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Is there any relation between quantitative traits interesting for ornamental breeding and genome size in dog roses (*Rosa* sect. Caninae)?

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Abstract

Ferus, P., Pachl, Š., Ďurišová, Ľ., Bartošová-Krajčovičová, D., Rovná, K. 2013. Is there any relation between quantitative traits interesting for ornamental breeding and genome size in dog roses (*Rosa* sect. Caninae)? *Folia oecol*., 40: 11–21.

To define participation of genome size as well as most important environmental factors in variability of quantitative characters interesting for ornamental breeding, a collection of wild dog roses (*Rosa* sect. Caninae) from Malé Karpaty mountains (localities Modra – Pažite and Vrbové – Baraní dvor) and Zobor hills (locality Zobor – Lyžiarska lúka) were analysed. We found a large variability in percentage of leaves longer than 70 mm (16–58%) and those of dark-green colour (28–78%), portion of half-full flowers (0–6%) and those of intense pink colour (0–100%), and percentage of hips longer than 20 mm (0–45%) and those of intense red colour (18–48%), among shrubs. Their genome size ranged from 2.33 to 2.92 pg. Our map survey revealed stagni-eutric cambisols in Modra – Pažite, haplic luvisols on loess in Vrbové – Baraní dvor, and rendzic/chromi-rendzic leptosols in Zobor – Lyžiarska lúka (increasing soil quality from stand to stand). Leaves and flowers grew in conditions of average temperature 15.3 °C (Modra – Pažite and Zobor – Lyžiarska lúka) and 14.5 °C (Vrbové – Baraní dvor). Precipitation ranged from approximately 300 mm in Modra – Pažite to 400 mm in Zobor – Lyžiarska lúka. Average temperature for hip formation varied from Zobor – Lyžiarska lúka (19.6 °C) to Modra – Pažite (20.4 °C). In this period, precipitation sum was round 200 mm in Zobor – Lyžiarska lúka and approximately 250 mm in the rest two stands. Quantitative traits of all dog roses were generally less correlated to genome size and environmental factors. However, in *R. canina* genotypes, leaf length was determined mainly by genome size (r = 0.437) and temperature (r = –0.316), and leaf colour by temperature (r = 0.777) and precipitation (r = 0.557), flower richness only by temperature (r = –0.320), flower colour by temperature (r = 0.606) and soil quality (r = –0.559), and hip colour was defined mainly by precipitation (r = 0.588), then by temperature (r = 0.427) and genome size (r = –0.362); but no factor had important influence on hip length. We can conclude that except for leaf size, all analysed quantitative traits were mainly determined by environmental factors.

Keywords

dog roses with breeding potential, quantitative traits, genome size, environment

Introduction

Roses are jewels of gardens, arboretums and urban vegetation for centuries (Kordes, 1966; Krüssmann, 1986). Till today, thousands of rose cultivars with different habitus, phenology, flower, leaf and prickle dimensions, shapes and colours have been bred. As summarises Gudin (2000), present rose breeding focusses on flower production, post-harvest longevity, resistance to pests and diseases, and to environmental constraints (particularly drought, cold), as well as cultivar-rootstock compatibility.

Dog roses (sect. Caninae) represent a specific group of roses with leaning liana or geyser shrub habitus, spiny sprouts, straight or hooked prickles, leaves of ±3 leaflet pairs, lobed outer sepals, pink or white petals, free style and irregular meiosis (2n = 28, 35, 42, 49). They can be found in sunny stands – forest edges and clearings, balks, fallows, dams, along road and railway communications, on rocks – in scrub communities (order Prunetalia), eventually grass communities (alliance Bromion erecti) (Větvička and Bertová, 1992; Větvička, 1995).

Many of them are attractive for breeders. MacPhail and Kevan (2009) list research teams from 60ties of the last century till present, analysing hip / flower percentage and ways of seed establishment (agamospermy, autogamy, geitonogamy, xenogamy) in different cross combinations between wild roses. Van Huylenbroeck et al. (2007) refer to test crosses of European wild roses with tetraploid cultivated roses. Interspecific hybridisation can occur among rose species at all ploidy levels (Nybom et al., 2005) but, as indicate Grossi and Jay (2002), best success can be expected in situations: parents of the same chromosome number, or triploid female and tetraploid male. In more works (Kroon and Zeilinga, 1974; Jičínská, 1976; Nybom et al., 1997; Olsson et al., 2000; Werlemark and Nybom, 2001), morphological consequences of hybridisation in offspring generations, were studied, as well.

