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CORRELATIONS AND HERITABILITY OF THE CHARACTERS DETERMINING
THE SEED YIELD OF THE PANICLE INFLORESCENCE FORMS
OF ALFALFA (*MEDICAGO X VARIA T. MARTYN*)

ABSTRACT

Phenotypic correlation coefficients and heritability of the characters determining seed yield of panicle inflorescence forms of alfalfa was examined. Seed yield per plant, which was positively correlated with 10 generative and morphological traits, depended upon the number of pods per panicle and the number of seeds per pod. Variability of these characters determined about 60% of the variability of seed yield. Multiple linear regression and phenotypic correlations show that simultaneous selection for increased pod number per panicle and increased seed number per pod and number of branches per panicle resulted in enhanced seed yield potential. The share of the additive genetic effects in the phenotypic variance for number of pods per panicle was low and about 23%, while for number of seeds per pod and seeds per panicle amounted to about 75-77% and 56-57% respectively.

Key words: alfalfa, expected genetic progress, heritability, interdependence, multiple regression, panicle inflorescence, seed yield.

INTRODUCTION

The main causes of low seed productivity of alfalfa are the poor pod setting as only 40 to 60 % of the flowers set pods, and the low number of seeds per pod, usually 3 to 4. These traits depend on weather conditions, especially temperature and insolation, and on the sum and distribution of rainfall during the flowering period, pod setting and seed ripening (Simon 1997, Djukić and Kraljevič-Balalič 1993). Significant improvements of seed yield can ensure a strict implementation of the recommendations concerning regionalization of seed industry and proper agricultural practices (Skalska 1993, Simon 1997).

The average number of inflorescences on stems and of flowers in inflorescence, are sufficient to assure high yields of alfalfa seeds (Skalska 1993, Dyba and Rogalska 1995). The investigations of Bocsa and Pummer (1994, 1997) indicate that improvement of pod and seed setting is possible by breeding. It is especially important to determine the effect of generative and morphological characters on seed yield, as well as on their interdependence and heritability. These properties determine the effectiveness of the selection of forms characterized by good pod and seed setting (Bodzon 2004).

The aim of the study was to estimate the phenotypic correlation coefficients and the inheritance of the characters determining the seed yield of panicle inflorescence forms of alfalfa. Panicles on mutant plants were consisted of a lot of branches that caused several fold increase of flower number in inflorescences. The panicle inflorescence character is controlled by a single recessive gene *pi* (Bodzon 2013). The knowledge of these relationships in new panicle inflorescence forms of alfalfa is essential in breeding for improved seed yield.

MATERIALS AND METHODS

The experimental material consisted of 5 panicle inflorescence BC₂ hybrids, constituting the components of the new synthetic population RAH 210.

These hybrids were obtained by crossing 5 clones, which were basic breeding material of the cultivar Radius, with 3 lines I₂ 21/1, used as donors of the panicle inflorescence character. The gene *pi* was introduced by backcrossing to the genotypes of the Radius clones. Two cycles of backcrossing were performed, and 5 panicle inflorescence BC₂ hybrids were obtained.

These BC₂ hybrids were examined in the second and third years of vegetation in a field trial set in a completely randomised block design in 3 replicates. Field experiments were conducted at Radzików in 2015-2016, on podzolic soil classified to the third class in the Polish system. The plot size was 10 m², row distance was 0.5 m and plant density 12 per m².

Six generative characters i.e.: number of pods per panicle, number of seeds per panicle, number of seeds per pod, 1000 seed weight, seed weight per panicle and seed yield per plant were tested. Likewise six morphological characters i.e.: number of branches per panicle, number of flowers per panicle, plant height, number of main stems, number of nodes and of inflorescences per main stem were evaluated.

Interdependence of the observed characters were examined by phenotypic correlation coefficients. Based on the multiple linear regression analysis, the effects of 6 characters conditioning the seed yield, i.e. number of pods per panicle, number of seeds per pod, 1000 seed weight, number of branches per panicle, number of flowers per panicle and number of panicles per stem were examined. This study was done on samples of 75 plants randomly selected from 3 plots (25 plants per plot). Correlation among characters and multiple linear regression was performed separately for each of the 5 BC₂ hybrids.

