UDC 575.633
https://doi.org/10.2298/GENSR23010203A
Original scientific article

ESTIMATION OF HETEROSIS, HETEROBELTIOSIS, AND GENE ACTION IN F1 PLANTS FROM SMALL-SEEDED SOYBEAN CROSSES

M. Muchlish ADIE[1]*, Arifin ARIFIN[2], Suyamto SUYAMTO[1], Ayda KRISNAWATI[1]

[1]Research Center for Food Crops, Research Organization for Agriculture and Food, National Research and Innovation Agency (BRIN), Indonesia
[2]Indonesian Legume Instrument Standard Testing, Indonesia

Adie M. M., A. Arifin, S. Suyamto, A. Krisnawati (2023). *Estimation of heterosis, heterobeltiosis, and gene action in F1 plants from small-seeded soybean crosses*. - Genetika, Vol 55, No.1, 203-215.

Soybeans with small seed sizes and high seed yield potential are crucial for addressing the needs of soybean-based industries. The objectives of the study were to investigate the maternal effect and quantify the value of heterosis, heterobeltiosis, and gene action in F1 plants from soybean crosses with small-seeded. In the present investigation, the experiment was conducted in the screen house of the Indonesian Legume and Tubers Crop Research Institute (ILETRI) located in Malang (East Java, Indonesia) from March to July 2021. The F1 plants were derived from crosses of Lokal Jember × Tidar, Tidar × Gepak Kuning, Gepak Kuning × Detam 3, and their reciprocals. The parental genotypes and F1 plants were all planted. The observed data were plant height, number of branches, number of nodes, number of filled pods, the weight of 10 seeds, and seed yield/plant. The performance of the F1 plants showed variation for all observed traits, which is mostly averaged between the two parents, including 10 seed weight and seed yield. There was no maternal effect for almost all agronomic traits on all crosses and their reciprocals, except for the number of nodes in the cross of Gepak Kuning × Detam 3. Heterosis (hMP) and

---

Corresponding author: M. Muchlish Adie, Research Center for Food Crops, Research Organization for Agriculture and Food, National Research and Innovation Agency (BRIN), Indonesia mm_adie@yahoo.com, +6281333220026

heterobeltiosis (hHP) of F1 derived from six cross combinations for seven agronomic traits ranged from -25.93 to 186.27 and -94.83 to 114.71, respectively. Based on the potence ratio, the gene action was differed from a cross to cross for seed yield and its components. The degree of dominance for seed size and seed yield varied from overdominance, incomplete dominance, and complete dominance. Thus, based on the present investigation, it is possible to develop soybean varieties with small seed sizes and high yield by using pedigree selection on F2.

Keywords: Agronomic character, degree of dominance, maternal effect, reciprocal crosses, yield

INTRODUCTION

Soybean is a legume with a variety of nutritional properties that is could be processed into a variety of food ingredients. Soybean seeds have different sizes classifications around the world. In Indonesia, a small seed size is defined as the weight of 100 seeds weighing less than 10 g (KRISNAWATI and ADIE, 2015). The small seed size is commonly used as raw material for soybean sprouts (GHANI *et al.,* 2016; SHURTLEFF and AOYAGI, 2021).

Seed size in soybean is an inherited trait controlled by multiple genes and influenced by environmental factors (KUMAWAT and XU, 2021; HINA *et al.,* 2020). A study by HU *et al.* (2013) revealed that seed size may be controlled by different genetic factors. The estimation of heritability for seed size in soybean was reported from medium to high (XU *et al.,* 2011; SULISTYO *et al.,* 2021). A study by NAYANA and FAKRUDIN (2020) found a high heritability coupled with high genetic advance as per cent mean for seed size in soybean. This data indicates that creating small seed-sized soybean cultivars has a high probability of success.

Seed size is one important factor influencing soybean yield. Breeding for soybean varieties with small seed sizes and high seed yields is possible to depend on the availability of the appropriate gene sources or parents as well as selection methods for segregated populations, and also the understanding of the fundamental biological and genetic architecture (ACQUAAH, 2009; TURNER-HISSONG *et al.,* 2020). Various genetic parameters on the determination of parents and the prediction of F1 plants from crosses between parents have been studied by researchers on a variety of plants (SAKILA and PANDIYAN, 2018; SURIN *et al.,* 2018; RAHANA *et al.,* 2021).

Soybean varieties with small seeds must be combined with high seed-yielding characteristics. As a result, the characteristics of the parents, as well as genetic studies of the progeny of the crosses, must be investigated further. Information on heterosis can serve as a foundation for the exploitation of valuable cross combinations in breeding programs, especially for seed size traits. A study in soybean by YAMGAR *et al.* (2021) found the cross of JS335 × SDP 30 exhibited the highest mid and better parent heterosis for 100 seed weight in F1, F2, and F3. Another study reported positive mid and better parent heterosis in soybean F1 of Devon × Dering for 100 seed weight (SULASTRI *et al.,* 2020). A study by SEN (2020) found the parental soybean variety L75-6648(P4) was a good combiner not only for earliness and plant height but also for 100-seed weight traits. Breeding for improved variety with small-seeded also carried out in other plants (TRUSTINAH *et al.*, 2021; SENBETAY and TESFAYE, 2015; KARAMI and TALEBI, 2013).

