Short communication. Assessing relationships between seed yield components in spring-sown field pea (*Pisum sativum* L.) cultivars in Bulgaria by correlation and path analysis

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Abstract

An analysis was carried out during 2007-2009 on nine spring-sown Bulgarian and Ukrainian field pea cultivars. Strongest positive phenotypic correlations were observed between number of fertile nodes per plant and numbers of pods ($r = 0.97$) and number of seeds per plant ($r = 0.97$) and between number of seeds and pods per plant ($r = 0.94$); between seed weight per plant and number of seeds ($r = 0.83$) and fertile nodes per plant ($r = 0.77$). High genetic correlations were found between plant height and first pod height ($r = 0.89$), between number of pods per plant and seed weight per plant ($r = 0.91$) and number of seeds per plant ($r = 0.96$) and between seed weight per plant and number of branches per plant ($r = 0.92$) and number of fertile nodes per plant ($r = 0.89$). The strongest and direct positive effect on seed yield was found in branch length (17.70), 1,000-seed weight (5.92) and number of seeds per pod (4.93). The highest positive indirect contribution was in branch length to number of seeds per pod (2,214.8), number of fertile nodes per plant (1,258.0) and number of seeds per plant (708.70). Based on the trait association and the path coefficients for seed yield and its components, it can be concluded that field pea breeders should pay attention to traits such as branch length, 1,000-seed weight and number of seeds per pod when selecting high-yielding genotypes in field pea.

Additional key words: breeding; genetic correlations; *Pisum sativum*; phenotypic correlations; seed yield; trait association.

Resumen

Comunicación corta. Evaluación mediante análisis de correlación y de sendero de las relaciones entre componentes del rendimiento en cultivares de guisante (*Pisum sativum* L.) de siembra primaveral en Bulgaria

Se ha realizado un estudio entre 2007 y 2009 sobre nueve cultivares de guisante de primavera búlgaros y ucranianos. Para la mayor parte de los caracteres considerados, los coeficientes de correlación genéticos resultaron mayores que los fenotípicos. Se han observado fuertes correlaciones fenotípicas positivas entre el número de nudos fértiles por planta y el número de vainas ($r = 0,97$) y el número de semillas por planta ($r = 0,97$); entre el número de semillas y el de vainas por planta ($r = 0,94$); entre el peso de la semilla por planta y el número de semillas ($r = 0,83$) y los nudos fértiles por planta ($r = 0,77$); entre el número de semillas por vaina y el número de ramas por planta ($r = 0,82$) y entre la altura de la planta y la altura de la primera vaina ($r = 0,77$). Se han encontrado altas correlaciones genéticas entre la altura de la planta y la de la primera vaina ($r = 0,89$); entre el número de vainas y el peso de semilla por planta ($r = 0,91$) y el número de semillas por planta ($r = 0,96$) y entre el peso de semillas y el número de ramas por planta ($r = 0,92$) y el número de nudos fértiles por planta ($r = 0,89$). Los efectos directos positivos más fuertes sobre el rendimiento de semilla se han observado en la longitud de la rama (17,70), el peso de 1.000 semillas (5,92) y el número de semillas por vaina (4,93). Los mayores efectos indirectos positivos se han observado en la longitud de la rama al número de semillas por vaina (2.214,8), al número de nudos fértiles por planta (1.258,0) y al número de semillas por planta (708,70). Sobre la base de la asociación de caracteres y sus modelos de relación con el rendimiento de semilla y sus componentes, se puede concluir que los mejoradores de guisante, para la selección

This work has one Supplementary Table that do not appear in the printed article but that accompany the paper online.

de genotipos de alto rendimiento, deben tener en cuenta caracteres como la longitud de la rama, el peso de 1.000 semillas y número de semillas por vaina.

Palabras clave adicionales: análisis de coeficientes de sendero; componentes de rendimiento; correlaciones fenotípicas; correlaciones genéticas; mejora genética; *Pisum sativum;* rendimiento de semilla.