A single plant was randomly selected from each BC₂ cross combination. These plants were cloned, thus giving 5 clones. These clones were crossed in 2012, according to the diallel crossing system using Griffing method 3. The obtained F₁ progenies were examined in a completely randomised block design with 3 replicates in the first and the second year of full utilisation. The analysis of data for the generative characters, i.e. number of seeds per panicle, number of seeds per pod, number of pods per panicle and number of branches per panicle, was performed according to the random Griffing model (Griffing 1956).

The heritability coefficients were calculated in a narrow (h^2_A) and broad (h^2_G) sense. The values of expected genetic progress R were calculated, assuming the following selection intensities: 10%, 30%, 50%, and 80%.

RESULTS

Multiple linear regression was used to estimate the effects of tested characters on seed yield per plant. It was found that both in the first and second year of full utilisation, the yield of seed from the plant, all tested BC₂ hybrids, was significantly dependent on the number of pods per panicle and on the number of seeds in the pod. The variance of these characters determined the variance of the seed yield per plant from ca 60.3% to ca 66.1% in the first year, and from ca 58.5% to ca 63.0% in the second year (Table 1).

Table 1
Determination coefficients (R^2) obtained from the analysis of multiple linear regression in the years of utilisation of alfalfa genotypes.

Genotypes BC ₂	R^2	
	First year	Second year
3088 × 21/1/3	0.6197	0.5988
3131 × 21/1/3	0.6225	0.6011
3139 × 21/1/4	0.6614	0.6305
3149 × 21/1/1	0.6028	0.5847
3015 × 21/1/1	0.6057	0.5944

The seed yield per plant of all the BC₂ hybrids was positively correlated with all generative and morphological characters tested in this experiment, in both years. The only exception was the lack of correlation with the number of nodes per stem (Table 2). Interdependence of the number of seeds per pod and number of branches per panicle, as well as those between the number of seeds per pod and the number of flowers per panicle, were insignificant in both years. Similarly, correlation coefficients between number of pods per panicle and the number of seeds per pod, was not statistically confirmed. However, the number of pods per panicle and the number of seeds per pod, were positively correlated with the number of seeds per panicle and with seed weight per panicle.

Table 2

The matrix of mean phenotypic correlation coefficients between 12 characters within panicle inflorescence BC₂ alfalfa populations (clones Radius × I₂ 21/1). Data above the diagonal are for 2015, below for 2016

Characters	1	2	3	4	5	6	7	8	9	10	11	12
1		0.82*	-0.08	0.09	0.67*	0.66*	0.53*	0.64*	0.35*	0.17	0.24	0.40*
2	0.89*		0.68*	0.04	0.84*	0.88*	0.63*	0.54*	0.38*	0.32*	0.33*	0.38*
3	-0.12	0.73*		0.05	0.59*	0.87*	-0.05	-0.09	0.07	0.27	0.05	0.06
4	0.09	0.02	0.02		0.85*	0.84*	0.12	0.17	0.33*	0.14	0.07	0.17
5	0.71*	0.81*	0.55*	0.83*		0.72*	0.35*	0.33*	0.11	0.08	0.03	0.08
6	0.63*	0.87*	0.77*	0.81*	0.83*		0.41*	0.38*	0.33*	0.36*	0.09	0.54*
7	0.66*	0.62*	-0.13	0.15	0.34*	0.37*		0.85*	0.42*	0.37*	0.10	0.27
8	0.72*	0.56*	-0.12	0.08	0.35*	0.36*	0.91*		0.35*	0.49*	0.16	0.38*
9	0.23	0.34*	0.05	0.16	0.08	0.35*	0.38*	0.33*		0.14	0.26	0.46*
10	0.05	0.34*	0.18	0.10	0.13	0.32*	0.24	0.37*	0.15		0.08	0.35*
11	0.32*	0.33*	0.06	0.04	0.05	0.07	0.08	0.11	0.33*	0.07		0.02
12	0.41*	0.37*	0.02	0.04	0.16	0.45*	0.27	0.33*	0.52*	0.28	0.17	

