

ASSESSING COMBINING ABILITIES AND BREEDING VALUE OF DRY PEA GENOTYPES

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Abstract

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Aim of the research was to assess a breeding value of 6 parental genotypes of dry pea and their F₁ progeny produced in a diallel fashion. The traits enquired were plant height, count of nodes till the 1st podded node, mass of 1000 seeds and grain yield per plant. Parental breeding values were assessed by means of their GCA effects, whilst the F₁ crosses were assessed upon their exhibited *per-se* values.

All the results were discussed with respect to the breeding goals. There were distinguished the most promising parents and cross-combinations for the improved RILs derivation.

Key words: dry pea, breeding value, grain yield

Introduction

Considering the produced quantity, dry pea (*Pisum sativum* L.) ranks as a third grain legume worldwide, with production about 10 million tons at 6 million hectares in 2008 (FAOSTAT 2010). Approximately half of the world production is fed to livestock while the remaining portion is used for human food, primarily in developing countries (McPhee, 2003). Average grain yield worldwide is about 1690 kg/ha (FAOSTAT 2010). The lowest yields are in African countries, 400-600 kg/ha, and the highest yields are in the west European countries, with averages 3000 to 4700 kg/ha.

Along with economic importance of pea grain, there are certain beneficial environmental impacts of growing pea, including symbiotic nitrogen fixation (Marohnić, 2006) and improved crop rotation.

Grain yield variation in the world is a consequence of various environmental conditions such as climate (Cupic et al., 2008), soil (Duzdemir et al., 2003) and genetic yield potential of cultivars grown (Karnwal and Kushwaha, 2010), and G×E interactions (Duparque et al., 1995) as well. Modern cultivar improvement is based on creation of new genetic variability in desirable direction, and subsequent selection of improved genotypes. Desirable genetic variability is being achieved by

crossing divergent parents with high breeding values or particular resistance or quality trait carriers. The breeding value of parents is being assessed using various crossing designs, like diallel crossing (Griffing, 1956) and line×tester analysis (Sharma, 1998). Breeding values of F₁ cross-combinations were assessed considering their *per-se* value of a trait. Namely, according to many research results (Kearsey and Pooni, 1996), the high value of a trait in F₁ cross, at many crop species, is the consequence of accumulation of additive genetic effects, which previously were dispersed among parents, what was especially proven in the pea (Sarawat et al., 1993). So, the high breeding value of a cross was assigned to the crosses with desirable *per-se* value of a trait.

The object of our study was to determine GCA and SCA among these dry pea genotypes, consequently, to identify the breeding value of investigated dry pea genotypes.

Materials and Methods

These studies were conducted at Agricultural Institute Osijek, Croatia (45°34'N, 18°41'E), during 2007-09. The characteristics of these varieties are reported in Table 1. Six parental lines of pea, *Pisum sativum* L., were selected, based on their diverse origin and background for yield and other

agronomic important characteristics in 2006 and 2007, for a diallel cross-made in 2008. The ready-to-open flower buds were hand-emasculated and pollinated to produce all possible combinations of F₁ hybrids, but without the reciprocals. The F₁ seeds were picked at full physiological maturity. Six parental genotypes (Anno, Gold, Joel, Junior, PF-G1 and Shawnee) and their 15 cross-combinations were grown 2009 in a field trial in complete random block design with 3 replicates. Each genotype was seeded in a single row (0.8 m long) at each replicate, with 20 seeds per row. Inter-row distance was 0.2 m. Plots were surrounded with distinct experimental line with purple nodes and brown seeds, to avoid edge effects and to allow for easy distinguishing the experimental plants. Harvesting plants, measuring and recording of investigated traits were done in the state of full ripening.

