



## Yield and stability for agronomic and seed quality traits of common bean genotypes under Mediterranean conditions

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### ABSTRACT

Common bean is the most significant pulse in Mediterranean countries and high yield performance is required to become commercially successful. Seven common bean genotypes were evaluated for yield and stability along with their interrelationship with agronomical, physicochemical and quality characteristics. An analysis of variance was conducted to test main effects and interactions between plant traits and environments. Significant variation among genotypes occurred for seed yield and a strong positive correlation was observed between seed yield and pods m<sup>-2</sup>. High Genetic Coefficient of Variation (GCV) values combined with high heritability for traits as seed yield, cooking time, hydration capacity and protein content were recorded. The GGE biplot analysis indicated two cultivars as superior genotypes that combine high yield, stability, short cooking time and high protein content. Furthermore, a local population assessed as promising genetic material for the selection of elite lines with high yield and short cooking time.

**Key words:** Common bean, Cooking time, Landraces, Protein content, Seed yield.

### INTRODUCTION

Grain legumes significantly contribute to total world food production providing a valuable source of proteins in many developing countries. Common bean (*Phaseolus vulgaris* L.) is the most consumed grain legume, and hold an important place in the Mediterranean diet considered as the "poor man's meat". Beans are the most significant among the other pulses in Greece and in the recent years the cultivated areas are increasing steadily, especially in Northern and Central regions of the country (Vakali *et al.*, 2017). In some cropping areas landraces are still cultivated, since they are adapted to specific low input environments and provide high tolerance to biotic and abiotic stresses, resulting in high yield stability but intermediate in yield potential (Zeven, 1998; Angioi *et al.*, 2010). However, modern agriculture depends on uniform crop varieties in order to meet a global growing demand for food. Hence, landraces have progressively been replaced by elite cultivars which have high agronomic performance and ensure high production and income (Mavromatis *et al.*, 2010).

The study of the sensory and chemical characteristics of beans is important because they affect the beans' culinary properties (González *et al.*, 2006; Mkanda *et al.*, 2007). Some of the most important characteristics are grain size, seed coat color and cooking time (Mkanda *et al.*, 2007). Another high quality factor related to bean quality is

the nutritional composition of dry seeds which includes proteins, fat and dietary fiber content (Kamboj and Nanda, 2018).

The aim of this work was to evaluate the seed yield performance, the agronomic, physicochemical and quality characteristics of seven dry bean genotypes. The results could permit us to select the most adapted and high yielding genotypes, rich in nutrients and presenting the lowest cooking time and to gain insights in determining future breeding objectives and selection criteria to be used in the breeding program employed.

### MATERIALS AND METHODS

Seven common dry bean genotypes, two landraces - *Chrysoupoli* (Ch), *Albanian Prespa* (APr)- and five commercial cultivars *viz.*, - *Iro* (Ir), *Mirsini* (Mi), *Lingot Suisse* (LS), *Pirgetos* (Pi), and *Lida* (Li) - cultivated in Greece were evaluated in a randomized complete blocks (RCB) design with four replications. Field experiments were performed over the years 2011 and 2012 in two main production areas in North Greece: Prespa (Pr) (40°49' N, 21°06' E, 859 m MSL) and Florina (FI) (40°46' N, 21°22' E, 707 m MSL). For each environment, soil properties, mean temperature and rainfall were recorded (Table 1). Across both treatments, basal fertilization was uniformly applied at rates of 44-60-60 Kg ha<sup>-1</sup> N, P, K at planting, and appropriate cultural practices were followed.

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**Table 1:** Climatic conditions during the cultivation period and soil characteristics of the field trial.

Environment	Mean temperature (°C)	Rainfall (mm)	Soil Type	pH	CaCO <sub>3</sub> (%)	EC (mS/cm)	Organic matter (%)
Prespa 2011 (Pr11)	16.54	237.3	SL	6.7	0.1	0.25	1.37
Florina 2011 (Fl11)	17.6	132.2	SL	6.3	3.5	1.31	1.4
Prespa 2012 (Pr12)	17.9	389.57	SL	6.7	0.1	0.25	1.37
Florina 2012 (Fl12)	18.34	70.2	SL	6.4	4	1.22	1.5

EC: electrical conductivity, L: loam, SL: sandy loam.