Qualitative and quantitative traits interesting for rose breeding have recently been studied particularly using genetic markers (Debener, 1999; Crespel et al., 2002). However, despite of many indicia from agricultural crop breeding (Laptev, 1988) and numerous karyological and cytometrical surveys in Rosaceae family and particularly genus *Rosa* have been accomplished (Dickson et al., 1992; Yokoya et al., 2000; Roberts et al., 2009; Jedrzejczyk and Sliwinska, 2010; Jian et al., 2012), there is almost no data on relation between quantitative characters and genome size. To ascertain the influence of genome size as well as the most important components of environment on leaf, flower and hip mass and their colour intensity, we analysed dog roses from western Slovakia.

Table 1. Taxonomic determination of selected wild roses from three research localities in western Slovakia

Locality	GPS coordinates	Height above sea level	Individual	Taxon
Modra – Pažitie	N 48°20'46.13" E 17°19'33.38"	229 m	1	*R. canina* L. *var. canina*
			2	*R. corymbifera* Borkh.
			3	*R. canina* var. *dumalis* Baker non Bechst.
			4	*R. canina* L. var. *canina*
Vrbové – Baraní dvor	N 48°37'23.3" E 17°41'29.98"	298 m	1	*R. canina L. var. canina*
			2	*R. canina var. dumalis* Baker non Bechst.
			3	*R. canina L. var. squarosa* Rau
			4	*R. canina var. dumalis* Baker non Bechst.
			5	*R. tomentosa* Sm.
Zobor – Lyžiarska lúka	N 48°20'56.27" E 18°05'47.71"	414 m	1	*R. canina* L. var. *squarosa* Rau
			2	*R. micrantha* var. *perparva* (Borbás) R. Keller in Asch. and Graeb.
			3	*R. dumalis* Bechst.
			4	*R. canina* var. *lapidicola* Heinr. Braun
			5	*R. canina* L.

Material and methods

Experimental area and plant material

For this study, localities with tradition of botanical rose research were chosen (Svobodová et al., 2007; Eliáš jun., 2009). In Malé Karpaty region we analysed wild roses from Modra part Pažite and planted botanical ones in Vrbové part Baraní dvor (Table 1). The third stand with natural occurrence of wild roses was Zobor hill part Lyžiarska lúka, one of the highest peak of Zobor hills belonging to Tríbeč mountains. All of them represent open sunny and warm sites, meeting needs of roses (Kordes, 1966; Walter, 2011). Soil types with bonity categorisation (Granec and Šurina, 1999; Hanes et al., 1999), as well as most important meteorological parameters influencing leaf, flower and hip formation (temperature averages and precipitation sums for period June–August 2009 and April–June 2010) were provided by Soil Science and Conservation Research Institute of the Slovak Republic and Slovak Hydrometeorological Institute, respectively. Scoring of soils was adapted to substrate requests of roses (Kordes, 1966; Walter, 2011). Meteorological data from the nearest meteo-stations to the research localities were applied: 1. Modra – Pažite: station Slovenský Grob; 2. Vrbové – Baraní dvor: station Piešťany; and 3. Zobor – Lyžiarska lúka: station Nitra.

In the middle of June 2009 (the most adequate term according to Větvička (2001)), rose shrubs with patulous – pendulous habitus and potential for ornamental breeding were selected and determined (Table 1) using determination key of Kerényi-Nagy (2012).

Morphological analyses

In August 2009, hundred hips per analysed rose shrub were collected and divided into size/shape categories according to Bauer (2005):

A) – spheric, very little (4–10 mm)
B) – spheric, middle large (13–20 mm)
C) – oval, middle large (15–20 mm)
D) – oval, large (20–30 mm)
E) – hippy, long (10–30 mm)
F) – hippy, oblong (more than 30 mm)
G) – apple shaped – spheric, large (30–40 mm).

Thereafter we defined percentage of hips larger than 20 mm (categories D, F, G) per shrub.

From hips coloured in following colour spectrum (Royal Horticultural Society, London),

A) – N 30 A
B) – N 30 B
C) – N 30 C
D) – 40 A
E) – 40 B
F) – 40 C,

portion of those with most intense red tones (highest concentration of carotenoids; Méndez and Mínguez-Mosquera, 2000) was determined (category A and D).