Traditionally, breeders of field pea (*Pisum sativum* L.) aimed at optimising seed yield mostly by empirical selection and with little regard for the physiological processes involved in its increase. More recently, strategies to optimise field pea seed yield have focused on the physiological mechanisms involved in seed setting and filling. However, developing high yielding field pea cultivars via specific traits requires knowledge of not only resulting yield but also on numerous compensation mechanisms among seed yield components resulting from ever changing genotypic, environmental and management factors. Seed yield in field pea is a quantitative trait affected by many genetic and environmental factors (Ranjan *et al.*, 2006; Espósito *et al.*, 2009) such as temperature, precipitations or soil type and moisture. Therefore, a priority of modern conventional field pea breeding programmes is searching for the donors of desirable traits able to answer all the challenges of specific environment (Mehandjiev *et al.*, 2006; Mikić *et al.*, 2011a). Contemporary breeding programs use field pea genotypes with a wide genetic base and a diversity of phenological, morphological and economic traits. One of the most important steps in developing novel field pea lines with stable seed yield is an adequate use of the available germplasm and a proper selection of the parents for hybridisation.

The path coefficient analysis, initially suggested by Wright (1921) and described by Dewey & Lu (1959), allows partitioning of each correlation coefficient into direct and indirect effects of various traits on the dependent variable and thus helps assessing the cause-effect relationship and an effective selection. The presence of correlations is considered important because they can be used as selection criterion resulting in more effective selection (Togay *et al.*, 2008). Path coefficient analyses correlate coefficients into direct and indirect effects of various seed yield components based on the assumption that relationships exist among yield components. Statistically, path coefficients are standardised partial-regression coefficients obtained from equations, where yield-related variables are expressed as deviations from the means in units of standard deviation (Steel & Torrie, 1982).

The aim of the presented study was to determine the relationships among seed yield components of field pea cultivars using correlation and path coefficient analysis.

A small-plot trial has been carried out from 2007 to 2009 at the Second Experimental Field of the Institute of Forage Crops, Pleven (43.41°N, 24.61°E), situated in the central part of the Danube hilly plain of Bulgaria. The trial included nine spring-sown, white-flowered and light-testa field pea cultivars of Bulgarian and Ukrainian origin, namely Amitie, Druzba, Harkovskii Etalon, Kerpo, Kristal, Picardi, Pleven 4, Rezonator and Usatii 90. Kerpo, Pleven 4 and Rezonator had normal leaf, while the others were semi-leafless. Also, all had short stems except Pleven 4, Rezonator and Usatii 90. All the cultivars were sown in March, according to a randomised complete block design method with four replications and a plot size of 5 m^2 (2.0 m × 2.5 m). Each plot had 11 rows spaced at 20 cm, sowing rate of 120 viable seeds m^{-2} and a sowing depth of 5 cm. All the agronomic practices during the trial were ordinary and officially approved by the Institute of Forage Crops.

According to the weather data during the trial, each of three trial years was drier, warmer and with less moisture in comparison to a long-term average (Suppl. Table 1, pdf). In individual trial years, the total annual precipitations were 233.9 mm, 236.4 mm and 282.8 mm respectively, the average temperatures were 23.9°C; 25.5°C and 24.1°C respectively, and the average relative humidity was 55.2%; 59.8% and 60.3% respectively.

