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RESEARCH ARTICLE

Multiple selection indices based identification of soybean (*Glycine max* L.) in early segregating generations

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Abstract

Selection towards an ideal plant progeny is a principal component in plant breeding programs. In this current study, a field experiment was conducted to select progenies that can produce superior advanced breeding lines of soybean (*Glycine max* L.). A total of 403 progenies of $F_{2:3}$ and $F_{2:4}$ generations derived from three different crosses, namely, JS 20-98 × JS 95-60, JS 20-34 × JS 95-60 and EC 457254 × JS 95-60 were evaluated along with their parents for the agronomic performance of soybean. Likelihood ratio test revealed significant genotypic effect for the traits viz., plant height, pods per plant and yield per plant in progenies of both generations. Ideotype selection based on MGIDI, FAI-BLUP and SH Index identified 15 progenies viz., VN20, VN35, VN39, VN45, VN57, VN75, VN90, VN92, VN93, VN95, VN96, VN112, VN170, VN176 and VN248 in $F_{2:3}$ generation and twenty progenies viz., VN18, VN40, VN42, VN85, VN91, VN96, VN103, VN109, VN111, VN113, VN123, VN124, VN126, VN140, VN141, VN152, VN170, VN179, VN189 and VN196 in $F_{2:4}$ generation. Two progenies, VN96 and VN 170 were found promising across both generations; such progenies are of immense potential in developing high-yielding varieties with a good agronomic base.

Keywords: Soybean, genetic gain, selection, progeny, segregating populations, multiple traits

Introduction

Soybean (*Glycine max* L.) production plays an essential role in meeting food and feed demand as it is the world's sixth most important field crop. Currently, South America contributes 55% to soybean production worldwide, where Argentina and Brazil are the main producing countries. In India, it is the number one oilseed crop, cultivated in an area of 12.93 mha with production of 13.36 mt and productivity of 1033 kg/ha during the year 2024 (ICAR-NSRI Annual report 2024). It contributes 40% to total oilseed production and 25% to total edible oil production. Currently, India is earning 73 billion rupees through soy-product exports (Anonymous 2024) and has contributed to the reduction of the quantum of import of edible oil in the country. As a short-duration and low-input cash crop, soybeans have provided great economic benefits to small and marginal farmers of this country.

During 1960–2020, the global average soybean yield has increased from ~1,128 to ~2,769 kg ha^{-1}, which was predominantly attributed to genetic improvement (Rowntree et al, 2013). Several field experiments were performed to select early generation soybean progenies that maximize the probability of extracting superior lines in the process of breeding for high-yielding soybean varieties (Volpato et al. 2018; Volpato et al. 2019).

Genetic improvement is directly influenced by the development and selection of diverse genetic materials in several segregating generations. Since grain yield is quantitatively inherited and its manifestation depends on both genotypic and environmental effects, indirect selection through other economically important traits is rewarding in identifying superior genotypes (Zali et al. 2023). It is a well-established fact that owing to its shrinkage property, the accuracy in predicting breeding values is higher in BLUP (Best linear unbiased predictions) as compared to BLUE (Best linear unbiased estimates) (Piepho et al. 2008; Viana et al. 2009).

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Random-effect mixed models are used as an optimum selection procedure, which involves estimation of variance components by means of the restricted maximum likelihood model (REML) (Patterson and Thompson 1971) and the prediction of genotypic values by the best linear unbiased prediction (BLUP) (Piepho et al. 2007). This results in a more accurate selection process (Resende 2002; Resende 2008; Santos et al. 2015). Accordingly, several BLUP-based selection indices were proposed based on various plant characters, such as the Smith–Hazel index (Smith 1936, Hazel 1943), the FAI-BLUP index (Rocha et al. 2018) and the genotype–ideotype distance index (MGIDI) (Olivoto and Nardino 2021) for selecting ideal progenies based on multiple traits and methods. The extensive application of Smith–Hazel index (Jahufer and Casler 2015), MGIDI index (Shivakumar et al. 2021) and FAI-BLUP index (Resende et al. 2014; Silva et al. 2018; Rocha et al. 2019; Woyann et al. 2020; Oliveira et al. 2021; Almeida et al. 2021) across different crops for multiple agronomic traits is evident from the literature. Further, several studies demonstrated the applicability of BLUP-based selection indices in early generation selection in several crops (Rocha et al. 2019; Volpato et al. 2019; Fronza et al. 2025). Therefore, with the hypothesis that selection gain can be achieved through direct and indirect selection for grain yield in early segregating generation, the current study was carried out to select superior soybean progenies using these indices for grain yield and attributing traits in soybean.

