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Crop Yield Potential Estimation under Too Low Density in Dry Bean Genotypes

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Abstract: The study was conducted to investigate the crop yield potential of 19 lines derived from two local dry bean populations (*Phaseolus vulgaris* L.). Lines evaluation by the honeycomb methodology method under the low density of 1.2 plants m⁻² in both greenhouse and open field conditions permitted to partition crop yield potential in three genetic components: i) progeny mean yield per plant (\bar{X}), reflecting the yield potential per plant, ii) progeny standardized mean ($\bar{X} s^{-1}$), which evaluates genes contributing to stability of performance and iii) progeny standardized selection differential $\{(\bar{X}_s - \bar{X}) s^{-1}\}$, which evaluates genes that control responsiveness to inputs. Performance of the lines at the typical dense stand of 2.4 plants m⁻² in three greenhouse and open air trials was also tested. The two approaches of entries crop yield potential differentiated entries in a similar way. Entries crop yield potential estimated by the honeycomb methodology were found to be consistent with their performance in dense stand. Exception existed for two out of the 19 lines, attributable partly to genotype by year interaction. Results were suggestive that crop yield potential estimated under very low density approximating total absence of competition may effectively predict performance under the typical crop production conditions, permitting application of honeycomb methodology in the absence of competition across the entire generations of a breeding program and exploitation of the following advantages: maximum phenotypic expression and differentiation that facilitates identification of the superior genotypes, erasure of the adverse impact of negative relationship between yielding and competitive ability on selection effectiveness, avoidance of biased judgment of crop yield potential in dense stand due to significant genotype by density interactions.

Key words: Honeycomb selection, absence of competition, yield potential per plant, tolerance to stresses, responsiveness to inputs

INTRODUCTION

Evans and Fischer (1999) defined crop yield potential (i.e., maximum yield per unit area) as the yield of a cultivar when grown in the most favourable environments. Thus, the commonly used method of its approach is estimation of cultivars grain yield per unit area under dense stand assumed to represent optimum density. However, crop yield potential is distinguished from maximum yield

reached in given environments (Evans and Fischer, 1999). Moreover, significant genotype by density interactions (Tollenaar, 1992; Lloveras *et al.*, 2004) might lead to biased judgment when crop yield potential is estimated under a single high plant density.

Honeycomb selection in the absence of competition has been suggested to overcome the environmental effects on phenotypic expression of quantitative characters (Fasoulas, 1993) that constitute the major obstacle breeders encounter in their attempt to identify the most promising genotypes. Honeycomb experimental designs to apply either single-plant selection or progeny evaluation in the absence of competition have been constructed to cope with the adverse effects of soil heterogeneity on phenotypic expression (Fasoulas and Fasoula, 1995). Consequently, Fasoula and Fasoula (2000, 2002) proposed the honeycomb approach of crop yield potential, by estimation of its three components under the objective conditions of absence of competition: yield potential per plant, tolerance to overall biotic and abiotic stresses and responsiveness to inputs. These parameters are predicted by the respective measurements: the entry mean (\bar{X}), standardized entry mean ($\bar{X} s^{-1}$), actually representing inverse value of Coefficient of Variation (CV) and the standardized entry selection differential $\{(\bar{X}_s - \bar{X}) s^{-1}\}$. Genotypes that combine high values for each single component are assumed to have incorporated genes for improved yield potential per plant, tolerance to stresses and responsiveness to inputs, respectively. Selection for the three crop yield components and quality across the target area of adaptation at all stages of the breeding program makes regional testing unnecessary and halves the time required to release a cultivar (Fasoula and Fasoula, 2002). Thus the question how performance in dense stands approaching densities that producers establish could be predicted from the performance in the absence of competition is reasonable.

The present study aimed to assess crop yield potential of dry bean genotypes by two approaches, firstly by the newly proposed honeycomb methodology under a single low density approximating absence of competition (CYP) and secondly under a single dense stand simulating field crop conditions. By this way it was possible to investigate if CYP is associated with performance under the dense stand and thus honeycomb method could effectively predict crop yield potential, as an alternative procedure of crop breeding due to its considerable advantages. For the purpose, 19 experimental lines were used, derived from two traditional landraces via honeycomb selection on the basis of single plant yield.

