

## PHENOTYPIC PERFORMANCE AND GENOTYPIC VARIANCE FOR REPRODUCTIVE CHARACTERISTICS IN HUNGARIAN VETCH (*VICIA PANNONICA* CRANTZ)

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### ABSTRACT

The objectives of this study were (1) to compare by seed yield and reproductive traits eight Hungarian vetch genotypes (populations and varieties) of both ssp. *pannonica* and ssp. *striata*, selected in previous stage by productivity of green forage; (2) to quantify broad-sense heritability and variance components of seed yield and reproductive traits in this group of genotypes; (3) to identify genotypes and pivotal traits for the seed yield improvement. A field experiment was established at the Experimental Station of Soybean, Northern Bulgaria, during three cropping seasons – 2009/10, 2010/11 and 2011/2012. Significant differences were observed at subspecies level regarding the values of the investigated reproductive traits. Subspecies *striata* located blossoms and pods at significantly lower height and formed significantly more pods per stem in comparison with subspecies *pannonica*. Pods were smaller in size and had less number of seeds in them, but significantly higher weight of 1000 seeds and high percentage of filled seeds. In Hungarian vetch of subspecies *striata*, the breeding for reproductive ability can be limited to breeding for simultaneous ripening and for non-shattering pods. The highest genotypic variance between the genotypes from subspecies *pannonica* was observed for the number of pods per stem, number of filled seeds per pod and weight of 1000 seeds. These traits had the highest heritability ( $H^2_{bs}=0.40$ ; 0.33 and 0.65, respectively) and should be used as criteria for effective breeding regarding the reproductive ability of the elites, selected for green forage production. Variety Angerner (Germany) can be used as improver of the number of seeds per pod and weight of seeds, and variety Pisareska Panonska (Czech) – as improver of the number of pods per stem.

**Key words:** *Vicia pannonica*, reproductive traits, heritability, variance components.

### INTRODUCTION

Hungarian vetch (*Vicia pannonica* Crantz) is a diploid ( $2n=2x=12$ ) annual leguminous species adapted to environments of large areas of Southern and Central Europe, Anatolia, North-west Africa, and Caucasia. It is among the vetch species of economic importance as forage crop (Zhang & Mosjidis, 1998) and as crop for improving soil fertility (Açikgöz, 2001). It is spread in dry areas with continental climate due to its excellent potential for extensive production of forage (Uzun et al., 2004, Sahin-Demirbag et al., 2008). The species has wide natural spreading in Bulgaria and is often found as weed. It is also considered as a very good nectariferous plant for the conditions of our country (Yancheva et al., 1994), forming qualitative nectar for a very long time (from the

beginning of April to the beginning of June). According to our previous results Hungarian vetches grown as a crop for green forage in the conditions of Northern Bulgaria are characterized by very good winter survival, early flowering and relatively good resistance to lodging. They do not differ in forage quality from Hairy and spring vetch. Compared with Hairy vetch, they are more suitable for growing in winter mixtures with widespread low-growing varieties of wheat and barley, because of the lower plant height and the correspondence of their periods of the beginning of the phase of flowering-pod formation and ear formation of the wheat component.

Seed yield is a key element of the agricultural potential of vetch species (Berger et al., 2002). Vetches are perhaps the most difficult of all annual forage legumes for

improvement of seed production, being notorious for its excessive and indeterminate growth, non-uniform maturity and large seed losses due to prominent pod dehiscence (Mihailović et al., 2010). It is important that Hungarian vetch often has higher seed yields than common and many other vetches due to a less prominent pod shattering. Hungarian vetch is not grown in Bulgaria and no data are available about its propagating coefficient, as well as about the possibilities for seed production using the practices spread in the country for growing vetch. Seed expenses have a major share in the expenses of growing vetch; therefore it is important that reproduction ability of genotypes is included as a supplementary selection criterion in our breeding program of winter vetch for green forage production. There are few investigations on the reproductive biology of Hungarian vetch. Zhang and Mosjidis (1995) determined it as no automatic self-fertilizing species, unlike common vetch because the

blossoms need insects visit to set higher percentage of ovaries.

The objectives of this study were (1) to be compare by seed yield and reproductive traits eight Hungarian vetch genotypes (populations and varieties) of both ssp. *pannonica* and ssp. *striata*, selected in previous stage by productivity of green forage; (2) to quantify broad-sense heritability and variance components of seed yield and reproductive traits in this group of genotypes; (3) to identify genotypes and pivotal traits for the seed yield improvement.

## MATERIAL AND METHODS

The experiment was carried out in ESS in Pavlikeni during the period 2009-2012. Characteristics of the region where the investigation took place, which in agro-climate terms is representative of conditions in Northern Bulgaria, are shown in Table 1.