* - significant at $p = 0.05$

1 - Pod no. 1er panicle; 2 - Seed no. per panicle; 3 - Seed no. per pod; 4 - Weight of 1000 seed ; 5 - Seeds weight per panicle; 6 - Seed yield per plant; 7 -Branch no. per panicle; 8 - Flower no. per panicle; 9 -Plant height; 10 - Main stem no. per plant; 11 - Node no. per main stem; 12 - Panicle no. per stem

The number of seeds per panicle was highly and positively correlated with seed yield per plant and with the number of branches per panicle. It was also positively correlated with all other generative and morphological characters, except of the 1000 seed weight. Seed weight per panicle was positively correlated with all generative characters, the number of branches per panicle and the number of flowers per panicle. No negative correlations were found between seed yield per plant or any generative character and the characters decisive for yield of green matter, i.e.: plant height, number of main stems and of nodes produced on the stems.

F₁ hybrids obtained from crossing five BC₂ clones were examined in terms of characters that significantly influence the seed yield per plant i.e. number of pods per panicle, number of seeds per pod and number of seeds per panicle in the first and second year of full utilisation under field conditions.

Significant deviations from zero were found for variance components concerning the effects of general combining ability, as well as and specific combining ability, in all studied characters in both years of utilisation (Table 3). This means that in the population of panicle inflorescence hybrids, were identified both additive and dominant genetic variability of the characters determining the seed yield per plant. The variance component responsible for the effects of reciprocal crossings in terms with respect to the number of seeds per panicle was also significantly deviated from zero. However the variance component responsible for the effects of reciprocal crossings (σ_r^2) of all other characters did not differ significantly from zero. Therefore, the female parents transmitted the genetic material controlling the number of seeds per panicle also via out of nuclear way.

Table 3
Estimates of variance components for characters determining seed yield per plant of alfalfa F₁ hybrids obtained by crossing clones in a diallel crossing system using Griffing's method 3

Component of variability	Year	Pod no. per panicle	Seed no. per pod	Seed no. per panicle
σ_g^2	2015	1.3261*	0.0398*	62.041*
	2016	1.2883*	0.0418*	56.034*
σ_s^2	2015	1.2517*	0.0154*	17.356*
	2016	1.1784*	0.0183*	14.214*
σ_r^2	2015	0.7028	0.0124	32.053*
	2016	0.8241	0.0133	22.857*
σ_e^2	2015	0.5319	0.0119	9.421
	2016	0.6853	0.0122	7.928

* - significantly different from zero

The heritability coefficients (in a narrow sense) for number of pods per panicle were low in both years of examination (Table 4). These results indicate, that the share of the additive genetic components in the phenotypic variance of the number of pods per panicle in the panicle inflorescence population was 23.1% and 23.8% in the following years. Therefore, the expected breeding progress for this character would be from about 1.7 with selection intensity 10% and about 0.4 with selection intensity 80%. The value of the broad sense heritability coefficient indicates that the share of genetic non additive effects in the genotypic variance was about three times as great as that of additive effects.

Table 4
Estimates of heritability coefficients in a narrow sense (h_A^2) and broad sense (h_G^2) of characters conditioning the seed yield of alfalfa and the expected genetic progress (R) at different selection intensity in subsequent years of utilisation

Character	Year	h_A^2	h_G^2	R			
				10%	30%	50%	80%
Pod no. per panicle	2015	0.231	0.634	1.73	1.12	0.72	0.35
	2016	0.238	0.649	1.76	1.14	0.73	0.35
Seed no. per pod	2015	0.534	0.775	0.55	0.35	0.25	0.13
	2016	0.507	0.756	0.53	0.29	0.23	0.12
Seed no. per panicle	2015	0.578	0.862	17.23	12.40	8.25	3.19
	2016	0.563	0.881	16.07	11.72	7.49	2.92