MATERIALS AND METHODS

Source Material and Experimental Treatments

Two local dry bean populations (i.e., traditional landraces) constituted the source material of the study. These populations concern a famous for bean quality region, located in Western Macedonia, Greece. The first population (A), named by producers *plaki Prespas* had been used mainly in the highlands until 1970 and thereafter it was replaced by the second population (B) named Chrisoupoli which was assumed more adaptable to lowlands neighbouring Prespa lakes in the region. Both populations belong to white-large-seed type with Thousand Kernel Weight of 690 (A) and 600 g (B), as well as to the indeterminate climbing type (IV). Experimentation was carried out in two regions of Greece, the Technological Education Institute Farm of Florina (40° 46' 7N, 21° 22' 8E, 705 m elevation) and the Prespa lakes region (40° 50' 1N, 21° 07' 2E, 856 m elevation). The first region involved a greenhouse constructed of glass (on a sandy loam soil with a pH of 6.4, 1.6% organic matter and a water-holding capacity of 0.35 cm³ cm⁻³) and an adjacent open field (field 1) on a sandy loam soil with a pH of 5.8, 2.06% organic matter and a water-holding capacity of 0.26 cm³ cm⁻³. The second region involved another open field (field 2) on a sandy loam soil with a pH of 6.8, 1.23% organic matter and a water-holding capacity of 0.39 cm³ cm⁻³. Two or three seeds were sowed in each hill and were thinned to a single plant at the four-leaf stage. Plants grown in small pots, being at the stage of two leaves, were transplanted to hills in a few cases of seed failure to emerge. Plants were staked on canes

of 200-230 cm height. Treatments like soil preparation, sowing depth, as well as weed, disease and insect control, irrigation and fertilisation, were applied carefully to ensure as uniform as possible plant growing conditions. Grain yield was measured after plants had been cut about 140 days from sowing date and left to dry for at least 10 days.

Line Formation

A total of 432 plants of each population were grown in the greenhouse (sowing date 13th of March 2003), in a nonreplicated (NR-0) honeycomb trial (Fasoulas and Fasoula, 1995) for each population, with plants spaced 80×80 cm (≈ 1.8 plants m^{-2}). Another similar two NR-0 trials were established on 3rd of May 2003 in the open air (field 1), each trial containing a total of about 500 plants spaced 100×100 cm (≈ 1.2 plants m^{-2}). Although the 100×100 cm density was assumed to approximate better real absence of competition, higher density in the greenhouse was preferred, because of limited area to include sufficient number of plants. The HONEY microcomputer program (Batzios and Roupakias, 1997) was used to apply the moving-circle selection of individual plants. By this way 19 high yielding plants were selected and seed of each constituted a separate line. Lines were coded according their origination, A or B for population and G or F for area (e.g., line BG1 was originated from a single plant selected from population B in the greenhouse).

Line Evaluation under Low Density

During 2004 growing season progeny evaluation was conducted in a R21 honeycomb trial in the greenhouse and another R21 honeycomb trial in the field 1. Each trial included the 19 lines and the original populations as checks, with plants being spaced 100×100 cm. A total of 532 plants (≈ 25 plants per entry) were established in the greenhouse (sowing date 15th of March) and another 994 plants (≈ 47 plants per entry) were similarly established in the field1 (sowing date 6th of May). In order the three crop yield components to be approached, the HONEY microcomputer program (Batzios and Roupakias, 1997) was used to compute entry mean yield per plant (\bar{X}), standardized entry mean ($\bar{X} s^{-1}$) and standardized entry selection differential $\{(\bar{X}_s - \bar{X}) s^{-1}\}$ with a 5.3% selection pressure. Each component value was expressed % of the respective value of the check population. The sum of the three components for each entry gave entry's Crop Yield Potential index (CYP).

Line Evaluation under Dense Stand

Entry evaluation under the dense stand of around 2.4 plants m^{-2} was performed during 2005 growing season in randomized complete blocks, each block replicated four times in three environments. In greenhouse sowing date was 12th of March with two rows per plot of 4.8 m length, 70 cm between rows and 60 cm between plants on each row. These intra- and inter-row distances are used by the producers in the region for commercially produced dry bean. Border plants were omitted in harvest and yield per plot was adjusted to yield per hectare (ha). In field 1 and 2 similar trials were established on 26th and 28th of April, respectively. Plots included four rows of 6.6 m length, 70 cm between rows and 60 cm between plants on each row. Plants of the two central rows of each plot were harvested and yield per plot was adjusted to yield per ha. Comparison of means was conducted by Duncans multiple range test after Analysis of Variance (ANOVA), for one-factor randomized complete block design combined over locations.