The traits investigated were: plant height, count of nodes till the 1st podded node (nodes), mass of 1000 seeds (g, M₁₀₀₀) and grain yield per plant (g/plant, yield). Estimation of combining ability effects was done according to the Griffing's (1956) model I (genotypes and blocks as fixed-effects), experimental method 2 (parents and one set of F₁ combinations included). Breeding value of parental genotypes was assessed considering their general combining ability (GCA) effects. Namely, a parent with high GCA effect is characterized by its better breeding value since the GCA effects represent the additive nature of gene action (Sharma, 1998). Deviations of F₁ cross-combination means from the values based on the sum of diallel mean and specific combining ability (SCA) effects of each cross-combination present GCA effects of both parents (GCAP1 and GCAP2). Statistical analyses were calculated with the statistical program MSTAT-C version 2.10.

Results and Discussion

A satisfactory divergence of parents used in the research was achieved since they differed in origin and significant-

ly differed in almost all the enquired traits, except the grain yield per plant (Table 1). The range of parent's means of investigated traits was similar to, or broader than in the researches of Ceyhan et al. (2008), Ceyhan and Avci (2005) and Bourion et al. (2002). A greater range of parent's M₁₀₀₀ was used in Lejeune-Henaut et al. (1992) and higher parent's grain yields per plant were achieved in Ceyhan et al. (2008), and Lejeune-Henaut et al. (1992) researches, probably due to wider plant spacing.

Significant positive and negative GCA effects (Table 2) were observed for almost all the traits, except for grain yield per plant. Junior was the most plant height-enlarging parent, nodes to 1st pod increasing, and M₁₀₀₀ and yield decreasing parent. Gold was the most plant height decreasing and M₁₀₀₀ increasing parent. Joel was the most nodes to 1st pod decreasing and yield increasing parent.

Considering the each investigated trait, SCA effects were found significant (Table 3), showing that particular cross-combinations performed differently from expectation based on the sum of diallel mean and GCA effects of both parents.

Assessment of the GCA and SCA effects and *per-se* values of cross-combinations, whether desirable or not, has to be done according to the breeding objectives. Regarding the plant height in dry pea, it is not generally defined what the most desirable range of values is. In North Dakota (which is the largest producer of pulse crops in the USA), prevailing plant height is in the range of 73 to 118 cm (Kandel and Endres, 2010), but in Croatia, there are prevailing lower cultivars, tall about 50 cm in full ripening. The higher grain yields are usually associated with the higher plant height (Dahiya et al., 1977; Espósito et al., 2009), since it allows for a higher number of podded nodes, what is considered as an important yield contributor (Bourion et al., 2002). Conversely, excessive plant height could be associated with greater lodging and loss of grain yield and quality. According to the breeder's experience at the Faculty of Agriculture in Osijek (prof. dr.

Table 1
Mean parental agronomics values, country of origin, leaf type and seed color

Parent	Height, cm	Nodes numbers	M ₁₀₀₀ , g	Yield, g	Country of origin	Leaf type	Seed color
Anno	44.3	13.95	202.6	3.34	Denmark	Afila	Yellow
Gold	35.1	11.80	243.3	3.77	Croatia	Afila	Yellow
Joel	73.5	11.75	214.6	3.72	USA	Wild	Green
Junior	90.1	18.91	144.3	3.77	Serbia	Wild	Yellow-black
PF-G1	46.6	12.96	239.3	3.98	Croatia	Wild	Yellow
Shawnee	65.9	10.68	200.6	4.08	USA	Wild	Yellow
LSD _{0,05}	6.5	1.59	30.16	1.07			
LSD _{0,01}	8.6	2.13	40.32	1.43			

Mirko Stjepanović, unpublished data, personal communication), the optimum plant height should be in range of 60 to 80 cm (with respect to the environmental conditions what can affect the plant height), so the promising cross-combinations should include at least one parent with progeny mean falling into the desired range (Shawnee, Joel, Junior). Number of nodes till the 1st podded node is an important morphological

trait, associated with earliness of onset of flowering. According to Bourion et al. (2002.), the more nodes till the 1st flowering node (which is usually the same as the 1st pod node), the longer will be the period till onset of flowering. Since the breeding objective is to avoid the coincidence of a pea flowering with a very frequent drought conditions during the late spring in mediterranean and continental types of cli-