Twenty plants per cultivar were harvested at full maturity from the middle of the sixth row of each plot for the analysis of seed components. Among the targeted traits related to seed yield were plant height (cm), first pod height (cm), number of branches per plant, number of pods per plant, number of seeds per plant, number of fertile nodes per plant, branch length (cm), number of seeds per pod, 1,000-seed weight (g), seed weight per plant (g) and lodging resistance (from 0 to 9, with 0 for all the plants resistant and 9 for all the plants susceptible). Genetic and phenotypic correlations were calculated by two-factor analysis of

Table 1. Phenotypic correlation coefficients (r) among the traits in the tested field pea cultivars in Pleven during 2007-2009

Trait	Plant height	First pod height	Number of branches per plant	Number of pods per plant	Number of seeds per plant	Number of fertile nodes per plant	Branch length	Number of seeds per pod	1,000-seed weight	Seed weight per plant
First pod height	0.77 ***									
Number of branches per plant	–0.38 *	–0.58 **								
Number of pods per plant	0.34 *	–0.22 *	0.10 *							
Number of seeds per plant	0.54 **	0.01 *	0.11 *	0.94 ***						
Number of fertile nodes per plant	0.36 **	–0.19 *	0.20 *	0.97 ***	0.97 ***					
Branch length	0.63 **	0.45**	–0.05 *	0.46 **	0.62 **	0.56 **				
Number of seeds per pod	–0.16 *	–0.18 *	0.82 ***	–0.17 *	0.02 *	0.02 *	0.09 *			
1,000-seed weight	–0.05 *	0.38 *	–0.30 *	–0.61 **	–0.70 **	–0.74 **	–0.44 **	–0.37 **		
Seed weight per plant	0.52 **	0.04 *	0.13 *	0.83 ***	0.83 ***	0.77 **	0.36 **	–0.07 *	–0.27 *	
Lodging resistance	0.27 *	–0.07 *	0.37 *	0.29 *	0.39 **	0.31 *	0.30 *	0.41 **	–0.30 *	0.47 **

* $p \le 0.05$, ** $p \le 0.01$, *** $p \le 0.001$.

variance (ANOVA) and path analysis (Genchev, 1975; Williams *et al.*, 1990).

All the experimental data were statistically processed using the computer software GENES 2009.7.0 for Windows XP (Cruz, 2009).

The phenotypic correlation is conditioned by the relationship among individual characters and the influence of environmental factors. The genotypic correlation is a function of the pleiotropic action of the genes involved and their related inheritance. Linked genes have additive, dominant and epistatic actions. It is generally regarded that the additive genes are of greatest value in breeding (Zhelyazkov & Tsvetanova, 2002).

The performed analysis of the relationships among the tested traits shows that the coefficients of phenotypic dependence for most of the traits were lower as compared to the coefficients of genotypic correlations (Table 1 and Table 2).

Strong positive phenotypic correlations were found between number of fertile nodes per plant and number of seeds ($r = 0.97$), number of pods per plant ($r = 0.97$) and number of seeds per pod ($r = 0.94$), between seed weight per plant and numbers of seeds ($r = 0.83$) and fertile nodes per plant ($r = 0.77$), between number of seeds per pod and number of branches per plant ($r = 0.82$) and between plant height and first pod height ($r = 0.77$). Relatively low phenotypic correlations were detected between number of branches per plant and number of pods ($r = 0.10$) and number of seeds per plant ($r = 0.10$) and seed weight per plant ($r = 0.13$). Positive but weak were the relationships between number of seeds per pod and branch length ($r = 0.09$), numbers of seeds ($r = 0.02$,) and fertile nodes per plant ($r = 0.02$). Negative correlations were found between 1,000-seed weight and numbers of fertile nodes ($r = –0.74$), number of seeds ($r = –0.70$) and number of pods per plant ($r = –0.61$).