Table 1. Geographic, soil and climatic data for the region of the investigation

Location	Latitude : 43 <sup>0</sup> 24' N Longitude : 25 <sup>0</sup> 32' E Altitude : 144 m
Soil characteristics	Soil type : leached chernozem Soil pH : 7,1 in H <sub>2</sub> O
Rainfall amount average for the period 2009-2012	Rainfall amount for March-June : 247 mm Autumn-winter rainfall amount (October - February) : 209 mm

Eight Hungarian vetch genotypes (populations and varieties) of both subsp. *pannonica* and subsp. *striata*, were included in the experiment: three wild Bulgarian populations – No. 2, 12 and 13, and varieties Angerner, Germany; Beta Pannonbukkony, Hungary; Pisarecka Panonska, Czech Republic; Siofoki, unknown origin and Maglodi, Hungary. These genotypes were selected in our previous investigations by productivity of green forage. The randomized block method was used, the number of replications was 4 and the area of the plot was 1m<sup>2</sup>. Mineral fertilization was not applied. The sowing was in rows, with 20 cm space between the rows and sowing rate was 200 g s.m<sup>-2</sup>. It was done during the period 15-30 October – during three cropping seasons – 2009/10, 2010/11 and 2011/12.

Determinations concerning the following traits were made: height of the first pod location, cm; number of branches per stem; number of blossoms per stem; number of pods per stem; pod length, mm; pod width, mm; number of seeds per pod; number of filled seeds per pod, weight of seeds (m<sub>1000</sub>), g; seed yield, g m<sup>-2</sup>.

Biometric measurements were done on 20 plants from every genotype, five from each replication. The average values for the populations regarding the studied traits were compared by Least Significant Difference at 5% level of probability (LSD 5%). The statistic program STATGRAPHICS PLUS was used.

For determination of the component composition of the variance ANOVA model including the factors G = genotype and Y = year, model 3 was used (Annicchiarico, 2002).

The variance components were calculated in the following way:

$$S^2_{GY} = (MS_{GY} - MS_E) / r;$$

$$S^2_G = (MS_G - MS_{GY}) / ry;$$

$$S^2_e = MS_E;$$

$$S^2_{Ph} = [S^2_G + (S^2_{GY}/y) + (S^2_e/ry)].$$

The coefficient of broad-sense heritability was calculated as a share of the genetic variance from the observed phenotypic variance  $H^2_{bs} = S^2_G / S^2_{Ph}$  regarding the studied characteristics in the conditions of the experiment and for the selected group genotypes.

## RESULTS AND DISCUSSION

The seed yield varied between 94 and 166 g m<sup>-2</sup> (Table 2). With one hectare seed-production sowing 12-20 ha can be sown, at sowing rate of 200 g.s. m<sup>-2</sup> (or 80 kg ha<sup>-1</sup>), having in mind the seed traits observed in the experiment. This determined the reproductive coefficient of Hungarian vetch as relatively good. Besides of seed yield, the genotypes of subspecies *pannonica* also differed significantly ( $P < 0.05$ ) regarding the following traits: number of pods per stem, pod size, total number of seeds and number of filled seeds per pod. The genotypes of this subspecies located 3-4 blossoms at a node, of which one or rarely two pods were formed and average 83% of the blossoms did not fertilize or aborted. According to Abd El Moneim (1993) this was caused by the high temperatures during the blossoming period. For the conditions of our investigation, significant falling of the blossoms was observed because of the plants lodging as a result of high rainfall amount in May. Therefore, it is recommended to grow the Hungarian vetch for seeds in mixtures with supporting crops. According to Iptas (2002), growing of this subspecies in mixtures with 20% participation of triticale increased the seed yield with 65%. The pods were formed at several consecutive fertile nodes at different height of the stems, depending on the period of beginning of favorable conditions for mating of blossoms and development of ovaries. The trait height of first pod location depended mainly on

random causes (insects causing self-fertilizing, density of the grass stands, etc.). The fertilizers should be specified as the most probable random cause with significant effect on the values of the discussed trait, because the plants were massively frequented by bees. The genotypes reacted significantly ( $P < 0.05$ ) to the conditions of the year.

The population belonging to subspecies *striata* located reproductive organs at significantly lower height and formed significantly more pods per stem. In this genotype fully developed pods were formed also at the branches of second grade. In comparison with the studied genotypes of subspecies *pannonica*, the pods had smaller size and less number of seeds per pod, also relatively smaller share of unfilled seeds. Hungarian vetch of subspecies *striata* had significantly higher weight of seeds ( $m_{1000} = 34.7$ g compared to 21.4 g average weight for subspecies *pannonica*). In comparison with foreign investigations, the selected genotype had very high values of the number of seeds per pod – 3.6, while Firincioğlu et al. (2011) specified a corresponding average value – 1.8. Two important unwanted characteristics should be reported, which decreased the seed yield – not simultaneous ripening and pod shattering. In common vetch non-shattering of pods is due to a homozygous recessive gene, which occurred as a natural mutation in wild ecotypes of the species (Abd El-Moneim, 1993). The trait was transferred in highly productive lines by backcrossing breeding. Probably the scheme could be also used for Hungarian vetch of subspecies *striata*.