Materials and methods

Plant material

In the current study, a total of 403 $F_{2:3}$ and 403 $F_{2:4}$ half-sib families derived from three crosses: JS 20–98 × JS 95–60, JS 20-34 × JS 95–60 and EC 457254 × JS 95–60, were evaluated for different agronomic traits. JS 20-98 is a high-yielding soybean variety that matures in 100-105 days with a yield potential of 25 to 28 quintals per hectare. It performs exceptionally well under both adverse and normal conditions, making it a versatile choice for farmers. This variety exhibits multiple resistances against key diseases such as anthracnose, Yellow Mosaic Disease (YMD) and charcoal rot. JS 95-60 is an early maturing soybean variety developed by JNKVV Jabalpur in 2007 and a donor for the *e1-as* allele (early maturity). It completes its growth cycle in about 90 days and is the most popular variety of Madhya Pradesh farmers to date. This variety is especially suited for the Soybean-potato/onion-wheat cropping system. JS 20-34 is a soybean variety known for its extra early maturity (90 days) and a donor for the *e2* allele (early maturity). It is insensitive to both temperature and light conditions, allowing it to grow under varying environmental factors. The variety is dwarf, has smooth (hairless) stems, and produces light-coloured pods. EC 457254 is a collection from USDA, having early maturity (90 days) and anthracnose resistant (Nataraj et al. 2020). This genotype was extensively used in the breeding programme for the development of anthracnose-resistant soybean genotypes in India. The number of F_3 and F_4 progenies evaluated in the field from the crosses was 265 from JS 20-98 × JS 95-60, 43 from JS 20-34 × JS 95-60 and 95 from EC 457254 × JS 95-60 cross.

Methods, measured traits and experimental site

The experiment was conducted at ICAR-National Soybean Research Institute, Indore, Madhya Pradesh. A total of 403 progenies, each from $F_{2:3}$ and $F_{2:4}$ generations derived from three crosses, were evaluated for yield and yield component traits in a randomised complete block design (RCBD). Each progeny was planted in a single row of one meter in length with two replications due to limited seed quantity. Four checks, JS 20-98, JS 20-34, JS 95-60 and EC 457254, were also used in the experiment. A total of 15 seeds from each progeny and checks were counted and sown in a one-meter row length and after full field emergence, only 10 plants were retained in each row. The data on days to maturity, plant height (cm), number of branches per plant, number of pods per plant, 100-seed weight (g), and seed yield per plant (g) were recorded and analysed through various statistical tools.

Statistical analysis

All the statistical analyses were carried out using the R package «metan» (Olivoto and Lúcio 2020). Progenies Selection was made based on three selection indices (Smith and Hazel index, FAI-BLUP index and MGIDI index) at a 15% selection index. Genetic parameters, viz., heritability, phenotypic variance, genotypic variance and genetic gain, were estimated using REML/BLUP, genotypes being random effects.

Results

Likelihood ratio test

Likelihood ratio test indicated traits viz., plant height, pods per plant, yield per plant in $F_{2:3}$ and $F_{2:4}$ generation found a highly significant genotypic effect. 100-seed weight was significant only in the $F_{2:4}$ generation. The traits, viz., number of branches per plant, number of nodes per plant, were found non-significant genotypic effect in both $F_{2:3}$ and $F_{2:4}$ generations.

Estimates of genetic parameters

Genetic estimates, viz., genotypic variance, phenotypic variance, heritability (broad sense and narrow sense), and coefficient of variation were estimated in the $F_{2:3}$ and $F_{2:4}$ generations of three different crosses. Genetic variance and phenotypic variance were higher for all the traits in $F_{2:3}$ generations than the $F_{2:4}$ generations. However, there was little or no difference in heritability, broad sense and narrow sense among the $F_{2:3}$ and $F_{2:4}$ generations. Low value