For each replication, observations for the following agronomical traits were recorded: seed yield (SY) expressed in grams per square meter, number of pods (P) per square meter and 100 seed weight (W100). Morphological characteristics determined on 20 seeds per plot were seed length (LEN), seed width in cross section (WID) and thickness (THI). Also, the following physicochemical characteristics were measured: hydration increase (HI) of bean seeds was calculated as the percentage of increase in mass of beans soaked in distilled water for 12h at room temperature; hydration capacity (HC) is determined after soaking in distilled water for 12 h (Bishnoi and Khetarpaul, 1993); seed coat proportion (SCP%) was determined on 10 seeds per plot, as the ratio in weight between coat and cotyledon expressed in percentage, after removing the seed coat from the cotyledons, both after soaking and keeping them for 24h at 105°C; cooking time (CT) was recorded according to the method described by Iliadis (2001). The nutritional quality traits determined in the finely grounded samples obtained from all plots for each genotype and location were protein content P (%) (measured with the Kjeldhal method) and mineral ash percentage A (%) (AOAC, 2000) calculated on a dry weight basis.

Data were subjected to over year two-way analysis of variance (ANOVA), using the mixed model considering genotypes as fixed effect and environments as random effect (McIntosh, 1983). The ANOVA treatment sum of squares ( $SS_{TRTMT} = SS_G + SS_E + SS_{G \times E}$ ), including the genotype (G), environment (E) and their interaction GxE (GEI), was partitioned into its components  $SS_G$ ,  $SS_E$ ,  $SS_{G \times E}$  (Sneller *et al.*, 1997). Furthermore, broad sense heritability (H) was calculated to assess the effectiveness of the testing program in differentiating between cultivars as follows:  $H = \sigma_g^2 / \sigma_p^2$ , in which phenotypic variance  $\sigma_p^2$  is estimated as  $\sigma_p^2 = \sigma_g^2 + (\sigma_{ge}^2/e) + (\sigma_c^2/re)$ , where e and r are the numbers of environments and replications per environment, respectively (McIntosh, 1983). The genotypic coefficient of variation

$$(GCV\% = \sqrt{\sigma_g^2} / x * 100)$$

was also calculated to indicate the useful genotypic variation. Varieties with high GCV for a particular character were assumed as the most responsive to breeding selection and genetic gains. The Student *t*-test at  $\alpha = 0.05$  was used to compare means. Pearson's correlation coefficients (*r*) were calculated to establish relationships between parameters. All the analyses were performed using the statistical software

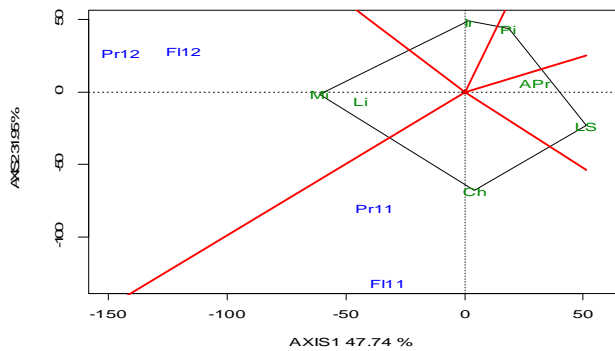
JMP 8 (SAS Institute, 2009). To determine stability across environments, a Genotype plus Genotype×Environment (GGE) biplot analysis was conducted using a free software package, GGE Biplots in R version 1.0-8 (Yan and Kang, 2003).