Narrow sense heritability estimates for numbers of seeds per pod were 0.53 in the first year and 0.51 in the second year of research. Therefore, the variability for this character due to the additive effects of genes consisted of about a half of the total phenotypic variation in the population of panicle inflorescence hybrids. The expected magnitude and the rate of genetic progress in recombination breeding will be at medium level and depending upon the intensity of selection. Its value may range from 0.5 to 0.1, if the proportion of individuals selected from the parental population would be 10% to 80%, respectively. In the case of the number of seeds per pod, the share of genotypic variance in phenotypic

variance was 77.5% and 75.6% in two years of research respectively, and was greater than the share of additive genetic effects because of a significant share of non additive effects.

The share of additive variance effects in the phenotypic variance of number of seeds per panicle was 57.8% and 56.3% in the two years of investigations. The expected genetic progress resulting from selection would be, according to the results from the first year, from ca 17.2 to ca 3.2, depending on the selection intensity. The expected progress in the number of seeds per panicle, according to the results obtained in the second year, would range from about 16.1 to 2.9 at the selection intensity 10% and 80%, respectively. Due to non additive effects the share of genotypic variance in total phenotypic variation for this character was 86.2% and 88.1% respectively in the two years of investigation.

DISCUSSION

The quantitative characters determining seed productivity are polygenically determined. For this reason determining of the effects of these characters on seed yield, their heritability and interdependence is decisive for the effectiveness of selection for increased seed yield.

The multiple linear regression analysis of the panicle inflorescence hybrids show that seed yield per plant depends on the number of pods per panicle and the number of seeds per pod. The variability of these characters determines about 60% of total variability of seed yield per plant. Similar dependence was demonstrated by Bodzon (2004), who studied the long-raceme forms of alfalfa. Dependence of the seed yield on the number of pods per inflorescence was also shown by Pomogajbo (1981), Bocsa and Buglos (1983) and Rosellini *et al.* (1990).

Seed yield from plant in panicle inflorescence hybrids was positively correlated with all examined characters except of the number of nodes on stems. These correlations are also confirmed by the study of Bodzon (2004). A positive correlation of seed yield per plant with the number of flowers and pods per plant was found by Mražkova and Vacek (1981), Pomogajbo (1981) and Vachunková *et al.* (1981). High correlation of seed yield with number of seeds per pod was also confirmed by Bocsa and Buglos (1983) and Rosellini *et al.* (1990). Puzio-Idzkowska (1993) showed high, positive correlation coefficients of seed yield with the number of inflorescences per stem, the number of pods per inflorescence and number of seeds per pod.

These correlations prove that selection for high seed yield of panicle inflorescence forms should include selection of plants with the highest number of pods per panicle and seeds per pod and at the same time the highest number of branches per panicle. The study of Huyghe *et al.* (1998, 1999) confirm that plants with high number of seeds per inflorescence gave also high seed yield. Increasing the number of seeds per inflorescence resulted both from the increase in the number of pods and seeds per pod. Jaranowski and Dyba (1983) and Bodzon (2004) confirm that selection for improved seed yield should be based on simultaneous selection for several characters closely connected with seed

yield. The most important characters for the seed yield potential are: the number of seeds per pod, number of pods per inflorescence, 1000 seed weight and the number of inflorescences per stem (Bocsa and Pummer 1994, Dyba and Rogalska 1995). Rotili *et al.* (1998) find a high correlation of seed yield with the number of formed pods and seeds. According to their opinion, selection for seed yield should include these two characters simultaneously.

The generative characters and characters affecting the green mass yield of panicle inflorescence hybrids are not negatively correlated. This demonstrates that selection for increased seed productivity does not necessarily reduce forage yield. These observations are consistent with the results of Veronesi and Falcinelli (1987) and Bocsa and Pummer (1997). However, positive correlation of seed yield and green mass was documented by Singh (1978) and Veronesi *et al.* (1986).