Morphologic analyses continued in May–June 2010 when quantitative parameters of fifty flowers and leaves were ascertained (morphology of selected rose shrubs and their flowers see in Fig. 1).

For evaluation of flower richness scale of Větvička (2001) was followed:

A) – simple (of 5 petals)
B) – half-full (of 6–14 petals)
C) – freely or moderate full (of 15–20 petals)
D) – full (of 21–40 petals)
E) – dense full (of more than 40 petals).

Since we found only A and B category, percentage of half-full flowers was expressed.

Flower corolla colour in respective individuals ranged in following scale (Royal Horticultural Society, London):

A) – 68 B
B) – 68 C
C) – 68 D
D) – 69 A
E) – 155 A
F) – 155 B.

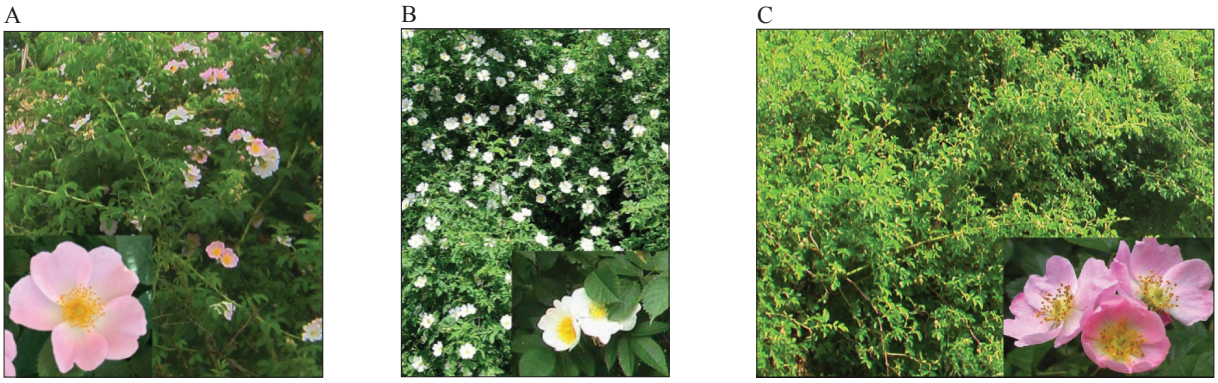

Fig. 1. Wild roses from Western Slovakia: a) *R. canina* var. *dumalis* Baker non Bechst. from Modra – Pažite; b) *R. canina* L. var. *canina* from Vrbové – Baraní dvor; and c) *R. canina* var. *lapidicola* Heinr. Braun from Zobor – Lyžiarska lúka.

We selected flowers of most intense pink tones (highest concentration of carotenoids and anthocyanins (Engster and Märki-Fisher, 1991); category A and B) and defined their portion in total number of analysed flowers.

Leaves were examined for length (Betten, 2003) and green colour intensity (Döpper and Unterlercher, 2007). Following leaf length and colour categories were identified:

A) – less than 40 mm – small
B) – 40–70 mm – middle large
C) – more than 70 mm – large

A) – dark green with glazy surface
B) – light green with glazy surface
C) – dark green with matt surface
D) – light green with matt surface.

We were interested in portion of leaves larger than 70 mm (category C) and those of dark green colour (categories A and C) per shrub.

Determination of genome size and ploidy level

Nuclear genome size of rose leaf samples was determined by flow cytometry using CyFlow cytometer (Partec GmbH., Germany) with argon laser emitting green light of wavelenght 532 nm (Doležel et al., 2007). As an internal standard we used pea leaves (*Pisum sativum* L. ´Ctirad´) of genome size 9.09 pg.

Rose cuttings from one-year old sprouts were collected in September 2010 and let overwinter in greenhouse in perlite-sand substrate. In early spring 2011, cuttings were transferred into lab and let sprout in water. Pea plants were cultivated in laboratory conditions in soil substrate.