Table 2
Offspring means and GCA effects (g_i) of investigated parents, and diallel mean (u)

Trait/ Parental	Height, cm		Nodes, n		M ₁₀₀₀ , g		Yield, g	
	mean	g _i	mean	g _i	mean	g _i	mean	g _i
Anno	55.8	-7.2**	12.90	0.03 ^{ns}	217.2	-1.5 ^{ns}	3.88	-0,08 ^{ns}
Gold	53.3	-10.2**	12.79	-0.33 ^{ns}	237.2	18.7**	4.01	0,07 ^{ns}
Joel	71.9	8.6**	11.84	-1.05**	232.5	11.5 *	4.16	0,18 ^{ns}
Junior	74.9	12.9**	15.87	2.87**	185.8	-32.3**	3.73	-0,14 ^{ns}
PF-G1	57.0	-6.0**	12.01	-0.77**	224.2	8.4 ^{ns}	3.80	-0,06 ^{ns}
Shawnee	64.3	1.9 *	12.41	-0.75**	213.1	-4.8 ^{ns}	3.88	0,02 ^{ns}
u =	62.3		13.02		216.8		3.89	
CD(g _i -g _j) _{0,05} =		2.9		0.72		13.6		0.48
CD(g _i -g _j) _{0,01} =		4.6		1.12		21.3		0.76

* - significant deviation from „u“ at P<0.05; ** - significant deviation from „u“ at P<0.01; ^{ns} - not significant deviation from „u“

Table 3
Means and SCA effects (s_{ij}) of F₁ cross-combinations

Trait	Height, cm		Nodes, n		M ₁₀₀₀ , g		Yield, g	
	mean	s _{ij}	mean	s _{ij}	mean	s _{ij}	mean	s _{ij}
Anno×Gold	35.2	-9.8**	10.31	-2.41**	229.6	-4.3 ^{ns}	3.42	-0,46 ^{ns}
Anno×Joel	80.4	16.7**	12.47	0.47 ^{ns}	259.7	32.9**	5.62	1,62**
Anno×Junior	71.3	3.3 ^{ns}	14.36	-1.56**	198.4	15.4 ^{ns}	3.12	-0,56 ^{ns}
Anno×PF-G1	40.7	-8.5**	13.88	1.60**	214.1	-9.5 ^{ns}	3.08	-0,67 ^{ns}
Anno×Shawnee	62.7	5.6 *	12.44	0.15 ^{ns}	198.4	-12.1 ^{ns}	4.69	0,87 *
Gold×Joel	69.5	8.8**	11.46	-0.18 ^{ns}	259.5	12.5 ^{ns}	4.19	0,04 ^{ns}
Gold×Junior	79.9	14.9**	17.75	2.19**	196.3	-6.9 ^{ns}	4.42	0,59 ^{ns}
Gold×PF-G1	38.4	-7.7**	12.69	0.76 ^{ns}	242.0	-1.8 ^{ns}	4.29	0,38 ^{ns}
Gold×Shawnee	61.5	7.5**	12.72	0.78 ^{ns}	252.6	22.0 *	3.97	-0,01 ^{ns}
Joel×Junior	66.6	-17.2**	13.53	-1.32 *	207.5	11.4 ^{ns}	3.73	-0,21 ^{ns}
Joel×PF-G1	76.3	11.4**	10.03	-1.18 *	239.1	2.5 ^{ns}	4.00	-0,02 ^{ns}
Joel×Shawnee	65.0	-7.8**	11.78	0.55 ^{ns}	214.6	-8.9 ^{ns}	3.70	-0,39 ^{ns}
Junior×PF-G1	75.3	6.1**	13.14	-1.98**	183.4	-9.5 ^{ns}	3.97	0,27 ^{ns}
Junior×Shawnee	66.1	-11.0**	17.50	2.36**	185.0	5.3 ^{ns}	3.35	-0,42 ^{ns}
PF-G1×Shawne	64.7	6.4**	9.35	-2.15**	227.1	6.8 ^{ns}	3.48	-0,37 ^{ns}
CD(s _{ij} -s _{ik}) _{0,05} =		6.4		1.57		29.8		1.06
CD(s _{ij} -s _{ik}) _{0,01} =		8.8		2.18		41.3		1.46
CD(s _{ij} -s _{kl}) _{0,05} =		5.9		1.46		27.6		0.98
CD(s _{ij} -s _{kl}) _{0,01} =		8.2		2.02		38.2		1.35