Table 1. **The *p-values* for the likelihood ratio test of the analysed traits**

Model complete	PHT	BRN	NOD	POD	HSW	YLD
Genotype effect (F_3 generation)	<0.001	0.441	0. 298	<0.001	0.625	<0.001
Genotype effect (F_4 generation)	<0.001	0.181	0.203	0.002	0.003	<0.001

of genotypic variance, phenotypic variance and heritability were recorded for traits, branches per plot and nodes per plot. High narrow sense heritability was found in plant height (0.54) and yield per plot (0.44) in the $F_{2:3}$ generation. Accuracy estimates for genetic values of progenies varied according to generation and the trait evaluated in the progenies (Table 3). $F_{2:3}$ generation presented the highest accuracy values for plant height (0.73), pods per plant (0.66), and grain yield (0.66). $F_{2:4}$ generation had the highest values for hundred seed weight (0.52), branches per plant (0.36), and nodes per plant (0.35). However, the 100 seed weight in the $F_{2:3}$ generation observed the lowest accuracy value (0.22) (Table 2).

Selection of inbred progenies MGIDI FAI-BLUP and SH Index

Based on the MGIDI selection index, in the $F_{2:3}$ generation, a total of 35 progenies were selected (Table 3). The highest genetic gain was recorded for the trait yield per plant (4.92), plant height (2.92), followed by number of nodes per plant (2.72) and number of pods per plant (2.72). There was no gain for the traits viz., 100 seed weight and number of branches per plant. Similarly, the FAI-BLUP Index was used in F_3 generation to select 35 progenies with the highest genetic gain for grain yield (7.92), followed by plant height (3.17) and number of pods per plant (3.00). There was little or no gain recorded for 100 seed weight, number of branches per plant and number of nodes per plant (Table 4). In case of SH index, the highest genetic gain was noted in case of grain yield (9.31), followed by plant height (3.59) and number of pods (2.36); little or no genetic gain was observed in case of no. of branches, no. of nodes and hundred seed weight. The details of $F_{2:3}$ progenies selected based on the SH index are given in Table 5. Overall, fifteen progenies viz., VN20, VN35, VN39, VN45, VN57, VN75, VN90, VN92, VN93, VN95, VN96, VN112, VN170, VN176 and VN248 were common in all the three indices used.

Similarly, in the case of $F_{2:4}$ progeny selection, the highest genetic gain through MGIDI was observed in grain yield (4.57), followed by plant height (1.59) and no of pods (1.05). There was no or little genetic gain observed in the case of hundred seed weight, no of branches and no of nodes. Details of $F_{2:4}$ progenies selected through MGIDI are given in Table 6. In case of FAI-BLUP, the highest genetic gain was observed in case of grain yield (4.5), followed by plant height (1.59) and no of pods (1.05), while no or little gain was noted in case of hundred seed weight, no of nodes and no of branches. Details of $F_{2:4}$ progenies selected through FAI-BLUP are given in Table 7. Similarly, using the SH index, the highest genetic gain was observed in the case of grain

Table 2. **Estimates of genetic and phenotypic parameters for seed yield per plot and component traits of soybean progeny in an $F_{2:3}$** and $F_{2:4}$ generations

Parameters	Generation	PHT	BRN	NOD	POD	HSW	YLD
GV	F_3	40.9	0.64	0.84	50.2	0.50	614
	F_4	24.7	0.1	0.22	24.4	0.57	373
PV	F_3	109.0	15.6	15.1	176	18.9	2156
	F_4	104.0	1.4	3.32	151	3.61	1711
h^2 (bs)	F_3	0.38	0.04	0.05	0.28	0.03	0.28
	F_4	0.23	0.07	0.06	0.16	0.15	0.21
h^2(ns)	F_3	0.54	0.08	0.1	0.44	0.05	0.44
	F_4	0.38	0.13	0.12	0.28	0.27	0.35
Accuracy	F_3	0.73	0.28	0.32	0.66	0.22	0.66
	F_4	0.61	0.36	0.35	0.53	0.52	0.60
EV	F_3	68.3	14.9	14.2	126	18.4	1542
	F_4	79.6	1.3	3.09	126	3.04	1338
C.V	F_3	15.6	16.5	8.77	15.3	5.56	27.2
	F_4	12.1	7.13	4.6	11.5	5.8	23.1

PHT= Plant height, BRN = No. of branches per plant, NOD = No. of nodes per plant, POD = No. of pods per plant; HSW = 100 seed weight, YLD = Grain yield per plant