## RESULTS AND DISCUSSION

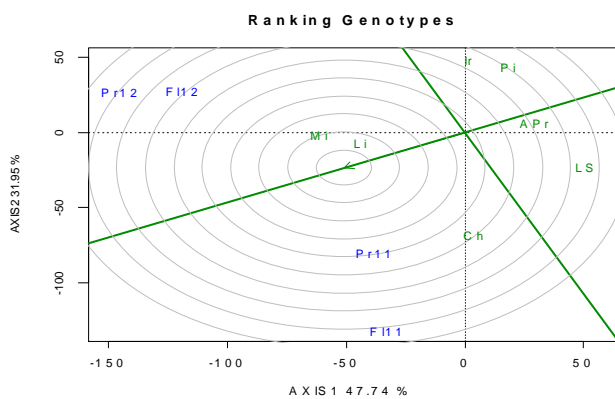
Analysis of variance revealed that SY and P were significantly affected by E, G, and its GEI (Table 2). The SY was affected equally by E and G, 30.07 and 30.33% of treatment SS respectively, whereas GEI was higher 39.60%. The P was also highly affected by GEI 44.03%. The coefficient of H was moderate for SY (0.56) and P (0.66), whereas the relatively high GCV% values for SY (GCV=15.67%) and P (GCV=23.32%) indicated the high potentiality of these traits for effective selection (Devi *et al.*, 2015; Razvi *et al.*, 2018).

Furthermore, the GGE biplot analyses revealed that the high GEI was due mainly, because of the differential performance of the genotypes in each year than in each location (Fig 1). The genotype Ch was the best in year 2011 in both locations (Florina, Prespa), whereas the Mi followed by Li were the best performing in 2012. For this reason, the results of SY and its component (P) were reported as means in each year (Table 3).

The highest mean value for SY in 2011 was recorded for Ch but not significantly higher than Mi, Li, Ls and Apr, whereas in 2012 the SY was significantly higher for Mi and Li (Table 3). The cultivars Ir, Pi, LS and the Apr constituted a low yielding group. The lower yield performance may be attributed to lower adaptation of these genotypes to the environmental conditions of North Greece. The GGE biplot analysis revealed that Li and Mi were most desirable for yield and stability whereas landrace Ch was high yielding but instable (Fig 2). These results indicate that the Li and Mi could be considered as wide adaptation cultivars, whereas Ch is a promising genetic material with high yield potential. Wide adapted cultivars are of great importance, especially due to the ongoing climate change (Tokatlidis and Vlachostergios, 2016). On the other hand, the landrace Ch constitutes a valuable source of genetic diversity and breeding efforts should be targeted in its exploitation. Besides, the selection of high yielding and stable across environments genotypes should be the main objective of a common bean breeding program (Mekbib, 2003).



**Fig 1:** Polygon view of genotype and genotype  $\times$  environment (GGE) biplot analysis for the best-performing in seed yield of seven dry bean genotypes, across two locations for two years



**Fig 2:** GGE biplot analysis for ranking seven dry bean genotypes and two years for stability and seed yield.

The W100, LEN, THI and WID were all significantly influenced by the G, E and GEI (Table 2). The influence of genetic factors in W100, LEN and THI was strong as was also indicated by the high H values (0.79 – 0.98), whereas the WID which was equally affected by E (34.27%) and GEI (34.43%) and its H was moderate (0.63). Cultivars that were high yielding (Mi, Li and Ch) showed the lowest weight in W100 (Table 3). Generally, there was a significant positive correlation between SY and P ( $r=0.77$ ,  $P\leq 0.01$ , Table 4). This seems to be an important observation since this trait could be recommended as an indirect selection criterion for high yield. These results are in accordance with those of other researchers (Devi *et al.*, 2015; Vakali *et al.*, 2017; Razvi *et al.*, 2018). In contrast W100 had a negative, significant contribution to the P ( $r=-0.28$ ,  $P\leq 0.05$ ) and this finding is in agreement with other references (White and Gonzales, 1990). González *et al.* (2006) reported that the correlation between W100 and SY affected by the environment, so the practical lack of correlation between SY and W100 ( $r=-0.04$ ) showed in this study is possible. This trait (W100) depended on genotype and had a positive correlation with the type and size of seeds (Graham and Ranalli, 1997). Our findings revealed that genotypes with lowest LEN and THI were Mi and Li (Table 3) and can be considered as small seeded genotypes. The W100 showed direct positive ( $r=0.59$ ,  $P\leq 0.01$ ) correlation with the LEN (data not shown). The negative correlation between the size of the seeds and the yield should be kept in mind when choosing

**Table 2:** Mean sum of squares (ss) percentage, genotypic coefficient of variation (GCV%) and heritability for seed yield, number of pods per square meter and seed character for seven dry bean genotypes.