In sample preparation and staining we followed procedure defined by the producer of Partec-CyStain PI Absolut P kit (Partec GmbH., Germany). Segments of young but expanded rose leaves of area 0.5 cm^2 were cut (into 0.5 mm pieces) in Petri dishes with 500 µl extraction buffer using fresh razor blade, and let incubate at lab temperature for 60–90 seconds. Mixture was filtered through nylon mesh of 42 µm pore size. Then 2 ml of staining buffer containing propidium iodide (PI) and RNAse, as well as 100 µl 1% polyvinylpyrrolidone (PVP) for nuclei stabilisation (Yokoya et al., 2000), were added to the filtrate. Nuclei were stained at 4 °C in the dark for 60 minutes. The same method (except of addition of PVP and with 15 min staining time) was applied for pea standard preparation and just before cytometric analysis sample and standard were mixed together in ratio 1 : 1. As outputs we obtained fluorescence intensity histograms made from at least 5,000 particles (Fig. 2). Their analysis provided FloMax software (Partec GmbH., Germany). Every sample was examined three times on three consecutive days.

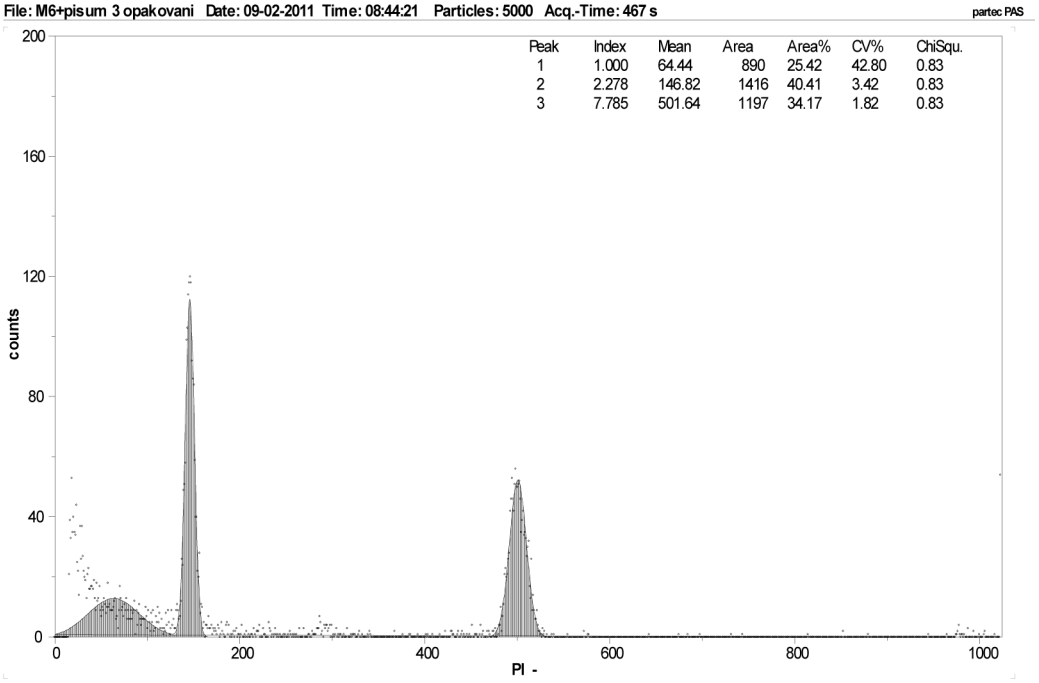

Fig. 2. Example of fluorescence histogram analysis in *R. canina* var. *dumalis* Baker non Bechst. from Modra – Pažite. From left: first wide peak of small subcellular particles binding PI, second peak – rose leaf cell nuclei, third peak – pea leaf cell nuclei. Determination accuracy is expressed by coefficients of variance (CV%), defining divergence from normal statistical distribution (CVs not exceeding 4% indicate clear genome size determination in Rosaceae family).

Genome size (pg) was calculated from relative peak position (fluorescence intensity) of standard and sample (Fig. 2), using formula:

$$GS(sample) = \frac{RP(sample) \,.\, GS(standard)}{RP(standard)},$$

where GS is genome size, RP is relative position of a peak and GS (standard) is 9.09 pg.

Ploidy level of rose samples we calculated from genome size determinations. In this case, *Rosa arvensis* Huds. (diploid (2x) of genome size 0.96 pg) served as standard. Stem cuttings, collected from Zobor hills in winter 2011, were let sprout as in analysed roses. Ploidy level calculation followed this form:

$$PL(sample) = \frac{GS(sample) \,.\, 2}{GS(standard)},$$

where PL is ploidy level, GS is genome size, GS (standard) is 0.96 pg, 2 – somatic tissues are diploid (2C).

