.8" E 18°45'07.6"	acidophilous oak forest
4	Augustów, Białobrzegi, site 1, Podlaskie region	N 53°47'00.4" E 22°57'23.3"	mixed forest
5	Szczecinek, Wierzchowo, site 1, Zachodniopomorskie region	N 53°46'55.4" E 16°35'53.7"	acidophilous beech forest
6	Krotoszyn, Gliśnica, site 1, Wielkopolska region	N 51°36'32.3" E 17°36'43.9"	acidophilous oak forest
7	Krotoszyn, Łówkowiec, site 1, Wielkopolska region	N 51°45'25.0" E 17°36'20.2"	acidophilous oak forest
8	Kudypy, Kudypki, site 1, Warmińsko-Mazurskie region	N 53°46'13.8" E 20°20'57.4"	mixed forest
9	Krotoszyn, Łówkowiec, site 2, Wielkopolska region	N 51°45'43.6" E 17°36'32.6"	acidophilous oak forest
10	Łopuchówko, Annowo, site 1, Wielkopolska region	N 52°29'04.8" E 17°00'28.9"	acidophilous oak forest
11	Łopuchówko, Annowo, site 2, Wielkopolska region	N 52°29'09.3" E 17°00'37.2"	acidophilous oak forest

Poland. While, hybridization between *C. arundinacea* and *C. canescens* was possible in populations nr 6, 7 and 9 (author's observations).

Thirty individuals from each population were collected every 10 meters along a transect and were analysed with regard to 10 morphological panicle traits (Table 2). From one panicle of each individual, five spikelets were isolated from the 4th node and another five from the 5th node (counting from the bottom node). Upper glumes, lower glumes, paleas and lemmas were taken from each spikelet separately. Glumes and paleas were transferred onto a microscope slide, submerged in a drop of water, covered by a cover slip, and measured under a stereoscopic microscope.

The data obtained were analysed statistically using STATISTICA 7.1 for Windows. Descriptive statistics (arithmetic means, standard deviation, minima and maxima), coefficients of variation (V) were computed to evaluate the range of variation of morphological traits. Multivariate analysis of variance (MANOVA), the one way (ANOVA) with *F*-statistics and Scheffe's test was used to analyse for interpopulation differences among means. Principal component analysis (PCA) was used to assess the relationship among populations along multivariate vectors. Cluster analysis based on Euclidean distances were performed to examine morphological similarity at the population level between the populations (Morrison 1990, Sokal and Rohlf 1997, Triola 1998, Łomnicki 2000).

Table 2. Studied morphological traits of *Calamagrostis arundinacea*

Trait no.	Trait description
1	Length of upper glume (*gluma superior*) in 4th node (mm)
2	Length of lower glume (*gluma inferior*) in 4th node (mm)
3	Length of palea (*palea superior*) in 4th node (mm)
4	Length of lemma (*palea inferior*) in 4th node (mm)
5	Length of upper glume in 5th node (mm)
6	Length of lower glume in 5th node (mm)
7	Length of palea in 5th node (mm)
8	Length of lemma in 5th node (mm)
9	Panicle length (mm)
10	Total number of nodes

RESULTS AND DISCUSSION

Descriptive statistics and coefficients of variation of all examined traits computed for each population are given in Table 3. We found that population 8 (from Warmińsko-Mazurskie region, mixed forest) has the lowest mean values for almost all traits except for trait 10 (total number of nodes). The highest mean values for traits 1-6 were found in population 9 (from Wielkopolska region; acidophilous oak forest), but plants from this population have a low mean value for traits 9 (panicle length) and 10. The longest panicles (trait 9) are in plants from population 11 (Wielkopolska region; acidophilous oak forest). It was found that there is no single character, among applied 10 morphological traits, which would characterise clearly any group of population. Traits 9 and 10 are the most variable in most populations, as their variation coefficients are usually higher than 10%, while mean values for traits 1-8 (lengths of glumes and paleas and lemmas) are usually lower than 10%. The highest variation coefficients (V%) for trait 9 and 10 are in population 6 (23.46% and 17.75%). The lowest V% have traits 1 (length of lower glume in 4th node) and 2 (length of palea in 4th node).