Source of variance	DF	SY(g m <sup>-2</sup> )	P	W100 (g)	LEN (mm)	THI (mm)	WID (mm)
Environment (E)	3	45113.98*	18133.17*	174.37*	1.38*	0.53*	0.86*
Genotypes (G)	6	22756.16*	29936.42*	218.33*	41.47*	2.30*	0.39*
G $\times$ E	18	9901.04*	10228.40*	46.39*	0.73*	0.16*	0.14**
Pooled Error	72	3357.7	2940.40	13.70	0.17	0.06	0.09
SS <sub>E</sub> %		30.07	13.01	19.60	1.56	8.80	34.27
SS <sub>G</sub> %		30.33	42.96	49.10	93.52	75.70	31.30
SS <sub>GEI</sub> %		39.60	44.03	31.30	4.92	15.50	34.43
GCV%		15.67	23.32	9.55	12.97	4.94	2.30
H		0.56	0.66	0.79	0.98	0.93	0.63

\*Significant at  $P\leq 0.05$  statistical level; \*\* Significant at  $P\leq 0.01$  statistical level.

**Table 3:** Mean values for seed yield, number of pods per square meter and seed characters for seven dry bean genotypes.

Genotype	SY (g m <sup>-2</sup> )		P		W100(g)	LEN(mm)	THI(mm)	WID(mm)
	2011	2012	2011	2012				
Mi	239.20 <sup>a</sup>	230.16 <sup>a</sup>	179.10 <sup>a</sup>	265.32 <sup>a</sup>	30.29 <sup>d</sup>	10.13 <sup>e</sup>	6.93 <sup>e</sup>	5.57 <sup>a</sup>
Li	237.78 <sup>a</sup>	206.38 <sup>ab</sup>	144.49 <sup>abc</sup>	247.05 <sup>a</sup>	29.25 <sup>d</sup>	10.27 <sup>e</sup>	7.01 <sup>e</sup>	5.58 <sup>a</sup>
Ch	276.74 <sup>a</sup>	126.25 <sup>cd</sup>	164.96 <sup>a</sup>	131.89 <sup>b</sup>	33.50 <sup>c</sup>	12.70 <sup>cd</sup>	7.69 <sup>b</sup>	5.44 <sup>ab</sup>
Ir	156.80 <sup>bc</sup>	160.40 <sup>bc</sup>	92.43 <sup>bc</sup>	157.76 <sup>b</sup>	34.36 <sup>bc</sup>	12.41 <sup>d</sup>	7.75 <sup>ab</sup>	5.25 <sup>bc</sup>
APr	208.83 <sup>abc</sup>	108.34 <sup>cd</sup>	156.16 <sup>ab</sup>	126.66 <sup>bc</sup>	36.92 <sup>b</sup>	12.79 <sup>c</sup>	7.90 <sup>a</sup>	5.32 <sup>bc</sup>
LS	220.83 <sup>ab</sup>	72.23 <sup>d</sup>	139.51 <sup>abc</sup>	72.74 <sup>bc</sup>	39.68 <sup>a</sup>	14.67 <sup>a</sup>	7.22 <sup>d</sup>	5.56 <sup>a</sup>
Pi	148.70 <sup>c</sup>	139.76 <sup>bcd</sup>	83.21 <sup>c</sup>	144.73 <sup>b</sup>	36.25 <sup>b</sup>	13.14 <sup>b</sup>	7.39 <sup>c</sup>	5.22 <sup>c</sup>
CV%	17.06	16.87	32.27	31.11	10.79	3.35	3.22	5.57 <sup>a</sup>

\* means with different letters are significantly different at  $\alpha=0.05$  level.

the best performing genotype since large seeded cultivars are preferred by consumers probably because they have been reported to hydrate rapidly and taste satisfactorily (Kigel, 1999).