Individual plant phenotypes can be influenced not only by genotype and environment but also by maternal effects. Maternal effects occur in plants when the maternal parent contributes to the phenotype of its offspring in addition to the equal chromosomal contribution from each parent (GILSINGER *et al.,* 2010). Soybean seed traits may be simultaneously controlled by nuclear genes, cytoplasm genes, and maternal nuclear genes (LI *et al.,* 2006). A study by RIX *et al*. (2012) found that both paternal and maternal effects affected the germination response, but the maternal parent had a stronger influence on the response to high-temperature stress than the paternal parent. NING *et al.* (2005) found that the matured soybean seed size was controlled by embryo, cytoplasm, and maternal effects simultaneously. A study in the investigation of soybean seed size traits in ten cross combinations showed five of them having no maternal effects (ISNAINI *et al.,* 2020).

In addition to the maternal effect, it is critical to investigate the gene action, particularly on F1 plants in comparison to the parents. Differences in gene action are likely to occur not just as a result of a difference in commodities, but also as a result of differences in a line's parental materials. The objectives of the study were to investigate the maternal effect and quantify the value of heterosis, heterobeltiosis, and gene action in F1 plants from soybean crosses with small-seeded.

MATERIALS AND METHODS

The research material comprised of F1 plants obtained from three cross combinations that were carried out reciprocally thus resulting in six cross combinations in total. The crosses were conducted in the screen house (made of galvanized iron pipes covered with 50 mesh size net) of the Indonesian Legume and Tubers Crop Research Institute (ILETRI) located in Malang (East Java, Indonesia) from March to July 2021. The F1 seeds were planted in ILETRI from September to December 2021 to produce F1 plants. The parent lines used to make these crosses were small-seeded soybean (Lokal Jember and Gepak Kuning) and small-seeded with high yield varieties (Tidar and Detam 3). The reciprocal crosses were Lokal Jember × Tidar, Tidar × Lokal Jember, Tidar × Gepak Kuning, Gepak Kuning ×Tidar, Gepak Kuning × Detam 3, and Detam 3 × Gepak Kuning. All the parental genotypes and the 558 F1 plants were planted.

The F1 seeds and their parents were planted in a plastic pot (Φ =18 cm) filled with soil and organic fertilizer (1:1). The NPK fertilizer dose was 2.0 g/pot, and it was applied at the time of showing. Plant maintenance (weeding, watering, pests, and diseases management) was performed optimally. Observations on all quantitative traits were made when the plants reached maturity (R8), and some were made after seed processing. Plant height, number of branches, number of nodes, number of filled pods, and number of empty pods were measured at maturity. The weight of 100 seeds and seed yield per plant was measured after seed processing.

All the data collected were subjected to descriptive statistics using Minitab® 17.1.0 (MINITAB, 2013). Heterosis was determined in the form of heterosis (mid-parent heterosis) and heterobeltiosis (high-parent heterosis) as proposed by FEHR (1987) and HAN *et al.* (2018).

Heterosis (%) = $\frac{F_1 - MPV}{MPV} x\ 100$

Heterobeltiosis (%) = $\frac{F_1 - BPV}{BPV} x\ 100$

The potency ratio (P) is used to determine the degree of dominance and its direction for various gene effects (PETR and FREY, 1966):

Potence Ratio *(P)* = $\frac{F_1 - MPV}{BPV - MPV}$

Where:
$\bar{F}_1$ = mean value of F1 hybrids
MPV = mid-parent value (the average performance of the two parents)
$BPV = \bar{F}_1$ better parent value (the highest performance of the parents)

The degree of dominance is classified based on the value of the potence ratio (PETR and FREY, 1966; IBRAHIM *et al.,* 2021). The positive and negative signs indicate the direction of the dominance of either parent.

$P = 0$, there is no dominance (additive)
$P = \pm 1$ = (negative or positive) complete dominance
$-1 > P > +1$ = partial dominance
$P > \pm 1$ = (negative or positive) overdominance

To determine the maternal effect, all the quantitative data were subjected to the unpaired t-test using Minitab® 17.1.0 (MINITAB, 2013). The non-significant differences between the unpaired t-test of F1 populations and the reciprocal crosses demonstrate the absence of the maternal effect, meanwhile, the significance difference implies the existence of the maternal effect (BADIARAJA *et al.,* 2020).