* - significant deviation from u+GCA_{p1}+GCA_{p2} at P<0,05; ** - significant deviation from u+GCA_{p1}+GCA_{p2} at P<0,01; ^{ns} - not significant deviation from u+GCA_{p1}+GCA_{p2}

mate, found in Croatia as well, breeding should be directed to the earlier flowering (what is called as the approach of stress avoidance (Araus et al., 2002). This is achievable through the breeding for smaller number of nodes till the 1st pod. According to this, a smaller GCA effect of a parent is characterized by its more desirable breeding value (Joel, PF-G1, Shawnee), as well as a smaller *per-se* value of a particular F₁ cross-combination (PF-G1×Shawnee, Joel×PF.G1). Increasing a seed size and its weight is, reasonably, the aim of dry pea breeding processes, since it is associated with higher grain yields (Dahiya et al., 1977; Gan and Liu, 2005), so among the desirable parents certainly are the Gold and Joel, and among the crosses are Anno×Joel, Gold×Joel and Gold×Shawnee. However, a breeder should bear on mind that overmuch increase of a seed size could be associated with compensation effects with the rest of yield components (Timmerman-Vaughan et al., 2005), or even with detrimental effects on yield. GCA effects for a grain yield per plant were not found significant, but the highest values belonged to the parents Joel, Gold and Shawnee. Among the cross-combinations, the highest values were found in the crosses Anno×Joel, Anno×Shawnee, Gold×Junior, Gold×PF-G1 and Gold×Joel. These are considered the most promising combinations for derivation of improved recombinant inbred lines since they combine parents with desirable GCA performance for almost all the enquired traits, which is in agreement with the results obtained by other authors (Singh et al., 1985; Kosev et al., 2012). The high *per-se* values of grain yield in these F₁ cross combinations provide a good potential for transgressive segregation in the future recombinant inbred lines (RILs), since their value is likely to be the consequence of an additive genetic effects accumulation, that previously were dispersed among parents (Sarawat et al., 1993; Kearsley and Pooni, 1996). A performance of future RILs will be reported upon their derivation and investigation.

Conclusions

Parental genotypes used in the research satisfactory covered the range of values of the traits of interest. They exhibited the desirable GCA performance and allowed for the appearance of particularly promising cross-combinations. For the plant height improvement, parents Shawnee, Joel and Junior were assessed to have a desirable breeding value, based on their average progeny performance, falling into the range 60 to 80 cm. For the number of nodes till the 1st podded node, parents Joel, PF-G1 and Shawnee, and their cross-combinations were found to be the most desirable, since they decreased the trait values, allowing for the earlier flowering onset and consequent avoidance of frequent late-spring

drought in Croatian conditions. Parents Gold and Joel, and their cross-combinations were found to desirably increase the seed weight, up to *per-se* value of 260 g/1000 grain in F₁ generation. Anno×Joel cross-combination exhibited the highest grain yield per plant, 5.62 g in average, in a dense stand. Therefore, this cross was assessed to be the most promising, what is explained by the assumption that its value is likely to be the consequence of accumulation of additive genetic effects, what is in line with previous genetic research in pea. A performance of future RILs will be reported upon their derivation and investigation.

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