Selection on the basis of SY alone is the simplest and most efficient method of selection, but cooking and quality parameters should be also considered. Table 5 shows that G accounted for 44.87% of the total variability in HI, 43.02% in HC, 74.15% in SCP and 85.16% in CT, although E and GEI were also significant except for SCP which proved to be insignificant. The coefficient of H was high ( $H > 0.82$ ) and the GCV% values were also high for HI, HC and CT (Table 5), indicated the high potential for genetic advancement for these characters. Cultivars Mi and Li recorded the highest values of HI% (Table 6) and this trait was found to be positively associated with HC ( $r = 0.65$ ,  $P \leq 0.01$ ) (Table 4). Del Valle *et al.* (1992) found that small

seeds hydrated even more than the large seeds during soaking, however Berrios *et al.* (1999) reported that small seeds did not hydrate after soaking for 24h and took a long time to soften during cooking. In our research, the large seeded cultivar LS had the maximum HC, whereas significant, positive correlation was found between HC and W100 ( $r = 0.49$ ,  $P \leq 0.001$ ).

Cooking time was mainly controlled by genotypic factors (Table 5) and was significantly longer in landrace Ch and cultivar Ir, whereas the shortest time obtained by Mi and Li (Table 6). Kigel (1999) and Sozen *et al.* (2018) reported that culinary and nutritional quality traits were strongly affected by geographic location, soil and climatic conditions. Beans grown in soils rich in Ca and Mg and with elevated average annual temperature (15-24°C) had higher cooking time and seed hardness compared to beans grown in a location with lower temperature (11-18°C) and soils with

**Table 4:** Correlation coefficient for seed yield and number of pods per square meter, seed character and quality parameters for seven dry bean genotypes.

	P	SY	W100	HI%	HC	CT	SCP%	P%
SY	0.77**							
W100	-0.28*	-0.04						
HI%	0.11	0.09	-0.04					
HC	-0.14	0.05	0.49**	0.65**				
CT	-0.30*	-0.17	0.15	-0.53**	-0.29*			
SCP%	-0.20	-0.21	0.13	0.07	0.29*	0.05		
P%	-0.09	-0.15	0.13	-0.08	0.02	-0.02	-0.003	
A%	-0.20	0.25*	0.27*	0.20	0.34**	0.19	-0.04	-0.05

When  $r \geq 0.23$ , correlation was significant at  $P \leq 0.05$  (\*) and at  $r \geq 0.31$ , correlations was significant at  $P \leq 0.01$  (\*\*) for  $n = 72$  degrees of freedom.

**Table 5:** Means Squares, partitioning of sum of squares (SS), heritability (H) and genetic coefficient of variation (GCV) for cooking and quality parameters for seven dry bean genotypes.

Source of variance	df	HI%	HC	SCP%	CT(min)	P%	A%
Environment (E)	3	2849.22*	0.06*	0.67ns	91.37*	14.79*	32.09*
Genotypes (G)	6	1985.23*	0.04*	5.64*	804.09*	11.57*	0.49*
G×E	18	338.05*	0.01*	0.54ns	31.47*	4.02ns	0.22*
Poolederror	72	57.28	0.00	0.48	14.91	3.02	0.07
SS <sub>E</sub> %		32.20	33.31	4.38	4.84	23.85	93.23
SS <sub>G</sub> %		44.87	43.02	74.15	85.16	37.30	2.87
SS <sub>GEI</sub> %		22.93	23.67	21.47	10.00	38.85	3.90
GCV%		10.91	14.41	6.54	18.94	2.76	2.55
H		0.83	0.82	0.90	0.96	0.65	0.55

\*Significant at 0.05 statistical level; \*\* Significant at 0.01 statistical level.