RESULTS AND DISCUSSION

Agronomic performance

The performance of the F1 plants derived from crossing showed variation for traits of plant height, number of branches, number of nodes, number of filled pods, 100 seed weight, and seed yield/plant (Table 1). The F1 plants from the Lokal Jember × Tidar had a lower average of agronomic performance than the two parents. However, the 100 seed weight was close to that of the female parent (Lokal Jember). Meanwhile, the reciprocal F1 plants (Tidar × Lokal Jember) had higher agronomic performance, except for seed yield which was between the two parents. The 100 seed weight was also close to that of the female parent (Lokal Jember). As a result, there was a low chance that this cross will produce a line with small seeds.

The F1 performance for all traits (including the seed size and yield) in the cross between Tidar × Gepak Kuning and its reciprocals were averaged between the two parents, except for the plant height which is higher than the two parents. Furthermore, the performance of F1 plants produced from Gepak Kuning × Detam 3 and its reciprocals are averaged between the two parents, except for plant height, which is higher than the two parents, and the seed yield of the Detam 3 × Gepak Kuning which was lower than the parents. Accordingly, the chance of getting lines with small seed size and high seed yield was greater in these cross combinations and their reciprocals (Tidar × Gepak Kuning, Gepak Kuning × Tidar, Gepak Kuning × Detam 3, Detam 3 × Gepak Kuning) than in the cross between Lokal Jember × Tidar and its reciprocals.

Table 1.The agronomic performance of F1 plants and their parental genotypes

Cross Combination	DS	Agronomic traits					
		PHG	NOB	NON	NFP	SWG	YLD
Parental:							
Lokal Jember	Mean	66.50	6.00	25.00	57.00	8.10	9.72
Tidar	Mean	47.00	4.00	28.00	83.00	6.10	16.04
Gepak Kuning	Mean	63.00	5.50	17.50	49.50	9.55	10.72
Detam 3	Mean	55.00	3.50	13.50	39.50	12.10	9.24
F1:							
Lokal Jember ×Tidar	Mean	68.67	6.25	32.25	83.25	8.10	14.49
	Min	50.00	5.00	26.00	62.00	6.90	9.73
	Max	82.00	7.00	42.00	99.00	10.00	22.20
	Std	9.04	0.60	5.15	13.57	0.85	3.89
Tidar × Lokal Jember	Mean	69.06	6.18	30.76	87.47	8.55	14.74
	Min	54.00	0.00	7.00	17.00	6.80	4.82
	Max	84.00	14.00	46.00	133.00	10.10	25.02
	Std	9.72	2.81	10.74	33.27	1.02	6.30
Tidar × Gepak Kuning	Mean	66.31	5.17	23.33	67.61	8.74	13.11
	Min	40.00	4.00	11.00	35.00	6.00	5.20
	Max	91.00	7.00	34.00	110.00	11.70	21.70
	Std	13.62	0.87	5.80	17.69	1.17	3.82
Gepak Kuning × Tidar	Mean	72.72	5.44	23.39	71.56	8.49	13.01
	Min	39.00	4.00	14.00	40.00	7.00	6.11
	Max	89.00	7.00	36.00	118.00	9.70	24.70
	Std	14.01	1.12	6.39	22.32	0.74	4.50
Gepak Kuning × Detam 3	Mean	63.31	5.06	19.31	43.56	10.59	9.67
	Min	43.00	3.00	13.00	31.00	9.60	7.29
	Max	76.00	6.00	24.00	55.00	11.80	16.42
	Std	8.48	0.97	3.58	7.00	0.56	2.24
Detam 3 × Gepak Kuning	Mean	65.75	4.50	15.88	40.00	11.78	8.68
	Min	61.00	2.00	10.00	27.00	9.60	6.08
	Max	71.00	6.00	20.00	50.00	19.00	10.41
	Std	18.07	1.68	5.50	13.22	5.04	3.44

DS = descriptive statistic, Min = minimal value, Max = maximum value, Std = standard deviation, PHG = plant height (cm), NOB = number of branches, NON = number of nodes, NFP = number of filled pods, SWG = 100 seeds weight (g), YLD = seed yield/plant (g)

Maternal effect

Maternal effect is a concept used to describe the influence of parental on their offspring. The maternal effects of three crossings on F1 plants and their reciprocals for agronomic traits in soybeans were presented in Table 2.