Statistical analysis

Quantitative morphological parameters of dog roses from all three experimental sites were submitted to correlation analysis (application MS Excell 2010) in order to characterize participation of genome size, soil and weather conditions in their determination. Variability in genome size of respective rose samples was examined by analysis of variance (LSD-test; application Statgraphics Centurion XVI).

Results

Quantitative morphological traits

In hips we analysed size and red colour intensity (Table 2). Length exceeding 20 mm were found in 0–45% examined hips in roses from Modra – Pažite, 0–25% in roses from Vrbové – Baraní dvor, and 13–32% in those from Zobor – Lyžiarska lúka. Percentage of hips with intense red colour ranged in intervals 18–43, 30–48 and 19–36 in Modra – Pažite, Vrbové – Baraní dvor and Zobor – Lyžiarska lúka, respectively.

Most commonly, studied roses established simple 5-petal flowers. Only in some cases (Modra – Pažite: individual 3; Vrbové – Baraní dvor: individuals 2 and 3; Zobor – Lyžiarska lúka: individual 2), half-full flowers were formed but their frequency was low (2–6%). On the other hand, except for roses from Vrbové – Baraní dvor (three of five shrubs did not form any flower), flowers coloured by intense tones of pink colour were found relatively often. In roses from Modra – Pažite we found 60–98% of them and in Zobor – Lyžiarska lúka from 32 to 60%.

Table 2. Quantitative trait analysis in leaves, flowers and hips of respective rose individuals with different origin (as percentage of samples with specified attribute)

Locality	Shrub	Hip longer than 20 mm	Intense red hip colour	Half-full flower	Intense pink flower colour	Leaf longer than 70 mm	Dark-green leaf
Modra – Pažite	1	45	43	0	60	32	58
	2	8	40	0	72	26	42
	3	8	35	4	84	16	44
	4	0	18	0	98	30	62
Vrbové – Baraní dvor	1	3	34	0	0	48	40
	2	25	30	6	0	42	28
	3	12	41	2	0	22	48
	4	15	48	0	78	20	42
	5	0	30	0	100	30	64
Zobor – Lyžiarska lúka	1	13	20	0	58	22	70
	2	29	23	4	60	42	40
	3	27	36	0	44	58	50
	4	23	19	0	46	36	70
	5	32	28	0	32	24	78

Focussing on leaf length, in wild roses from Modra – Pažite we observed only 16–32% and in Vrbové – Baraní dvor 20–48% of leaves longer than 70 mm, respectively. The highest variability of this parameter (24–58%) exhibited roses from Zobor – Lyžiarska lúka. Portion of dark green leaves was generally much higher: in Modra – Pažite it ranged between 42 and 62%, in Vrbové – Baraní dvor 28 and 64% and in Zobor – Lyžiarska lúka it was in interval 40–78%.

Genome size and ploidy level

Analysis of variance in genome size of whole wild rose collection revealed more groups of individuals (Table 3). Both extremes (group *a* with values round 2.35 pg, and group *g* with value slightly exceeding 2.90 pg) were observed in Vrbové – Baraní dvor. This mirrored in calculated ploidy level (4.85x and 4.92x as minimum values and 6.07x as maximum value).

Environmental conditions

Soils in respective research localities showed relative homogenity (Table 4). Our soil map survey revealed stagni-eutric cambisols with unsaturated sorption complex, slightly acidic reaction and middle humus content in Modra – Pažite, haplic luvisols on loess with saturated sorption complex, neutral reaction and middle humus content in Vrbové – Baraní dvor, and rendzic/chromi-rendzic leptosols of saturated sorption complex, slightly basic reaction and high humus content in Zobor – Lyžiarska lúka.

Hip formation generally realized in relatively warm conditions – average June–August 2009 temperature ranged from 19.6 (Zobor – Lyžiarska lúka) to 20.4 °C (Modra – Pažite), and precipitation sum for the same period was 199–247.4 mm (Table 5). On the other hand, flowers and leaves grew in very wet conditions – average April–June 2010 temperature inVrbové – Baraní dvor was 14.5 °C, and for Modra – Pažite and Zobor – Lyžiarska lúka we calculated 15.3 °C. Precipitation sum for this period ranged between 305.7 mm in Modra –Pažite and 409.9 mm in Zobor – Lyžiarska lúka.