Firincioğlu et al. (2011), who investigated quantitatively the phenotypic variation of 45 genotypes of Hungarian vetch, considered that the seed yield would increase essentially if traits of two subspecies of Hungarian vetch were combined by combinative selection. The corresponding traits were the early ripening, the larger number of pods and seed size of var. *purpurascens* (var. *purpurascens* = subsp. *striata*) with longer stems and pods of var. *pannonica*. According to our previous and

not published results, the hybridization of two subspecies is difficult. We consider as more perspective the breeding by reproductive ability inside the subspecies. In subspecies

*striata*, which already possesses the mentioned above values of the reproductive traits, it should be sufficient to breed for non-shattering of pods.

Table 2. Mean values for investigated traits

Genotypes	Wild population №2	Angerner	Beta Pannonbukkony	Pisarecka Panonska	Siofoki	Wild population №12	Wild population №13	Maglodi	LSD <sub>0.05</sub>
Traits	subsp. <i>striata</i>	subsp. <i>pannonica</i>							
Seed yield, g m <sup>-2</sup>	124 <sup>c</sup>	166 <sup>a</sup>	152 <sup>ab</sup>	131 <sup>bc</sup>	132 <sup>bc</sup>	118 <sup>c</sup>	155 <sup>a</sup>	94 <sup>d</sup>	22.0
Height of first pod location, cm	39.9 <sup>c</sup>	69.8 <sup>ab</sup>	68.2 <sup>ab</sup>	68.5 <sup>ab</sup>	68.6 <sup>ab</sup>	68.7 <sup>ab</sup>	75.1 <sup>a</sup>	65.1 <sup>b</sup>	7.2
Number of branches per stem	2.1 <sup>a</sup>	1.5 <sup>a-d</sup>	1.5 <sup>bcd</sup>	1.3 <sup>cd</sup>	1.0 <sup>d</sup>	1.6 <sup>abc</sup>	2.0 <sup>ab</sup>	0.9 <sup>d</sup>	0.6
Number of blossoms per stem	17.4 <sup>ab</sup>	17.6 <sup>ab</sup>	15.0 <sup>b</sup>	20.1 <sup>ab</sup>	22.5 <sup>a</sup>	21.7 <sup>a</sup>	20.8 <sup>ab</sup>	19.2 <sup>ab</sup>	3.5
Number of pods per stem	7.7 <sup>a</sup>	3.1 <sup>c</sup>	2.9 <sup>c</sup>	5.3 <sup>b</sup>	2.6 <sup>c</sup>	2.8 <sup>c</sup>	3.8 <sup>bc</sup>	2.6 <sup>c</sup>	1.5
Pod length, mm	24.0 <sup>d</sup>	28.9 <sup>b</sup>	29.1 <sup>ab</sup>	28.2 <sup>b</sup>	27.0 <sup>c</sup>	30.1 <sup>a</sup>	29.1 <sup>ab</sup>	28.5 <sup>b</sup>	1.2
Pod width, mm	6.4 <sup>d</sup>	6.9 <sup>bc</sup>	7.2 <sup>ab</sup>	6.6 <sup>cd</sup>	7.0 <sup>bc</sup>	7.4 <sup>a</sup>	7.7 <sup>a</sup>	7.3 <sup>ab</sup>	0.4
Number of seeds per pod	3.6 <sup>d</sup>	4.9 <sup>abc</sup>	4.8 <sup>bc</sup>	5.6 <sup>a</sup>	4.4 <sup>c</sup>	4.9 <sup>abc</sup>	4.6 <sup>bc</sup>	5.2 <sup>ab</sup>	0.7
Number of filled seeds per pod	3.1 <sup>cd</sup>	4.2 <sup>a</sup>	3.7 <sup>abc</sup>	4.1 <sup>ab</sup>	2.8 <sup>de</sup>	2.2 <sup>e</sup>	3.4 <sup>bcd</sup>	3.9 <sup>ab</sup>	0.8
1000-seed weight, g	34.7 <sup>a</sup>	25.2 <sup>b</sup>	22.4 <sup>bc</sup>	21.1 <sup>bc</sup>	21.9 <sup>bc</sup>	21.7 <sup>bc</sup>	20.5 <sup>bc</sup>	17.3 <sup>c</sup>	3.8
Pod shattering	yes	no	no	no	no	no	no	no	

The average values followed by same letters did not differ significantly, P=0.05.