Table 2. Maternal effect of the agronomic traits of six cross combinations in soybean

Agronomic character	Mean (P1×P2 vs P2×P1)		
	Lokal Jember × Tidar	Tidar × Gepak Kuning	Gepak Kuning × Detam 3
Plant height (cm)	68.67 vs 69.06^{ns}	66.31 vs 72.72^{ns}	63.31 vs 65.75^{ns}
Number of branches	6.25 vs 6.18^{ns}	5.17 vs 5.44^{ns}	5.06 vs 4.50^{ns}
Number of nodes	32.25 vs 30.76^{ns}	23.33 vs 23.39^{ns}	19.31 vs 15.88*
Number of filled pods	83.25 vs 87.47^{ns}	67.61 vs 71.56^{ns}	43.56 vs 40.00^{ns}
10 seed weight (g)	8.10 vs 8.55^{ns}	8.74 vs 8.49^{ns}	10.59 vs 11.78^{ns}
Seed yield/plant (g)	14.49 vs 14.74^{ns}	13.11 vs 13.01^{ns}	9.67 vs 8.68^{ns}

ns = not significant and * = significant at the t-test 5%

The non-significant differences were found for almost all agronomic traits on all crosses and their reciprocals, except for the number of nodes in the cross of Gepak Kuning × Detam 3. However, similar to the results of this study, other studies also reported no maternal effect on the number of branches (ISNAINI *et al.,* 2020; BADIARAJA *et al.,* 2021). The lack of a significant difference indicated the absence of maternal effects, implying that those traits were most likely regulated by a combination of genes from both male and female parents (GILSINGER *et al.,* 2010).

In this study, maternal effect influenced the characteristics of the number of empty pods and the number of nodes in some crosses but not in others. This difference could be attributed to differences in the varieties of genotypes used in the study (BADIARAJA *et al.,* 2021). A maternal effect on the number of nodes, and other agronomic traits (plant height, number of filled pods, seed weight per plant, and 100-seed weight) was also reported in another study which caused the cluster structure to differ between cross and its reciprocal (BADIARAJA *et al.,* 2021). Meanwhile, another study reported that cytoplasmic effects controlled the inheritance of 100-seed weight, seed length, length/width, length/thickness, and width/thickness, whereas maternal effects influenced the inheritance of seed width and thickness (LIANG *et al.,* 2005). A maternal effect on seed size-related features was also observed by GE *et al.* (2016).

The agronomic traits in this study were not affected by maternal effect. Thus, the implication was that all of the parental genotypes used in this study could be used as female or male parents to develop a line with small seed size and a high seed yield.

Heterosis (hMP) and heterobeltiosis (hHP)

Heterosis values (hMP) of F1 derived from six cross combinations ranged from -25.93 to 186.27 for seven agronomic traits (Table 3). All agronomic traits were observed to have positive hMP values in F1 derived from a cross between Gepak Kuning × Tidar and their reciprocals.

Meanwhile, the Tidar × Gepak Kuning cross and its reciprocals had positive hMP values for agronomic traits, except for seed yield. In the cross between Gepak Kuning × Detam 3 and its reciprocals, the positive hMP values were found for almost all yield components, except for the number of filled pods and seed yield.

Table 3. Heterosis (hMP) value of agronomic traits in F1 soybean

Cross Combination	Heterosis (%) for agronomic traits					
	PHG	NOB	NON	NFP	SWG	YLD
Lokal Jember × Tidar	21.00	25.00	21.70	18.93	14.08	12.49
Tidar × Lokal Jember	21.69	23.53	16.09	24.96	20.46	14.45
Tidar × Gepak Kuning	20.56	8.77	2.56	2.05	11.64	-2.00
Gepak Kuning × Tidar	32.22	14.62	2.81	8.01	8.56	-2.75
Gepak Kuning × Detam 3	7.31	12.50	24.60	-2.11	-2.19	-3.02
Detam 3 × Gepak Kuning	11.44	0.00	2.42	-10.11	8.78	-12.98

PHG = plant height (cm), NOB = number of branches, NON = number of nodes, NFP = number of filled pods, SWG = 100 seeds weight (g), YLD = seed yield/plant (g)

High yield is a desirable trait for any crop. In this study, the highest hMP for seed yield was for the cross of Tidar × Lokal Jember (14.45%) and its reciprocal (12.49%). Another study found the highest hMP for seed yield per plant in soybean reached 77.35% (MARANNA *et al.*, 2019). The yield components with high value were also shown by the cross of Tidar × Lokal Jember and its reciprocal, but not in other crosses. According to PUNEWAR *et al.* (2017), a high degree of heterosis for seed yield could be attributed to heterosis for these yield component traits. Further study suggested that even a small magnitude of hybrid vigor in individual yield components may have a synergistic effect on the end product (SHIVANI *et al.*, 2011).