RESULTS AND DISCUSSION

Crop yield potential components, as they were computed on the basis of performance under the low density of 1.2 plants m^{-2} and considering overall data from greenhouse and field 1, are presented in Table 1a. Each component, as well as their sum representing the Crop Yield Potential (CYP) index,

Table 1: Comparative data obtained under 1.2 (a) and 2.4 plants m⁻² (b). a: The three components of crop yield potential, mean yield per plant (\bar{x}), standardised entry mean ($\bar{\bar{x}}$) and standardised mean differential $\{(\bar{x}_s - \bar{\bar{x}}) s^{-1}\}$, expressed % of the respective check's value and their sum resulting in crop yield potential combined index (CYP) expressed also % of the respective check's value. b: Mean yield per ha expressed % of the respective check's value (Decreasing order according yield in dense stand)

Line	a: Ultra-low density			b: Dense stand	
	$\bar{\bar{x}}$ (%)	$\bar{x} s^{-1}$ (%)	$(\bar{x}_s - \bar{\bar{x}}) s^{-1}$ (%)	CYP (%)	Yield per ha ⁻¹ (%)
Population A					
AF4	173	164	79	138	132*
AF2	106	94	73	91	130*
AG4	143	136	85	121	122*
AF5	163	126	81	123	118*
AG2	141	141	74	118	113
AG1	114	116	92	108	105
check A	100	100	100	100	100
AF1	84	95	80	86	92
AF3	100	106	82	96	86
AG3	80	116	57	84	78*
100%=	171 g	1.92	2.91	300	2059 kg
Population B					
BG4	103	141	91	112	118*
BF3	127	140	104	124	114*
BG5	102	111	92	101	113
BG2	112	149	105	122	108
BF4	119	134	115	123	105
BF5	99	130	91	107	102
check B	100	100	100	100	100
BG3	98	138	87	107	99
BF2	79	98	104	94	92
BG1	83	119	70	91	92
BF1	107	144	117	123	89
100%=	243 g	1.87	2.24	300	2529 kg

*: Lines differ significantly from the respective check population (Duncans test, p<0.05)

is expressed as a percentage of the respective check population value. For the first crop yield potential component ($\bar{\bar{x}}$), that reflects yield potential per plant as it is expressed when any plant-to-plant interference of environmental inputs is erased, the check . A gave 171 g plant⁻¹ and the check B 243 g plant⁻¹. In relevance with the respective check population, this particular component ranged from 80 (line AG3) to 173% (line AF4) in case of entries A and from 79 (line BF2) to 127% (line BF3) for entries B. In other words differentiation among members of set A was wider compared with that of set B. Regarding the second component, that constitutes a measure of tolerance to stresses, $\bar{x} s^{-1}$ values ranged from 94 (AF2) to 164% (AF4) for entries A and from 98 (BF2) to 149% (BG2) for entries B, when expressed % of the respective values of the check A and the check B. For this particular component differentiation of entries A was greater either. The obtained $\bar{x} s^{-1}$ values reflect partly tolerance to environmental effects, since part of phenotypic variation resulted from genetic variation (wider in check populations). Obviously lines AF2 and AF1 could be assumed the most vulnerable to environmental fluctuations among the entries A, as well as line BF2 among the entries B. As far as the third component is concerned, reflecting responsiveness to inputs, differentiation extent of the two sets of entries was similar. A lines exhibited relevant $(\bar{x}_s - \bar{\bar{x}}) s^{-1}$ values ranging from 57 (AG3) to 92% (AG1). Relevant $(\bar{x}_s - \bar{\bar{x}}) s^{-1}$ values of B lines were 70% (BG1) till 117% (BF1). Thus, A lines, as well as five out of the 10 B lines exhibited lower $(\bar{x}_s - \bar{\bar{x}}) s^{-1}$ values than the respective populations. This result is reasonable because the difference $(\bar{x}_s - \bar{\bar{x}})$ is expected greater within wide genetic pool (i.e., population) than within narrow genetic pool (i.e., lines originating from single plants). Concerning CYP index and in comparison with the check A, five out of the nine A lines had higher CYP values, with line AF4 having the highest (138%), whereas four of the A lines exhibited lower CYP values, with the lowest being 84% for line AG3. In terms of B lines, CYP values ranged