According to the results of MANOVA, the general hypothesis stating that there are no significant differences between studied populations with respect to all the traits together was rejected, as the Rao statistic was equal to 5.79 ($p < 0.05$). Univariate analysis of variance (ANOVA) shows that the populations studied differ significantly with respect to means of individual traits. The highest *F* values were observed for traits: 10 (total number of nodes), 1 (length of upper glume in 4th node), 2 (length

Table 3. Arithmetic means (M), minimum, maximum (min, max) and variation coefficients (V%) of the investigated traits of *Calamagrostis arundinacea* in populations no. 1-11

Population no.	Trait 1				Trait 2				Trait 3				Trait 4				Trait 5			
	M	min	max	V%	M	min	max	V%	M	min	max	V%	sM	min	max	V%	M	min	max	V%
1	4.30	3.66	5.32	8.56	4.57	3.83	5.63	9.23	3.26	2.56	3.85	8.21	3.56	2.86	4.10	8.00	4.28	3.67	5.03	8.72
2	4.15	3.56	5.17	9.62	4.41	3.78	5.46	9.65	3.44	3.09	3.90	7.06	3.61	3.19	4.10	6.82	4.13	3.52	5.05	8.51
3	4.20	3.62	4.91	8.16	4.47	3.84	5.18	9.16	3.21	2.68	3.74	8.55	3.49	2.92	3.98	7.63	4.21	3.57	5.24	9.02
4	4.43	3.70	5.04	6.80	4.73	3.83	5.68	7.34	3.45	2.55	4.21	9.24	3.69	3.00	4.53	8.06	4.41	3.25	5.10	7.27
5	3.94	3.43	4.47	6.35	4.26	3.65	4.78	6.37	3.30	2.90	3.58	5.08	3.48	3.00	3.88	5.63	3.87	3.38	4.45	6.13
6	3.98	3.36	4.68	7.41	4.31	3.65	4.98	7.52	3.12	2.49	3.67	8.90	3.36	2.63	3.88	9.02	4.03	3.37	4.85	8.77
7	4.37	3.75	5.59	11.32	4.64	3.92	5.80	11.53	3.46	2.77	4.41	10.93	3.77	3.32	4.73	9.97	4.40	3.57	5.65	11.54
8	3.74	3.18	4.36	8.61	3.96	3.34	4.57	8.19	3.23	2.59	3.79	8.52	3.44	2.87	3.89	8.23	3.73	3.01	4.40	8.51
9	4.47	3.52	5.37	8.25	4.80	3.74	5.60	8.13	3.55	2.88	4.11	7.16	3.79	3.02	4.41	7.21	4.53	3.65	5.13	7.65
10	4.01	3.19	4.62	10.38	4.25	3.33	5.13	11.55	3.36	2.63	4.03	9.54	3.57	2.78	4.20	9.34	4.00	3.18	4.89	10.94
11	4.41	3.81	5.04	6.44	4.73	4.11	5.14	5.05	3.40	2.88	3.97	8.10	3.63	3.10	4.17	7.02	4.31	3.71	4.91	6.53

Trait 6				Trait 7				Trait 8				Trait 9				Trait 10			
M	min	max	V%	M	min	max	V%	M	min	max	V%	M	min	max	V%	M	min	max	V%
4.55	3.90	5.41	9.32	3.27	2.85	3.87	8.35	3.53	3.13	4.07	7.47	148.8	112.00	195.00	12.00	11.07	10.00	12.00	6.25
4.40	3.75	5.47	8.98	3.37	3.00	3.84	6.59	3.56	3.13	4.03	6.45	163.23	114.00	240.00	16.95	12.03	3.00	13.00	15.74
4.48	3.69	5.36	9.23	3.21	2.60	4.04	10.31	3.49	2.99	4.31	9.42	133.55	92.00	180.00	18.48	12.44	11.00	14.00	7.16
4.75	3.51	5.87	8.10	3.43	2.62	4.34	10.76	3.68	2.81	4.98	8.58	161.56	122.00	202.00	19.67	13.28	11.00	16.00	9.40
4.18	3.74	4.69	5.85	3.26	2.91	3.66	5.74	3.43	3.04	3.89	5.00	132.66	91.00	174.00	16.01	11.80	10.00	15.00	10.77
4.38	3.73	5.13	8.47	3.16	2.50	3.83	9.54	3.39	2.68	4.01	10.19	146.99	99.00	221.00	23.46	12.30	3.00	16.00	17.75
4.67	3.81	5.83	11.19	3.51	2.95	4.45	9.87	3.80	3.27	4.66	9.10	152.53	96.00	188.00	15.67	14.47	10.00	18.00	11.87
3.99	3.22	4.78	8.73	3.21	2.45	3.88	9.83	3.43	2.77	4.11	9.11	121.04	78.00	170.00	19.71	12.58	11.00	14.00	6.43
4.87	3.80	5.50	7.41	3.62	2.77	4.31	8.26	3.87	3.14	4.52	7.32	128.87	101.00	178.00	15.04	13.47	11.00	16.00	9.50
4.26	3.38	5.23	11.84	3.35	2.82	3.84	8.63	3.56	3.01	4.04	8.31	159.44	98.00	212.00	21.00	14.16	9.00	18.00	13.63
4.63	4.08	5.19	6.00	3.40	2.93	4.03	8.40	3.56	3.04	4.24	7.91	166.64	112.00	241.00	20.15	13.52	11.00	17.00	10.70