Table 4. Heterobeltiosis (hHP) valu eof agronomic traits in F1 soybean

Cross Combination	Heterobeltiosis (%) for agronomic character					
	PHG	NOB	NON	NFP	SWG	YLD
Lokal Jember × Tidar	3.26	4.17	15.18	0.30	0.00	-9.67
Tidar × Lokal Jember	3.85	2.94	9.87	5.39	5.59	-8.09
Tidar × Gepak Kuning	5.25	-94.83	-16.67	-18.54	-8.52	-18.27
Gepak Kuning × Tidar	15.43	-1.01	-16.47	-13.79	-11.05	-18.89
Gepak Kuning × Detam 3	0.50	-7.95	10.36	-11.99	-12.50	-9.72
Detam 3 × Gepak Kuning	4.37	-18.18	-9.29	-19.19	-2.69	-18.99

PHG = plant height (cm), NOB = number of branches, NON = number of nodes, NFP = number of filled pods, SWG = 100 seeds weight (g), YLD = seed yield/plant (g)

Heterobeltiosis values (hHP) of F1 derived from six cross combinations ranged from -94.83 to 114.71 (Table 4). The F1 plants from the cross of Tidar × Lokal Jember and its reciprocal showed positive hHP values for all the yield components, but a negative value of hHP for seed yield per plant. It showed that the average seed yield of F1 is lower than the best parent. The negative hHP for seed yield was also found in other crosses. The cross of Tidar × Gepak Kuning and its reciprocal had a negative hHP value, except for the plant height. Almost all of the traits in the cross of Gepak Kuning × Detam 3 and its reciprocals are negative, except for plant height and the number of empty pods, which are positive. Other studies have also reported on the differential expression of heterosis in agronomic traits of soybean (PEREZ *et al.,* 2009; SEN, 2020; YAMGAR *et al.,* 2021). High heterosis in some crosses and low heterosis in others revealed that the nature of gene action varied depending on the genetic makeup of the parents involved in the cross (SHIVANI *et al.,* 2011). According to PEREZ *et al*. (2009), heterosis exists in soybean [*Glycine max* (L.) Merr.], and soybean hybrid technology is possible if appropriate parent combinations and a cost-effective method of producing hybrid seed are identified.

The degree of dominance

The degree of dominance of the seven agronomic traits in F1 plants varied among cross combinations, including its reciprocals (Table 5). The F1 derived from a cross of Lokal Jember × Tidar showed four agronomic traits with positive overdominant gene action type, the number of empty pods and seed yield with incomplete positive dominant gene action type, and 10 seed weight with complete positive dominant gene action type. Positive complete dominance consistently controlled the reciprocal cross for the 10 seed weight, while positive overdominance controlled the seed yield character.

Table 5. The degree of dominance of agronomic traits of F1 plants

Cross Combination	The degree of dominance of agronomic traits					
	PHG	NOB	NON	NFP	SWG	YLD
Lokal Jember ×Tidar	1.22	1.25	3.83	1.02	1.00	0.51
	ODP	ODP	ODP	ODP	PDF	PDUF
Tidar × Lokal Jember	9.75	1.00	1.50	13.00	1.00	3.16
	ODP	PDF	ODP	ODP	PDF	ODP
Tidar × Gepak Kuning	8.00	0.75	5.25	16.75	1.73	2.66
	ODP	PDUF	ODP	ODP	ODP	ODP
Gepak Kuning × Tidar	2.22	0.93	0.12	0.32	0.39	-0.14
	ODP	PDUF	PDUF	PDUF	PDUF	NDUF
Gepak Kuning × Detam 3	1.08	0.56	1.91	-0.19	-0.02	-0.41
	ODP	PDUF	ODP	NDUF	NDUF	NDUF
Detam 3 × Gepak Kuning	1.69	0.00	0.19	-0.90	0.75	-1.75
	ODP	ADT	PDUF	NDUF	PDUF	NDUF

ADT = additive, PDF or NDF = positive or negative complete dominance, PDUF = positive incomplete dominance, NDUF = negative incomplete dominance, ODP or ODN = positive overdominance or negative overdominance, PHG = plant height (cm), NOB = number of branches, NON = number of nodes, NFP = number of filled pods, SWG = 100 seeds weight (g), YLD = seed yield/plant (g)

The cross Tidar × Gepak Kuning exhibited the positive overdominance type of gene action for the character of 10 seed weight as well as for the seed yield, but the reciprocal indicated the presence of the incomplete dominance gene action. Most of the agronomic traits in the cross of Gepak Kuning × Tidar exhibited incomplete dominance gene action. In the cross of Gepak Kuning × Detam 3 and its reciprocals, the incomplete dominance gene action was observed for the character of the number of filled pods, 10 seed weight, and seed yield. Another study found the additive and dominance gene effects controlled the yield and yield components in soybean (PANDINI *et al.,* 2002; ADSUL *et al.,* 2016; OTUSANYA *et al.,* 2020). The additive gene action was also reported for the days to 50% flowering, days to maturity, the number of pods/plant, and 100-seed weight in soybean (UMAR *et al.*,2017). In other crops, such as chickpea, both additive and dominance genetic effects were significant for days to flowering, days to maturity, biomass, 100-seed weight, harvest index, number of pods, seeds, and seed yield per plant (KARAMI and TALEBI, 2013). Meanwhile, in rice, plant height, panicle length, seed set, grain yield, dry matter production, and 1000-grain weight were mainly regulated by dominance variance (SHAHID *et al.*, 2012).