from 91-124%, with the highest being for lines BG4, BF3, BG2, BF4 and BF1 ($\geq 112\%$), while lines BG1 and BF2 had the lowest and equal to 91 and 94%, respectively. Greater differentiation among entries A for the first and the second component resulted to greater differentiation for CYP values as well, when compared to entries B (Table 1).

Analysis of variance of data regarding grain yield across the three environments under the dense stand of 2.4 plants m^{-2} depicted significant mean square for entries ($p < 0.001$) and entry by environment interaction ($p < 0.001$), but not for locations ($p < 0.14$). That means that the three experiments yielded on average the same, significant differences between entries existed and entries responded differently to the three environments. The entry by environment interaction was qualitative since entries were ranked differently across the three environments (not shown). Grain yield per unit area of the A and B entries, averaged across the three locations and expressed as percentage of the respective check population, are given in Table 1b. As it happened in case of CYP values, A entries appeared to differentiate more extensively than B entries. Average yield of the check A was 2059 kg ha^{-1} and that of the check B was 2529 kg ha^{-1} . Compared to the check A, four out of the nine A lines gave significantly higher yield (118-132%), with line AF4 that gave the highest CYP index under the low density being the highest yielding. On the other hand, one A line gave significantly lower (78%) yield per unit area than the check A and that was AG3 with the lowest CYP index either. Six out of the 10 B lines yielded higher than the check B, with two of them being significantly superior by 14 and 18%, including line BF3 that gave the highest CYP index under the low density. Even though four B lines yielded lower (89-99%) than the respective check B, none of them was significantly inferior.

Considering CYP values with the respective relative yields per unit area, the following inferences are drawn. The two parameters differentiated the two sets of entries to similar extent. With regard to set A, CYP values ranged from 84 to 138% and relative yields per unit area from 78-132%. As far as set of entries B is concerned, CYP values ranged from 91-124% and relative yields per unit area from 89-118%. In comparison with the check population A, the three of the four A lines that were found to be significantly superior in dense stand, having by 32% (AF4), 22% (AG4) and 18% (AF5) higher yield, had also the highest CYP values (by 38, 21 and 23%, respectively). Line AG3 with the lowest CYP value, that was by 16% lower than that of the check population, was found to be significantly inferior to the check population in dense stand (by 22%). Compared with the check population, lines AF1 and AF3 that had by 14 and 4% lower CYP values, respectively, gave also by 8 and 14% lower yield in dense stand. Discrepant was line AF2, which with 9% lower CYP value than the check A, gave significantly higher yield in dense stand. Consequently, line AF2 excepted, CYP values of entries A seem to be consistent with the respective yields in dense stand. Simple correlation coefficient between CYP and yield in dense stand was positive and significant ($R = 0.71$, $p < 0.03$), increasing to $R = 0.97$ ($p < 0.001$) if line AF2 was omitted. In case of entries B, lines BG4 and BF3, which outdid check B in CYP by 12 and 24%, yielded also by 18 and 14% higher in dense stand being significantly superior. Lines BG2 and BF4 also, which outdid check B in CYP by 22 and 23%, yielded by 8 and 5% higher in dense stand, respectively. On the contrary, line BF1 having of the highest CYP values, gave the lowest yield in dense stand. Considering also lines BG5 and BG3, it seems that consistence of CYP with yield in dense stand was not as clear as it was in set A. Nevertheless, if line BF1 was not included, simple correlation coefficient between CYP and yield in dense stand was computed to be $R = 0.66$ ($p < 0.04$).