of lower glume in 4th node), 5 (length of upper glume in 5th node) and 6 (length of lower glume in 5th node) (Table 4).

Our study showed degree of morphological variation within and between natural populations of *C. arundinacea*. The observed morphological variation between individuals may be caused by a phenotypic response to edaphic conditions as well as can result from genetic differentiation of the species. Besides, as a result of crossing with other species of the genus *Calamagrostis*, the gene pools of populations are enriched by new genes, which may induce a significant morphological variation (Frey and Paszko 1999). Studies on genetic variability in local populations of *C. arundinacea* based on peroxidases were earlier perform and described extent genetic variability (Krzakowa et al. 2005). Results of this study support earlier reports about its significant morphological variation (Frey and Paszko 1999). The present study also aimed to answer the question whether variation between particular populations is related to habitat. Cluster analysis, using phenetic distances between populations indicate two groups of populations (Fig. 1). The first group consists of populations 3 (near Koło), 5 (near Szczecinek), 8 (near Olsztyn) and 9 (near Krotoszyn). Population 5 inhabits acidophilous beech forest, population 8 were collected in mixed forest, whereas populations 3, and 9 are found in acidophilous oak forests. The second group consists of two subgroups. The first subgroup includes populations 4 (near Białobrzegi), 10 (near Łopuchówko), populations 2 (near Białobrzegi) and 11 (near Łopuchówko). Population 4 was found in a mixed forest, while population 10 is associated

Table 4. Results of variance analysis (ANOVA) of studied populations of *Calamagrostis arundinacea*: *F*-statistics for studied traits (*p ≤ 0.05; **p ≤ 0.01)

Trait no.	PCA1	PCA2
1	**0.88**	0.18
2	**0.88**	0.18
3	**0.87**	0.07
4	**0.90**	0.11
5	**0.91**	0.17
6	**0.89**	0.18
7	**0.86**	0.13
8	**0.89**	0.13
9	0.22	**0.75**
10	0.04	**0.83**