In the present study, the gene action was differed from a cross to cross for seed yield and its components. According to DAS *et al.* (2014), the difference in the gene action for each character was determined by the parental genotypes of the cross. Furthemore, GIOI *et al.* (2017) proposed that the nature of gene action and the direction of expression are important factors in the design of introgression and hybrid breeding programs. Hence, to increase the chances of a successful soybean varietal breeding program, it is important to understand the various genetic parameters such as the relationship between F1 and its parental genotypes, the position of the parents as female or male donors, and the gene action.

CONCLUSIONS

The genetic background of the parental genotypes determines the success of developing small-seeded soybean with a high seed yield. Crosses of Lokal Jember × Tidar, Tidar × Gepak Kuning, Gepak Kuning × Detam 3 and their reciprocals show no maternal effect, notably for seed weight and seed yield. The heterosis and heterobeltiosis, as well as gene action, were observed to differ between crosses and agronomic characteristics. It is possible to develop soybean varieties with small seed sizes and high yield by using pedigree selection on F2.

ACKNOWLEDGEMENTS

The authors would like to express sincere thanks to Indonesian Agency for Agricultural Research and Development (IAARD), Ministry of Agriculture, Republic of Indonesia, for the financial support.

Received, January 29th, 2022.
Accepted December 28th, 2022.

REFERENCE

ACQUAAH, G. (2009): Principles of Plant Genetics and Breeding. John Wiley & Sons.

ADSUL, A.T., V.P., CHIMOTE, M.P., DESHMUKH, D.S., THAKARE (2016): Genetic analysis of yield and its components in soybean. SABRAO J. Breed. Genet., *48*: 247-257.

BADIARAJA, P.H., S., ZUBAIDAH, H., KUSWANTORO (2021): Maternal effect of agronomic and morphological traits on cluster structure of F3 soybean lines. Biodiversitas, *22*: 969-982.

DAS, T.S., S.V., DURWAS, S., DUTTA, A., CHATTOPADHYAY, B., SINGH (2014): Gene action and combining ability for yield and yield component traits in Dolichos bean (*Dolichos lablab*var. typicus). SABRAO J. Breed. Genet., *46*:293-304.

FEHR, W.R. (1987): Principles of Cultivar Development. Vol.1 Theory and Technique. Macmillan, New York.

GE, L., J., YU, H., WANG, D., LUTH, G., BAI, K., WANG, R., CHEN (2016): Increasing seed size and quality by manipulating BIG SEEDS1 in legume species. Proc. Natl. Acad. Sci. USA, *113*:12414-12419.

GHANI, M., K.P., KULKARNI, J.T., SONG, J.G., SHANNON, J.D., LEE (2016): Soybean sprouts: A review of nutrient composition, health benefits and genetic variation. Plant Breed. Biotechnol., *4*: 398-412.

GILSINGER, J.J., J.W., BURTON, T.E., CARTER (2010): Maternal effects on fatty acid composition of soybean seed oil. Crop Sci., *50*:1874-1881.

HINA, A., Y., CAO, S., SONG, S., LI, R.A., SHARMIN, M.A., ELATTAR, J.A., BHAT,T., ZHAO (2020): High-resolution mapping in two RIL populations refines major "QTL Hotspot" regions for seed size and shape in soybean (*Glycine max* L.). Int. J. Mol. Sci., *21*: 1040.

HU, Z., H., ZHANG, G., KAN, D., MA, D., ZHANG, G., SHI, D., HONG, G., ZHANG, D.D., YU (2013): Determination of the genetic architecture of seed size and shape via linkage and association analysis in soybean (*Glycine max* L. Merr.). Genetica, *141*: 247–254.

IBRAHIM, S., M.A., ABDELSATAR, M., AHMED, M.M., NIAZY (2021): Genetic behavior for seed yield and yield components in sesame (*Sesamumindicum* L.) under normal irrigation and water stress conditions. Peruv. J. Agron., *5*: 1-17.

ISNAINI, A., S., ZUBAIDAH, H., KUSWANTORO (2020): Maternal effect of agronomical traits of F1 soybean derived from Panderman variety and CpMMV-resistant soybean lines. AIP Conf. Proc., *2231*: 040053.

KARAMI, E., R., TALEBI (2013): Nature of gene action and genetic parameters for yield and its components in chickpea. Afr. J. Biotechnol., *12*: 7038-7042.

KRISNAWATI, A., M.M., ADIE (2015): Selection of soybean genotypes by seed size and its prospects for industrial raw material in Indonesia. Procedia Food Sci., *3*: 355-363.

KUMAWAT, G., D., XU (2021): A major and stable quantitative trait locus qSS2 for seed size and shape traits in a soybean RIL population. Front. Genet., *12*: 550.