On the basis of the analysis of variance of the characters determining seed yield per plant, there was a significant deviation from zero of variance components regarding half-sibs variability (GCA effect) and the variability effects of parental pairs (SCA effect) on these characters. This demonstrates that in the panicle inflorescence hybrids both additive and dominant genes are controlled seed yield per plant. Similar results for the number of seeds per inflorescence were obtained by Peterson and Barnes (1983) and He and Campbell (1994), who reported that variability of the GCA effects is more important for expression of this character than the effects of specific combining ability. In their opinion the number of formed pods and the number of seeds per pod are determined both by additive and non-additive effects of the genes but the variability of additive effects is more important for expression of these characters.

In this study it was found that the share of the additive genetic effects in the phenotypic variance for number of pods per panicle was low and about 23%, while for number of seeds per pod and seeds per panicle amounted to about 75-77% and 56-57% respectively. This means that the magnitude and the pace rate of genetic progress in recombination breeding, which can be expected in the number of seeds per pod and in the number of seeds per panicle, will be at an average level. However we can not expect rapid and considerable progress in terms of the number of pods per panicle. Similar results with respect of genetic progress were obtained by Bodzon (2004), who studied the long-raceme forms of alfalfa.

CONCLUSIONS

The seed yield per plant of the panicle inflorescence hybrids was significantly dependent on the number of pods per panicle and seeds per pod and the variability of these characters determined more than 60% of the overall variability of the seed yield per plant. The results of study show that simultaneous selection for increasing the number of pods per panicle, the number of seeds per pod, and the number of branches per panicle leads to increased seed yield potential. The number of branches per panicle, which was positively correlated with the number of pods and seeds per panicle can be an important criterion in selection of

plants with high seed yield. Studies have shown that the expected genetic progress in respect to the number of pods per panicle will be small, while greater progress through selection in the panicle inflorescence hybrids population is expected for the number of seeds per pod and seeds per panicle.

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GROWTH AND YIELD RESPONSE OF FIELD PEA (*PISUM SATIVUM* L.) TO GAMMA IRRADIATION STRESS

ABSTRACT

Ionizing radiation has extensive applications in agriculture for inducing mutagenic changes in major field crops, potential breeding purposes, varietal development and crop improvement. This study was conducted to test the efficacy of 0.8, 1.6, 2.4 and 3.6 kGy gamma irradiation doses (Cobalt-60) upon growth and yield performance of edible pea (*Pisum sativum* L.) in pot culture experiment during 2009. Results demonstrated that higher radiation doses (1.6 and 3.2 kGy) significantly influenced the studied attributes of *P. sativum*. It was observed that 3.2 kGy had detrimental effects on shoot and pod lengths of pea which were reduced by 14.60 and 17.71 % respectively when compared to control. Differential response of the number of seeds pod⁻¹, 1000 grain weight and dry biomass of pea were recorded at the applied doses. Significant reduction in number of seeds (-14.21 %) but increase in 1000 grain weight (+13.93 %) and dry biomass (+11.32 %) of pea were recorded at 1.6 kGy which revealed stimulatory effects on grain weight and dry biomass. Conversely, radiation dose 3.2 kGy was found detrimental to all the studied parameters except number of pods plant⁻¹ and number of seeds pod⁻¹ which were not affected.

Key words: Biotechnology, Genetic variation, Ionizing radiation, Legumes, Mutation

INTRODUCTION

Pisum sativum L. in the family *Leguminosae*, holds an important position in human diet and agriculture. It possesses significant concentrations of proteins and other nutrients and is widely used as a food, vegetable and animal fodder (Schroeder *et al.*, 1993; Murtaza *et al.*, 2007). It is the most extensively grown crop in the world, ranked the 2nd in terms of cultivation after soybean (Smykal *et al.*, 2012). Nevertheless, having significant impact on human food and agricultural activities, global pea