Relations

Comparing correlation analyses in *R. canina* individuals, only, and all roses, much stronger relations could be seen for the former ones (Table 6). The only exceptions were negative moderate correlations of hip size to average June–August 2009 temperature ($r = –0.318$) and precipitation sum for this period ($r = –0.420$), as well as positive moderate correlation of leaf size to soil quality ($r = 0.351$).

Table 3. Genome size and ploidy level (calculated using genome size of *Rosa arvensis* Huds. standard) of wild roses from traditional research localities in Western Slovakia. Letters indicate statistically significant difference at $P < 0.05$

Locality	Individual	Genome size [pg]	Calculated ploidy (x)
Modra – Pažite	1	*2.45 ± 0.05 ab	5.09
	2	2.70 ± 0.04 ef	5.62
	3	2.52 ± 0.12 bc	5.25
	4	2.70 ± 0.02 ef	5.61
Vrbové – Baraní dvor	1	2.92 ± 0.06 g	6.07
	2	2.62 ± 0.10 cde	5.45
	3	2.33 ± 0.03 a	4.85
	4	2.61 ± 0.08 cde	5.43
	5	2.36 ± 0.03 a	4.92
Zobor – Lyžiarska lúka	1	2.66 ± 0.03 def	5.54
	2	2.72 ± 0.05 ef	5.66
	3	2.53 ± 0.07 bcd	5.27
	4	2.53 ± 0.02 bcd	5.26
	5	2.79 ± 0.04 fg	5.80

* Average ± SD.

Table 4. Soil quality in studied locations. Soil bonity code comprises characteristics of climatic region (first two numbers), soil type determination (second two numbers), then slope, skelet content and grain size distribution (the last three numbers)

Locality	Soil bonity code	Soil type	SCS [%]	pH	HC [%]	Score
Modra – Pažite	0171232	Stagni-eutric cambisols	40	5.6–6.5	2	3
Vrbové – Baraní dvor	0244202	Haplic luvisols on loess	>75	6.6–7.2	2.5	5.31
Zobor – Lyžiarska lúka	0292682	Rendzic leptosols and chromi-rendzic leptosols	>75	7.3–7.7	5.5	5.84

SCS, sorption complex saturation; HC, humus content in the soil. Soil scoring adapted to rose requests (Kordes, 1966; Walter, 2011): SCS 40% – 1, SCS > 75 – 2.125; pH 5.6–6.5 – 3, pH 6.6–7.2 – 2, pH 7.3–7.7 – 1; HC 2 – 1, HC 2.5 – 1.25, HC 5.5 – 2.75.

Table 5. Average air temperatures (t) and precipitation sums (p) in analysed locations in periods important for formation of respective plant organs (June–August 2009: hips; April–June 2010: leaves)

Locality	June–August 2009		April–June 2010	
	t [°C]	p [mm]	t [°C]	p [mm]
Modra – Pažite	20.4	247.4	15.3	305.7
Vrbové – Baraní dvor	20.0	240.0	14.5	346.7
Zobor – Lyžiarska lúka	19.6	199.0	15.3	409.9

Table 6. Correlation coefficients (r) between quantitative morphological traits of roses and their genome size as well as soil and weather conditions during formation of respective plant organs

Trait	Genome size	Soil quality	Temperature	Precipitation
Rosa canina				
Hip size	–0.294*	0.049	–0.148*	–0.232*
Hip colour	–0.362**	–0.217*	0.427**	0.588***
Flower richness	–0.268*	–0.117*	–0.320**	–0.294*
Flower colour	–0.070	–0.559***	0.606***	–0.277*
Leaf size	0.437**	0.166*	–0.316**	0.01
Leaf colour	0.075	0.139*	0.777***	0.557***
All analysed roses				
Hip size	–0.077	0.176*	–0.318**	–0.420**
Hip colour	–0.280*	–0.251*	0.410**	0.517***
Flower richness	–0.069	–0.014	–0.174*	–0.073
Flower colour	–0.158*	–0.463**	0.376**	–0.289*
Leaf size	0.160*	0.351**	–0.026	0.348**
Leaf colour	–0.088	0.146*	0.435**	0.365**