LI, W., H., NING, W., LI, W., LU (2006): Developmental genetic analysis of seed size in soybean (*Glycine max*). Acta Genetica Sinica, *33*:746-756.

LIANG, H.Z.,W.D., LI, H., WANG, X.J., FANG (2005): Genetic effects on seed traits in soybean. Yi chuanxuebao. Acta Genetica Sinica, *32*: 1199-1204.

MARANNA, S., G., KUMAWAT, V., NATARAJ, C., GIREESH, S., GUPTA, G.K., SATPUTE, M.B., RATNAPARKHE, D.P., YADAV (2019): NAM population–a novel genetic resource for soybean improvement: development and characterization for yield and attributing traits. Plant Genet. Resour., *17*:545-553.

MINITAB (2013): *Minitab® 17.1.0*. Minitab Ltd. UK.

NAYANA, R.S., B., FAKRUDIN (2020): Genetic variability, heritability and correlation studies in soybean (Glycine max). Indian J Agric. Sci., *90*:704–707.

NING, H., W.B., LI, W.X., LI, J., WANG, D., ZHANG,S., WEI, X., MENG, Y. ZHANG (2005): Genetic effects analysis of seed weight in soybean (*G. max*). Chinese J. Oil Crop Sci., *27*: 69-71.

OTUSANYA, G.O., G., CHIGEZA,S. CHANDER (2020): Combining ability of selected soybean [*Glycine max* (L.) Merrill] parental lines. Indian J. Agric. Res., *1*: 5.

PANDINI, F., N.A., VELLO, Â.C., LOPES (2002): Heterosis in soybeans for seed yield components and associated traits. Braz. Arch. Biol. Technol., *45*: 401-412.

PEREZ, P.T., R.C., SILVIA, G.P., REID (2009): Evaluation of Soybean [*Glycine max* (L.) Merr.] F1 Hybrids. J. Crop Improv., *23*:11–18.

PETR, F.C., K.J., FREY (1966): Genotypic, correlation, dominance and heritability of quantitative character in oats. Crop Sci., *6*:259-262.

PUNEWAR, A., A.S., PATIL, H.R., NANDANWAR, S.M., PATEL, B.N., PATEL (2017): Genetic dissection of heterosis and combining ability in castor (*Ricinuscommunis* L.) with line × tester analysis. J. Exp. Biol. Agric. Sci., *5*: 78-86.

RAHANA, S.N., B., THOMAS (2021): Exploitation of heterosis for drought tolerance in snake bean. Pharma Innov. J., *10*: 1658-1662.

RIX, K.D., A.J., GRACIE, B.M., POTTS, P.H., BROWN,C.J., SPURR, P.L., GORE (2012):Paternal and maternal effects on the response of seed germination to high temperatures in *Eucalyptus globulus*. Ann. For. Sci., *69*:673-679.

SAKILA, M., M., PANDIYAN (2018): Realization of facts and profiteering of black gram through different breeding methods. Int. J. Chem. Stud., *6*: 3359-3369.

SEN, T.M.A (2020): Gene action and combining ability analysis in some soybean quantitative traits. J. Plant Prod. Mansoura Univ., *11*: 579-586.

SENBETAY, T., A., TESFAYE (2015): eterosis at F_2 generation and combining abilities of white pea bean genotypes for important traits. J. Biol. Agric. Healthc., *5*: 22-33.

SHAHID, M.Q., X., HAI-MING, L., SHUN-QUAN, C., ZHI-XIONG, M., NAEEM, L., YA-JUAN, L., XIANG-DONG (2012): Genetic analysis and hybrid vigor study of grain yield and other quantitative traits in autotetraploid rice. Pak. J. Bot., *44*: 237-246.

SHIVANI, D., C., SREELAKSHMI, C.V.S., KUMAR (2011): Combining ability studies and heterosis for yield and its component traits in safflower [*Carthamustinctorius* L.)]. Electron. J. Plant Breed., *2*:377- 383.

SHURTLEFF, W., A., AOYAGI (2021): History of the Use of Soybean Plants as Forage for Livestock (510 CE to 2021): Extensively Annotated Bibliography and Sourcebook. Soyinfo Center.

SULASTRI, D., F., KUSMIYATI, KARNO (2020): Heterosis, heterobeltiosis, and the action of F1 generation genes resulting from crosses of soybeans (*Glycine max* (L.) Merrill) Devon and Dering varieties. J. Agro Complex., *4*:1-6.

SULISTYO, A., PURWANTORO, I.M.J., MEJAYA, N., NUGRAHAENI, SUHARTINA (2021): Determination of genetic parameters of seed characteristics in edible soybean. Legume Res., *44*: 522-526.

SURIN, S., A., KUMAR, S., KUMARI, Y., KUMAR, A., TUTI, A., SUMAN (2018): Heterosis for yield and its component in Indian mustard (*Brassica juncea* (L.) Czern&Coss). Int. J. Curr. Microbiol. App. Sci., *7*: 3866-7381.