Table 2. Genotypic correlation coefficients (r) among the traits in the tested field pea cultivars in Pleven during 2007-2009

Trait	Plant height	First pod height	Number of branches per plant	Number of pods per plant	Number of seeds per plant	Number of fertile nodes per plant	Branch length	Number of seeds per pod	1,000-seed weight	Seed weight per plant
First pod height	0.90***									
Number of branches per plant	–0.18 *	–0.27*								
Number of pods per plant	0.36 *	–0.17 *	0.34*							
Number of seeds per plant	0.55 **	0.07 *	0.43 **	0.96 ***						
Number of fertile nodes per plant	0.47 *	–0.14 *	0.79 **	0.10*	0.11*					
Branch length	0.65 **	0.65 **	–0.45 *	0.53 **	0.69 **	0.83 ***				
Number of seeds per pod	–0.40 *	–0.35 *	0.11*	–0.19 *	0.02 *	0.29 *	–0.01*			
1,000-seed weight	–0.04 *	0.39 **	–0.13*	–0.72 **	–0.79 **	–0.94 ***	–0.51 **	–0.64 **		
Seed weight per plant	0.59 **	0.04 *	0.92 ***	0.91 ***	0.89 ***	0.89 ***	0.57 **	–0.10 *	–0.41*	
Lodging resistance	0.17 *	–0.01 *	0.19*	0.34 *	0.51**	0.53 **	0.24 *	0.90 ***	–0.31 *	0.85 ***

* $p \le 0.05$, ** $p \le 0.01$, *** $p \le 0.001$.

High genetic correlations were detected between plant height and first pod height ($r = 0.89$), between number of pods per plant and seed weight per plant ($r = 0.91$) and number of seeds per plant ($r = 0.96$), between seed weight per plant and numbers of branches ($r = 0.92$) and fertile nodes per plant ($r = 0.89$). Low correlations were detected between seed weight per plant and first pod height ($r = 0.04$) and between number of fertile nodes and number of pods ($r = 0.10$) and seeds per plant ($r = 0.11$). Negative genetic correlation coefficients were detected between 1,000-seed weight and number of fertile nodes per plant ($r = -0.94$), number of seeds per plant ($r = -0.79$), branch length ($r = -0.51$) and number of seeds per pod ($r = -0.64$).

The presented data demonstrate that the seed yield in field pea is a complex trait and is the result of the combined effect of all seed yield components (Kalapchieva, 2002; Sardana *et al.*, 2007; Sultana *et al.*, 2009). They also confirm the earlier reports that seed weight per plant is highly and positively correlated to number of pods per plant and number of seeds per plant (Abnasan *et al.*, 1987; Raudseping & Puhm, 1996; Nisar & Ghafoor, 2009). In a similar complex study with ten field pea cultivars of diverse geographic origin carried out in Novi Sad (Mihailović *et al.*, 2007), the significant correlations at a level of 0.05 were between green forage yields per area unit and per plant ($r = 0.695$), forage dry matter yield per area unit and green forage yield per area unit ($r = 0.650$), seed yield per plant and green forage yield per plant ($r = 0.824$), forage dry matter per plant ($r = 0.825$) and number of pods ($r = 0.694$) and seed yields per area unit and per plant ($r = 0.617$).

Lodging resistance was highly correlated to seed weight per plant, with a phenotypic correlation of 0.47 and a genotypic correlation of 0.85. In that way, it was confirmed that any morphological change in field pea plants, such as short stem or afila leaf type, significantly contributes to increased seed yield (Mikić *et al.*, 2011b). This has highly practical implications in field pea breeding by developing novel cultivars with essentially transformed plant architecture in comparison to traditional field pea landraces with long stems and high seed yield losses during the harvest (Mihailović & Mikić, 2010).

In a study with cultivars of common vetch (*Vicia sativa* L.), a close botanical relative of pea and important grain legume, in the Mediterranean coastal region of Turkey, 1000 seed weight and harvest index showed significant positive correlation (Çakmakci & Açikgöz, 1994). Similar results were obtained in the trials with common vetch in Syria, where high grain yield was strongly correlated with harvest index (Abd El-Moneim, 1993). In addition, in numerous trials in various regions of Turkey, it was also found that grain yield was significantly and positively correlated to both number of pods per plant and number of grain per plant (Cakmakci *et al.*, 2003, 2006; Fırıncıoğlu *et al.*, 2009). This points out the significance of the role these two yield components may play in developing the common vetch cultivars with high and stable grain yield (Blum & Lehrer, 1972).