*** strong ($1 > r \geq 0.5$), ** moderate ($0.5 > r \geq 0.3$) and * weak linear correlation ($0.3 > r \geq 0.1$).

Despite of weak relations, hip size in *R. canina* individuals was mostly determined by genome size (r = –0.294) and precipitation sum (r = –0.232). On the other hand, its colour was strongly correlated to precipitation sum (r = 0.588) and moderately to average temperature and genome size (r = 0.427 and r = –0.362, respectively). Flower richness seemed to be dependent mainly on temperature (r = 0.320) and less on genome size (r = –0.268). However, most important influence on flower colour intensity had soil quality (r = –0.559) and temperature (r = 0.606). Although leaf size was determined mostly by genome size (r = 0.437) and temperature (r = –0.316), leaf colour intensity mostly by atmospheric conditions (r = 0.777 for average temperature and r = 0.557 for precipitation sum).

Discussion

Rosa sect. Caninae comprises alloploid species resulting from unbalanced, so called caninae meiosis, autopolyploidisation, hybridisation and apomixis. They transmit only seven chromosomes (from seven bivalents) through pollen whereas 21, 28 or 35 chromosomes (from seven bivalents and 14, 21 or 28 univalents (depending on ploidy level)) come from egg cell. Therefore, most of genetically determined traits are expected to be matroclinally inherited (Nybom et al., 2004, 2006; Popek, 2007; Wissemann and Ritz, 2007; Kovarik et al., 2008; Ritz et al., 2011). Present knowledge on maternal and paternal inheritance of rose characters review Wissemann and Ritz (2007). From those related to traits analysed by us, leaf shape, epicuticular waxes as well as hip form and size were inherited maternally, and colour and size of flowers were of intermediate inheritance. As indicate Pécrix et al. (2011), high temperature has potential to increase gamete ploidy level in roses. Decrease in pollen viability, pollen ectexine defects and appearance of diploid pollen grains as a result of spindle misorientation in telophase II, were induced by temperature 36 °C during early meiosis. Formation of unreduced gametes is often associated with spontaneous hybridisation (Ritz and Wissemann, 2011) of commonly selfing dog roses (Nybom et al., 2005). Ueda and Akimoto (2001) refer to breaking down self-incompatibility in the genus *Rosa* with polyploidisation. Heterogamy and apomixis in *R. canina* rootstocks was widely described in a morphological and cytological work of Kroon and Zeilinga (1974). Recently, Werlemark (2000) pointed to possible occurrence of apomixis when in 10% of progenies coming from reciprocal crosses between *R. dumalis* and *R. rubiginosa* (both from sect. Caninae) was not found any of RAPD marker from pollen donor plant. Using the same methodology, Nybom et al. (2006) detected 5% of apomicts and 49% of hybrids in interspecific crosses of dog roses. Moreover, level of sexual reproduction in dog roses, as facultative apomicts, can be strongly affected by environmental factors, as well (Marshall and Brown, 1981).

In our study, ploidy level of 4.85–6.07x was calculated for wild roses. Since a classical karyological work of Májovský and Murín (1987) indicates 2n = 35 chromosomes in all analysed taxa, this large variation in calculated ploidy level could be explained by different length of repeating non-coding DNA sequences – retrotransposons (Vitte and Panaud, 2005; Bennetzen et al., 2005), modifying nuclear genome size. As review Kumar and Bennetzen (1999), retrotransposon length depends on numerous biotic and abiotic stress factors (high temperature among them). Our data on genome size are relatively consistent with literature. Genome size survey in angiosperms made by Bennett and Leitch (1995) revealed 2.90 pg for *R. canina*. Yokoya et al. (2000) analysed a scale of rose species from different sections and their result for *R. canina* genome size was very similar (2.91 pg). Roberts (2007), testing effects of plant part selection as well as tissue herbarisation on genome size in more species, obtained the same values. Next work of Roberts et al. (2009) added information on genome size of *R. corymbifera*, *R. dumalis* and *R. micrantha* – 2.82–3.11 pg, 2.83–3.09 pg and 2.78 pg, respectively (higher than in our study). However, among *R. canina* clones they also identified such ones with genome size ranging in interval 3.38–3.55 pg, and took them for hexaploids. This result support our notion that calculated ploidy levels nearing to 6x do not mean real hexaploidy but are consequents of longer retrotransposon chains and use of concrete standard karyotype for calculation (genome size of *R. arvensis* varies as well (1.12 pg in work of Yokoya et al., 2000)). Thus, it is difficult to determine rose ploidy level from genome size because of high genomic diversity (Roberts et al., 2009).