TRUSTINAH, R., ISWANTO, R.T., HAPSARI, N., NUGRAHAENI, R., SOEHENDI, T., SUNDARI, SUHARTINA, F.C., INDRIANI, M.J., MEJAYA (2021): Genetic parameters for determining useful parents in mungbean (V*ignaradiata*(L.) Wilczek) breeding for early maturity, small seed size, and high seed yield. Scientifica.

TURNER-HISSONG, S.D., M.E., MABRY, T.M., BEISSINGER, J., ROSS-IBARRA, J.C., PIRES (2020): Evolutionary insights into plant breeding. Curr. Opin. Plant Biol., *54*: 93-100.

UMAR, F.A., M.S., MOHAMMED, M., OYEKUNLE, I.S., USMAN, M.N., ISHAQ, S.N., DACHI (2017): Estimates of combining ability for resistance to pod shattering in soybean (*Glycine max* (L.) Merrill) genotypes. J. Plant Breed. Crop Sci., *9*: 217-223.

VAN GIOI, H., M.G., MALLIKARJUNA, M., SHIKHA, B., POOJA, S.K., J.H.A., P.K., DASH, A.M., BASAPPA, R.N., GADAG, A.R., RAO, T., NEPOLEAN (2017): Variable level of dominance of candidate genes controlling drought functional traits in maize hybrids. Front. Plant Sci., *8*:940.

XU, Y., H.N., LI, G.J.,LI, X., WANG, L.G., CHENG, Y.M., ZHANG (2011): Mapping quantitative trait loci for seed size traits in soybean (*Glycine max* L. Merr.). TAG, *122*: 581-594.

YAMGAR, S.V., S.V., PAWAR, V.P., CHIMOTE, M.P., DESHMUKH, G.C., SHINDE, C.A., NIMBALKAR (2021): Expression of heterosis, residual heterosis and specific combining ability in yield and yield contributing traits of soybean (*Glycine max* (L.) Merrill). J. Pharmacogn. Phytochem., *10*: 2711-2714.

PROCENA HETEROZISA, HETEROBELTIOZISA I DELOVANJA GENA U F1 BILJAKAMA SITNOSEMENIH UKRŠTANJA SOJE

M. Muchlish ADIE[1]*, Arifin ARIFIN[2], Suyamto SUYAMTO[1], Ayda KRISNAWATI[1]

[1] Istreživački centar za jestive biljke, Istraživačka organizacija za poljoporiredu i hranu, Nacionalna istraživačka i inovaciona agencija (BRIN), Indonezija
[2]Indonežansko leguminoze instrument standard testiranje, Indonezija

Izvod

Soja sa malim veličinama semena i visokim potencijalom prinosa je ključna za zadovoljavanje potreba industrije zasnovane na soji. Ciljevi istraživanja bili su da se ispita materinski efekat i kvantifikuje vrednost heterozisa, heterobeltiozisa i delovanja gena kod F1 biljaka iz ukrštanja soje sa sitnim semenom. U ovom radu eksperiment je sproveden u Indonežanskom institutu za istraživanje leguminoza i krtolastih biljaka (ILETRI) koji se nalazi u Malangu (Istočna Java, Indonezija) od marta do jula 2021. Biljke F1 su izvedene iz ukrštanja Lokal Jember × Tidar, Tidar × Gepak Kuning, Gepak Kuning × Detam 3 i njihovih recipročnih ukrštanja. Roditeljski genotipovi i biljke F1 su posejane. Posmatrani podaci su visina biljke, broj grana, broj nodusa, broj napunjenih mahuna, masa 10 semena i prinos semena/biljci. F1 biljke su pokazale je varijaciju za sve posmatrane osobine, što je uglavnom u proseku između dva roditelja, uključujući težinu 10 semena i prinos semena. Nije bilo majčinskog efekta za skoro sve agronomske osobine na svim ukrštanjima i njihovim recipročnim kombinacijama, osim za broj nodusa u ukrštanju Gepak Kuning × Detam 3. Heterozis (hMP) i heterobeltiozis (hHP) F1 izvedene iz šest ukrštenih kombinacija za sedam agronomskih osobina kretao se od -25,93 do 186,27 i od 94,83 do 114,71, respektivno. Delovanje gena se razlikovalo od ukrštanja do ukrštanja za prinos semena i njegove komponente. Stepen dominacije za veličinu semena i prinos semena varirao je od superdominantnosti, nepotpune dominantnosti i potpune dominantnosti. Na osnovu sadašnjeg istraživanja, moguće je razviti sorte soje sa malim semenom i visokim prinosom korišćenjem pedigre selekcije u F2 genereciji.

Primljeno 09.VI.2022.
Odobreno 21. II 2023.