The analysis of variance in subspecies *pannonica* revealed highly significant effects of the genotype (P<0.001) for seed yield, number of reproductive organs (blossoms and pods) per stem, pod size and quantity of filled seeds per stem (Table 3). Significant genotype X year interaction variance was also detected for all evaluated traits, except for weight of seeds. According to the values of the coefficient of heritability (H<sup>2</sup><sub>bs</sub>), the genotypic variance was relatively the highest regarding the number of pods per stem, number of filled seed per pod and weight of 1000 seeds. These traits had the highest heritability in the investigated group of genotypes (H<sup>2</sup><sub>bs</sub>=0.40; 0.33 and 0.65, respectively) and should be used as selection criteria for effective breeding by reproductive ability of the elites, selected for green forage production. Firincioğlu et al. (2011) also specified the number of pods per plant and the number of seeds per pod as the most important characteristics for

improvement of the seed yield. We do not have data regarding the genetic base of these traits of Hungarian vetch. In other annual leguminous forage species the genotypic variance for seed weight was due predominantly to additive genetic effects and the high broad-sense heritability was connected with high narrow-sense heritability, which was a precondition for effectiveness of the pedigree method in the selection of this trait (Ulloa et al., 2010; Tchiagam et al., 2011).

Variety Angerner can be used as improver of the number of seeds per pod and the seed weight, and variety Pisareska Panonska – as improver of the number of pods per stem. Because of the excellent productivity of forage and their suitability for rapid and cheap selection process, Bulgarian populations 12 and 13 were specified as suitable for direct use as varieties after assessment of their reproductive ability.

Population 12 had the highest yield of green forage and it formed the largest pods, but it had significantly lower values of the traits number of pods per stem and number of seeds per pod, and it had very high share of unfilled seeds. Single not shattered pods were observed in this population.

Its seed yield was significantly lower (Table 2). The other Bulgarian population (13)

had high seed yield, relatively high values of its structuring elements, but needed improvement regarding the share of filled seeds and the weight of 1000 seeds. If the genotype was used only as a green forage variety, the small seeds in the reported high seed yield should be considered as a desirable characteristic because it determined high reproductive coefficient.

Table 3. Variance components and coefficient of broad-sense heritability ( $H^2_{bs}$ ) regarding seed yield and reproductive traits of *Vicia pannonica* subsp. *Pannonica*

Traits	Significance of the factorial influences			Estimates of variance components				Heritability
	G	Y	GxY	$S_G^2$	$S_{GY}^2$	$S_e^2$	$S_{Ph}^2$	$H^2_{bs}$
Seed yield	P<0.001	P<0.05	P<0.01	23.1	588.6	47.2	283.0	0.08
Height of first pod location	P>0.05	P>0.05	P<0.05					
Number of blossoms per stem	P<0.001	P<0.001	P<0.001	0.96	12.80	45.44	6.74	0.16
Number of pods per stem	P<0.001	P<0.001	P<0.01	0.38	1.00	15.22	0.97	0.40
Pod length	P<0.001	P>0.05	P<0.001	0.17	1.27	6.33	0.96	0.24
Pod width	P<0.001	P<0.05	P<0.01	0.05	0.13	1.04	0.14	0.45
Number of seeds per pod	P<0.05	P<0.01	P<0.01	0.002	0.36	2.70	0.16	0.01
Number of filled seeds	P<0.001	P<0.001	P<0.001	0.14	0.67	3.14	0.55	0.33
1000 seed weight	P<0.05	P<0.001	P>0.05	2.67	3.57	15.88	5.55	0.65

$S_G^2$  – genotypic variance;  $S_{GY}^2$  – variance for interaction of genotype with conditions of the year;  $S_e^2$  – variance for error;  $S_{Ph}^2$  – phenotypic variance;  $H^2_{bs}$  – coefficient of broad-sense heritability.

## CONCLUSIONS

Significant differences at subspecies level were observed regarding the values of the investigated reproductive traits. Subspecies *striata*, in comparison with subspecies *pannonica*, located pods at significantly lower height, and formed significantly more pods per stem. The pods were of smaller size and had less number of seeds in them, but significantly higher weight of 1000 seeds and high percentage of filled seeds. In the Hungarian vetch of subspecies *striata*, the breeding for seed yield improvement can be directed to breeding for uniform maturity and non-shattering of pods.

The highest genotypic variance between the genotypes from subspecies *pannonica* was observed for the number of pods per stem, number of filled seeds and weight of 1000 seeds.

These traits had the highest heritability ( $H^2_{bs}$ =0.40; 0.33 and 0.65, respectively) and

should be used as criteria for effective breeding by the reproductive ability of the elite plants, selected for green forage production. Variety Angerner can be used as improver of the number of seeds per pod and seed weight, and variety Pisareska Panonska – as improver of the number of pods per stem.

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