In general, seed yield in crops may be regarded as a complex character with polygenic inheritance that, from a crop physiology perspective, is the culmination of a series of environment-affected processes such as phenological and canopy development, radiation interception, biomass production and partitioning (Charles-Edwards, 1982). The ultimate performance of a genotype is determined by how it integrates genotype and environmental influences. The end result is seed yield, which has often been described as the product of its components such as plant number per unit area, number of pods per plant, number of seeds per pod, number of seeds per pod and mean seed weight. These yield components show interdependence or plasticity (Moot & McNeil, 1995).

In general, the genetic correlations for most of the traits in field pea have higher coefficients than the phenotypic correlations. Specifically strong positive phenotypic correlations were found between number of fertile nodes per plant and numbers of seeds ($r = 0.972$) and pods per plant ($r = 0.971$). The highest genetic correlations were determined between plant height and first pod height ($r = 0.890$), number of pods per plant and number of seeds per plant ($r = 0.960$). The strongest and direct positive effects over seed yield were by branch length (17.70), 1,000-seed weight (5.92) and number of seeds per pod (4.93). The highest positive indirect contribution were in branch length via number of seeds per pod (2,214.8), number of fertile nodes per plant (1,258.0) and number of seeds per plant (708.70).

The path coefficient analysis (Table 3) revealed that branch length (17.7), 1000 seed weigh (5.9) and number seeds per pod (4.9) were the yield components possessing the highest positive direct effects on seed yield. They can be important criterion for selecting desirable traits for the genetic improvement of the field

Table 3. Path coefficients among the traits related to seed yield in the tested field pea cultivars in Pleven during 2007-2009

Trait	Direct effect	Indirect effects									Total effect
		Plant height	First pod height	Number of branches per plant	Number of pods per plant	Number of seeds per plant	Number of fertile nodes per plant	Branch length	Number of seeds per pod	1,000-seed weight	
Plant height	0.14		−53.2	−127.3	−226.4	−3.2	−367.7	301.2	49.4	414.6	2
First pod height	−0.97	1.5		−26.8	−90.6	−456.8	−300.3	177.2	182.8	604.1	33
Number of branches per plant	−6.70	4.2	−23.2		0.0	305.6	−36.8	708.7	113.6	29.6	256
Number of pods per plant	−7.54	−7.5	6.3	−2.9		−388.6	0.0	−18.4	177.2	1,131.2	50
Number of seeds per plant	−3.21	3.9	−70.7	0.0	−664.0		−61.3	708.7	84.0	35.5	4
Number of fertile nodes per plant	−6.12	0.4	−91.0	−1072.1	−399.9	−19.3		1,258.0	24.7	337.6	20
Branch length	17.71	4.2	−24.2	0.0	−377.3	−25.7	−245.2		321.1	23.7	279
Number of seeds per pod	4.93	0.6	−11.6	−1,735.4	−633.9	−25.7	−214.5	2,214.8		183.6	5
1,000-seed weight	5.92	1.8	−33.9	−6.7	−113.2	−25.7	−459.7	354.4	296.4		43

pea crop. The strongest indirect effects were by branch length via number of seeds per pod (2,214.8), number of fertile nodes per plant (1258.0) and number of seeds per plant (708.7). Negative indirect effects were found in number of branches per plant via number of seeds per pod (−1,735.4) and number of fertile nodes (1,072.1).

The results of the presented study hopefully represent a contribution to a better knowledge on seed yield components in field pea. Collecting data on the mutual relationships among individual seed yield components and their effect on seed yield remains crucial for their optimisation and development of improved field pea genotypes with high, quality and stable seed yields. Based on the trait association and the path coefficients for seed yield and its components, it can be concluded that field pea breeders should pay attention to the traits such as branch length, 1,000-seed weight and number of seeds per pod when selecting high-yielding genotypes.

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