**Table 6:** Mean values for cooking and quality parameters for seven dry bean genotypes.

Genotype	HI%	HC	SCP%	CT(min)	P%	A%
Mi	107.0 <sup>a</sup>	0.30 <sup>cd</sup>	8.34 <sup>cd</sup>	29.06 <sup>e</sup>	24.51 <sup>a</sup>	5.08 <sup>bc</sup>
Li	106.1 <sup>a</sup>	0.31 <sup>bc</sup>	8.58 <sup>bc</sup>	30.31 <sup>de</sup>	24.79 <sup>a</sup>	5.04 <sup>c</sup>
Ch	85.4 <sup>cd</sup>	0.28 <sup>d</sup>	8.30 <sup>cd</sup>	46.56 <sup>a</sup>	25.73 <sup>a</sup>	5.41 <sup>a</sup>
Ir	80.8 <sup>d</sup>	0.29 <sup>cd</sup>	8.97 <sup>b</sup>	45.00 <sup>a</sup>	23.27 <sup>b</sup>	5.23 <sup>ab</sup>
APr	81.9 <sup>d</sup>	0.30 <sup>cd</sup>	8.64 <sup>bc</sup>	39.69 <sup>b</sup>	25.73 <sup>a</sup>	5.11 <sup>bc</sup>
LS	99.3 <sup>b</sup>	0.43 <sup>a</sup>	9.73 <sup>a</sup>	32.19 <sup>cd</sup>	25.23 <sup>a</sup>	4.84 <sup>d</sup>
Pi	90.3 <sup>c</sup>	0.32 <sup>b</sup>	7.86 <sup>d</sup>	34.06 <sup>c</sup>	24.71 <sup>a</sup>	5.08 <sup>bc</sup>
CV%	8.14	10.63	8.03	10.52	6.99	5.32

\* means with different letters are significantly different at  $\alpha = 0.05$  level.

low level in Mg and Ca (Kigel, 1999). Our results were in accordance with these findings, varieties cultivated in F111 and F112 where soils characterized by CaCO<sub>3</sub> concentration 3.5-4% recorded longer cooking time in comparison with Pr11 and Pr12 where soils were poor in Ca (0.1%). As described by Elia *et al.* (1997) the high, negative phenotypic correlation between CT and HC (-0.82) justifies using the HC trait as an indirect selection criterion for CT. In the current work, HI% had significant, negative contribution ( $r=-0.53$ ,  $P\leq 0.01$ ) to CT, while HC had negative, relative low but significant correlation ( $r=-0.29$ ,  $P\leq 0.05$ ) with CT (Table 4). According to these results the feature HC cannot be used as an indirect selection criterion for short cooking time and other factors might be influencing the process (Barros *et al.*, 2016).

Seed protein content differed slightly among genotypes from 23.27% to 25.73% with a mean of 24.85% (Table 6). Mavromatis *et al.* (2010) found wider ranges for this trait (22.36-28.58%) with mean value 25.25%. The differences in protein content were due to a combination of genetic and environmental factors (Table 5). All varieties,

except for cultivar Ir, constituted a high protein content group (Table 6). Many researchers have reported different kinds of association (negative, positive or neutral) between P% and SY (Osborn and Brown, 1988; González *et al.*, 2006). In our results a small negative but not significant correlation ( $r=-0.15$ ) between P% and SY was found and P% did not show a strong correlation with other characters (Table 4). Generally, consumers are interested in beans rich in nutrients with low cooking time and therefore, breeders should include the seed quality characters in their research targets.

## CONCLUSION

The results of this study indicate that cultivars Lida and Mirsini showed the best performance for agronomic and seed quality traits while, landrace Chrysoupoli seems to be a promising genetic material for selection of superior advanced lines. The P was highly associated with SY and could be proposed as indirect selection criterion for increasing yield. Valuable genetic variability for short CT and high protein content have been identified and could be exploited in future breeding programs.

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