Data of the study, particularly those of entries A, showed a relatively good fit between CYP predicted on the basis of single-plant yields at the low density representing absence of competition and yield per unit area obtained at the dense stand representing crop density conditions. Genotype by environment interaction is almost always present and thus discrepant behaviour of lines AF2 and BF1 might be partly attributed to different years of experimentation at low density and dense stand. Simultaneous evaluation of CYP and yield in dense stand perhaps might lead to better coincidence of them. However, considering entries A and B in overall, simple correlation coefficient between the two parameters was positive and significant ($R = 0.58$, $p < 0.006$), increasing to $R = 0.72$ ($p < 0.001$) if the

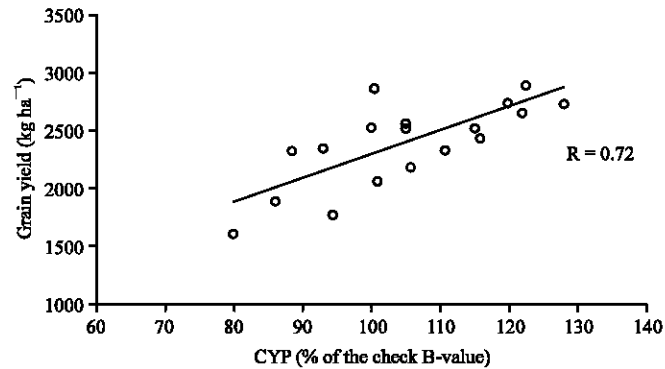


Fig. 1: Correlation between crop yield potential estimated on the basis of single-plant yields under low density (CYP) and grain yield per unit area obtained under dense stand

aforementioned discrepant lines AF2 and BF1 were omitted (Fig. 1). Consequently, results are supportive that crop yield potential could be sufficiently predicted on the basis of single-plant yields under the absence of competition and open the possibility that honeycomb selection and progeny evaluation could be applied across the entire generations of a breeding program. Given that, particularly in crops that strongly respond to density changes (i.e., density-dependent crops), optimum dense stand to measure crop yield potential may differ among different genotypes, the risk of biased judgment exists when genotypes are evaluated under a single dense stand, due to significant genotype by density interactions (Fasoula and Fasoula, 2000, 2002). Significant interactions between cultivars and densities for grain yield were reported in maize and wheat (Faris and De Pauw, 1981; Tollenaar, 1992; Lloveras *et al.*, 2004). Interference between plots in cultivar trials can distort yield and result in misleading conclusions from yield comparisons (Clarke *et al.*, 1998). So possibility to predict crop yield potential under the comparable conditions that absence of competition ensure, is of paramount importance for breeders and agronomists. Absence of competition allows maximum phenotypic expression and differentiation that facilitates identification of superior genotypes (Fasoula and Fasoula, 2000, 2002). Duggan *et al.* (2000) appraised small the differences in grain yield they found under dryland conditions among wheat genotypes with widely different yield potential. For breeding purposes, absence of competition also erases the adverse impact of negative relationship between yielding and competitive ability on selection effectiveness, by allowing genotypes potent to give the highest yield to express their capacity (Fasoula and Fasoula, 1997, 2000; Janick, 1999). On the other hand, selection for yield under interplant competition is counterproductive because the high competitors are selected instead of high yielders due to negative relationship between yielding and competitive ability (Fasoula and Fasoula, 1997; Janick, 1999). Furthermore, it is now well established that ability of genotypes to compete in a stress environment does not predict their performance in uniform stand (Janick, 1999). In case prospective studies in bean and other crops are supportive of the hypothesis, two possibilities are offered: beneficial utilization of honeycomb methodology of breeding in the absence of competition, thanks to the aforementioned advantages and avoidance of the risk of biased judgement of crop yield potential due to strong genotype by density interactions, particularly in density-dependent crops. Honeycomb methodology in the absence of competition has been found so far effective in breeding of various crops. For example to improve yield potential per plant and stability across densities in maize (*Zea mays* L.) when applied at the ultra-low density of 0.74 plants m⁻² (Tokatlidis *et al.*, 2001), to improve yield per unit area in snap bean at the density of 1.8 plants m⁻² (Traka *et al.*, 2000) and to develop at the ultra-low density of 0.59 plants m⁻² F₅-F₆ tomato (*Lycopersicon esculentum* L.) recombinant lines that out yielded their hybrid (Christakis and

Fasoulas, 2002). In case of rice (*Oryza sativa* L.) honeycomb selection at the density of 1.2 plants m⁻² was more effective than panicle-to-row selection at the density of 50-60 plants m⁻² to improve grain yield and quality and to extract lines that significantly over yielded their hybrid (Ntanos and Roupakias, 2001).

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