Zlesak (2009) tested possibilities to define sporophytic and gametophytic ploidy levels in diverse rose genotypes from pollen diameter and guard cell length. He found out that polled diameter was useful in gametophyte ploidy prediction, only, but because of large variability, guard cell length cannot serve for any ploidy level estimation. This is partly consistent with generalisation of Knight and Beaulieu (2008) that genome size correlations are relatively strong at the cellular level (guard and epidermal cell size) but decrease in predicting power with increasing phenotypic scale (stomatal density, seed mass, leaf mass/area and wood density, photosynthetic rate, maximum height). From studied quantitative traits, only hip colour intensity and leaf size of *R. canina* genotypes were determined by genome size in larger extent. Soil quality significantly influenced flower colour intensity, only. The widest effect among factors had temperature. It importantly affected all traits, except for hip size. Precipitation had marked effect on hip and leaf colour intensity. Thus, the

effect of environmental factors was decisive for almost all studied quantitative traits interesting for ornamental breeding, except for leaf size.

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Sú kvantitatívne znaky divo rastúcich ruží (*Rosa* sect. *Caninae*), zaujímavé pre okrasné šľachtenie, určené veľkosťou genómu?

Súhrn

Za účelom definovania podielu veľkosti genómu ako aj významných environmentálnych faktorov na variabilite kvantitatívnych znakov zaujímavých pre okrasné šľachtenie ruží, boli analyzované divo rastúce ruže (*Rosa* sect. Caninae) z Malých Karpát (lokality Modra – Pažite a Vrbové – Baraní dvor) a Zoborských vrchov (lokalita Zobor – Lyžiarska lúka). Medzi krami bola zistená značná variabilita v podiele listov dlhších ako 70 mm (16 – 58 %) a listov tmavozelenej farby (28 – 78 %), v podiele poloplných kvetov (0 – 6 %) a kvetov intenzívnej ružovej farby (0 – 100 %), ako aj v podiele šípok dlhších ako 20 mm (0 – 45 %) a šípok intenzívnej červenej farby (18 – 48 %). Veľkosť genómu študovaných ruží sa pohybovala v intervale 2,33 – 2,92 pg. Prieskum pôdnych máp odhalil kambizeme pseudoglejové na lokalite Modra – Pažite, hnedozeme typické na spraši ach vo Vrbovom na Baraňom dvore a rendziny typické na výrazných svahoch na lokalite Zobor – Lyžiarska lúka (rastúcu bonitu pôdy od lokality k lokalite). Listy a kvety rástli v podmienkach s priemernou teplotou 15,3 °C (Modra – Pažite a Zobor – Lyžiarska lúka) resp. 14,5 °C (Vrbové – Baraní dvor) a úhrnom zrážok od 300 mm (Modra – Pažite) do 400 mm (Zobor – Lyžiarska lúka). Priemerná teplota pre obdobie formovania šípok sa pohybovala medzi 19,6 °C pre Zobor – Lyžiarsku lúku a 20,4 °C pre Modru – Pažite, pričom suma zrážok dosiahla asi 200 mm na Zobori – Lyžiarskej lúke a 250 mm na ostatných dvoch lokalitách.

Kvantitatívne znaky analyzovaných ruží vykazovali relatívne slabé vzťahy k veľkosti genómu a environmentálnym faktorom. Ak sme však analýzu obmedzili na genotypy *R. canina*, korelačné koeficienty vzrástli. Z nich vyplynulo, že veľkosť listov bola v rozhodujúcej miere určená veľkosťou genómu (r = 0,437) a teplotou (r = –0,316), farba listu predovšetkým teplotou (r = 0,777) a množstvom zrážok (r = 0,557), plnosť kvetu hlavne teplotou (r = –0,320), jeho farba teplotou (r = 0,606) a kvalitatívnymi vlastnosťami pôdy (r = –0,559), a farba šípky sumou zrážok (r = 0,588), teplotou (r = 0,427) a veľkosťou genómu (r = –0,362). Žiadny z faktorov však nemal významný vplyv na dĺžku šípky. Tieto výsledky naznačujú, že okrem veľkosti listov, sú analyzované kvantitatívne znaku závislé takmer výhradne od environmentálnych faktorov.

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