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

V. Kosev\(^1\) and A. Mikić\(^2\)

\(^1\) Institute for Field Crops, Pleven, Bulgaria
\(^2\) Institute of Field and Vegetable Crops, Novi Sad, Serbia

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 fértil 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 fériles 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 fériles 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 fériles 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

---

\*Corresponding author: aleksandar.mikich@gmail.com
Received: 21-04-12. Accepted: 07-11-12

This work has one Supplementary Table that do not appear in the printed article but that accompany the paper online.
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 m² (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
Short communication. Correlation and path analysis of seed yield components in spring-sown field pea cultivars

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 \((r = 0.13)\). 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 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 *                | 0.41 **           | –0.30 *              | 0.47 ** |
| Lodging resistance           | 0.27 *       | –0.07 *          | 0.37 *                       | 0.29 *                   | 0.39 **                   | 0.31 *                            | 0.30 *        | 0.41 **                | –0.30 *           |                      |

* \(p \leq 0.05\), ** \(p \leq 0.01\), *** \(p \leq 0.001\).

**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 *           | 0.11 *                       | –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 **       | –0.01 *                | –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 ***              |

* \(p \leq 0.05\), ** \(p \leq 0.01\), *** \(p \leq 0.001\).
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, 1,000 seed weight and harvest index showed significant positive correlation (Çakmakçı & Açıkgöz, 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 (Çakmakci et al., 2003, 2006; Firincioglu 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 weight \( (5.9) \) 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
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 per plant (–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.

### Acknowledgements

Authors acknowledge the Ministry of Science and Education in Bulgaria for funding the study (contract MSE No.CC 1604/2006).

### References

Abd El-Moneim AM, 1993. Agronomic potential of three vetches (*Vicia* spp.) under rainfed conditions. J Agron Crop Sci 170: 113-120.

Abnasan NT, Garin CS, Tandang LL, 1987. Varietal evaluation and correlation studies in fifteen lines of garden pea. Philipp J Crop Sci 1: 11.

Blum A, Lehrer W, 1972. Genetic and environmental variability in some agronomical and botanical characters of common vetch (*Vicia sativa* L.). Euphytica 22: 89-97.

Çakmakci S, Açıkgöz E, 1994. Components of seed and straw yield in common vetch (*Vicia sativa* L.). Plant Breed 113: 71-74.

Çakmakci S, Aydinoglu B, Karaca M, 2003. Determining relationships among yield and yield components using correlation and path coefficient analyses in summer sown common vetch (*Vicia sativa* L.) genotypes. Pak J Bot 35: 387-400.

Çakmakci S, Aydinoglu B, Karaca M, Bilgen M, 2006. Heritability of yield components in common vetch (*Vicia sativa* L.). Acta Agrie Scand Sect B Plant Soil Sci 56: 54-59.

Charles-Edwards DA, 1982. Physiological determinants of crop growth. Academic Press, Sydney.

Cruz CD, 2009. Programa Genes: Biometria. version 7.0. University of Federal Viçosa, Viçosa, Brazil.

Dewey D, Lu Kh, 1959. A correlation and path-coefficient analysis of components of crested wheatgrass seed production Agron J 51: 515-518.

Espósito MA, Alejandra ME, Pamela CV, López LD, Sebastián AF, Luis CE, 2009. Relationships among agronomic traits and seed yield in pea. BAG J Basic Appl Genet 20: 1.

Fırıncıoğlu HK, Erbektaş E, Doğruyol L, Mutlu Z, Ünal S, Karakurt E, 2009. Phenotypic variation of autumn and spring-sown vetch (*Vicia sativa* ssp.) populations in central Turkey. Span J Agric Res 7: 596-606.

Genchev G, Marinkov E, Yovcheva V, Ogyanova A, 1975. Biometrichni metodi v rastenievadstvoto, genetikata i selektsiyata. Zemizdat, Sofia. [In Bulgarian].
Kalapchieva S, 2002. Korelatsionni zavisimosti mezhdu kolichestveni priznatsi pri sortove gradinski grah. Proc Int Conf 120 Years of Agriculture Science in Sadovo, Sadovo-Plovdiv, Bulgaria, 21-22 May, I, pp: 264-267. [In Bulgarian].

Mehandjiev A, Mihov M, Noveva S, Rodeva R, Kosturkova G, 2006. Some results from the investigation on genetic improvement of pea (Pisum sativum L.). Field Crop Stud 3: 397-403.

Mihailović V, Mikić A, 2010. Novel directions of breeding annual feed legumes in Serbia. Proc XII Int Symp on Forage Crops of Republic of Serbia, Kruševac, Serbia, 26-28 May, 1, pp: 81-90.

Mihailović V, Ćupina B, Mikić A, Katić S, Karagić D, 2007. Relationships between agronomic characteristics in dual-purpose pea. Book of Abstracts 6th Eur Conf Grain Legumes Integrating Legume Biology for Sustainable Agriculture, Lisbon, Portugal, 12-16 November, p: 116.

Mikić A, Mihailović V, Ćupina B, Đorđević V, Milić D, Duc G, Stoddard FL, Lejeune-Hénaut I, Marjet P, Hanoqc E, 2011a. Achievements in breeding autumn-sown annual legumes for temperate regions with emphasis on the continental Balkans. Euphytica 180: 57-67.

Mikić A, Mihailović V, Ćupina B, Kosev V, Warkentin T, McPhee K, Ambrose M, Hofer J, Ellis N, 2011b. Genetic background and agronomic value of leaf types in pea (Pisum sativum). Rat povrt / Field Veg Crop Res 48: 275-284.

Moot DJ, McNeil DL, 1995. Yield components, harvest index and plant type in relation to yield differences in field pea genotypes of partial resistance to field epidemics of ascochyta blight of pea. Euphytica 86: 31-40.

Nisar M, Ghafoor A, 2009. Inheritance studies of Pisum sativum F1, F2 and F3 generation based on morphological traits and selection of high yielding powdery mildew resistant lines. Mol Plant Breed 7: 335-340.

Ranjan S, Kumar M, Pandey SS, 2006. Genetic variability in peas (Pisum sativum L.). Legume Res 29: 311-312.

Raudseping M, Puhm M, 1996. Correlation between yield, morphological and biochemical characteristics of the garden pea and its importance for breeding work. Trans Est Acad Agric Soc 1: 18-21.

Sardana S, Mahajan RK, Gautam NK, Ram B, 2007. Genetic variability in pea (Pisum sativum L.). SABRAO J Breed Genet 39: 31-41.

Steel RG, Torrie JH, 1982. Principles and procedures of statistics: a biometrical approach. McGraw-Hill, Tokyo.

Sultana Z, Islam AKMA, Hasan Mitu MK, Mian MAK, 2009. Genetic variability and character association in garden pea (Pisum sativum L. spp. hortense) genotypes. Available in http://aminulgpb.faculty.bsmrau.edu.bd/files/2009/07/Zakia-paper_Genet-Var-BJAR.pdf.

Togay N, Togay Y, Yildirim B, Dogan Y, 2008. Relationships between yield and some yield components in pea (Pisum sativum ssp arvense L.) genotypes by using correlation and path analysis. Afr J Biotechnol 7: 4285-4287.

Williams WA, Demment MW, Jones MB, 1990. A concise table for path analysis statistics. Agron J 82: 1022-1024.

Wright S, 1921. Correlation and causation. J Agric Res 20: 557-585.

Zhelyazkov E, Tsvetanova Y, 2002. Rakovodstvo za uprazhneniya pa genetika. Trakian University, Stara Zagora. [In Bulgarian].