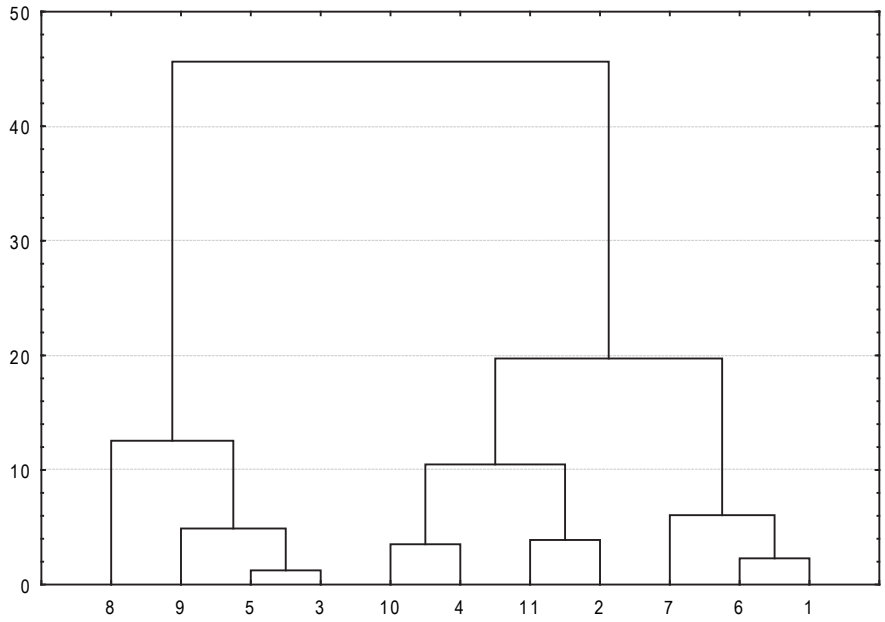

Fig. 1. Results of the cluster analysis (UPGMA), with the Euclidean distances for the 11 populations of *Calamagrostis arundinacea*

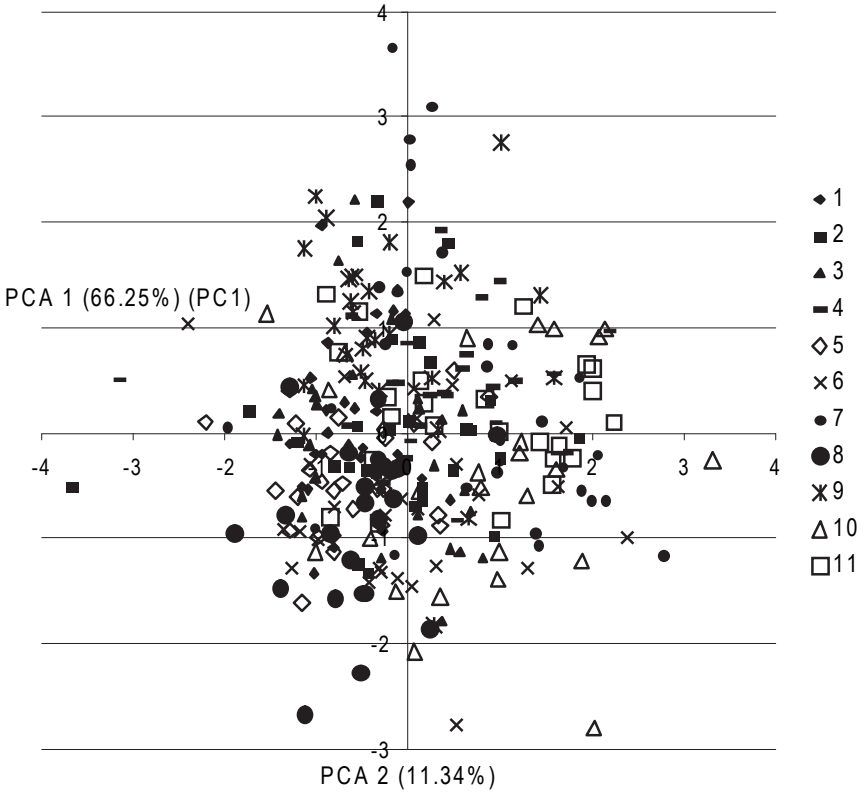

Fig. 2. Principal Component Analysis (PCA). Scatter diagram of 11 populations with centroids of the studied samples of *C. arundinacea* in the first two principal components (PCA1, PCA2)

with acidophilous oak forest, population 11 occupying areas with predominant oaks but population 2 originating from a mixed forest. The second subgroup includes three populations: 6 and 7 (near Krotoszyn), they are collected in acidophilous oak forest, and population 1 (near Koło) from thermophilous oak forest. According to Principal Component Analysis (PCA) (two principal components contain 77.59% information – V1 = 66.25%, V2 = 11.34%), the distribution of samples from 11 *C. arundinacea* populations in the space of the first two axes indicates that morphological variability of the studied populations of *C. arundinacea* is continuous, there is no clearly separated groups of populations distinguished by the analysis (Fig. 2).

It can be concluded that on the basis of morphological trait analysis, the studied populations of *C. arundinacea*

are significantly different. However, edaphic differences had probably a small influence on the morphological variation of the studied *C. arundinacea* populations.

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