Table 3. Predicted genetic gain for soybean progenies selected based on MGIDI in the $F_{2:3}$ generation

Variables	Xo	Xs	SD	SG	Selected genotypes
PHT	41	46.3	5.35	2.92	VN212, VN90, VN94, VN68, VN57, VN93, VN20, VN61, VN70, VN248, VN95, VN143, VN96, VN35, VN92, VN67, VN107, VN195, VN125, VN196, VN239, VN75, VN45, VN215, VN39, VN170, VN112, VN218, VN217, VN176, VN188 ,VN172, VN71, VN184 and VN175
BRN	4.87	4.87	0.21	0.01	
NOD	10.3	10.8	0.31	2.72	
POD	46.2	52.3	6.12	2.72	
HSW	12.7	12.7	0.006	0	
YLD	91.1	96.4	11.1	4.92	

X0 = Population mean; Xs = Selected progeny mean; SD =Selection differential and SG = Selection gain

Table 4. Predicted genetic gain for soybean progenies selected based on the FAI-BLUP index in $F_{2:3}$ generation

Variables	Xo	Xs	SD	SG	Selected genotypes
PHT	41	46.3	5.82	3.17	VN212, VN90, VN20, VN39 ,VN96, VN239, VN176, VN93, VN248, VN57, VN61, VN94, VN108, VN92, VN262, VN45, VN42, VN170, VN35, VN95, VN141, VN143, VN215, VN169, VN157, VN70, VN54, VN163, VN75, VN180, VN112, VN73, VN28, VN228 and VN107
BRN	4.87	4.87	0.2	0.01	
NOD	10.4	10.8	0.31	0.03	
POD	46.2	52.3	6.76	3.00	
HSW	12.7	12.7	0.02	0.00	
YLD	91.1	96.4	11.1	7.96	

Table 5. Predicted genetic gain for soybean progenies selected based on the Smith-Hazel index in $F_{2:3}$ generation

Variables	Xo	Xs	SD	SG	Selected genotypes
PHT	41.0	47.6	6.58	3.59	VN39, VN20, VN239, VN202, VN96, VN42, VN262, VN176, VN92, VN108, VN112, VN169, VN158, VN97, VN93, VN90, VN157, VN248, VN173, VN207, VN180, VN22, VN57, VN129, VN170, VN31, VN28, VN35, VN95, VN75, VN71 and VN54
BRN	4.87	4.93	0.06	0.005	
NOD	10.4	10.6	0.145	0.01	
POD	46.2	51.5	5.32	2.36	
HSW	12.7	12.7	0.02	0.001	
YLD	91.1	112.0	21.0	9.31	

Table 6. Predicted genetic gain for soybean progenies selected based on the MGIDI in $F_{2:4}$ generation

Variables	Xo	Xs	SD	SG	Selected genotypes
PHT	41	45.1	4.15	1.59	VN91, VN123, VN124, VN42, VN96, VN189, VN179, VN140, VN109, VN162, VN113, VN196, VN217, VN141, VN152, VN142, VN25, VN18, VN165, VN10, VN100, VN175, VN170, VN254, VN126, VN255, VN103, VN41, VN40, VN171, VN256, VN111, VN157, VN9 and VN85
BRN	4.47	4.6	0.13	0.01	
NOD	10.3	10.6	0.25	0.03	
POD	43.1	46.9	3.76	1.05	
HSW	13	13.2	0.2	0.05	
YLD	83.7	96.4	12.8	4.57	

Table 7. Predicted genetic gain for soybean progenies selected based on the FAI-BLUP index in $F_{2:4}$ generation

Variables	Xo	Xs	SD	SG	Selected genotypes
PHT	41	45.1	4.15	1.59	VN91, VN123, VN124, VN42, VN96, VN189, VN179, VN140, VN109, VN162, VN113, VN196, VN217, VN141, VN152, VN142, VN25, VN18, VN165, VN10, VN100, VN175, VN170, VN254, VN126, VN255, VN103, VN41, VN40, VN171, VN256, VN111, VN157, VN9 and VN85
BRN	4.47	4.6	0.13	0.01	
NOD	10.3	10.6	0.25	0.03	
POD	43.1	46.9	3.76	1.05	
HSW	13	13.2	0.2	0.05	
YLD	83.7	96.4	12.8	4.5	

Table 8. Predicted genetic gain for soybean progenies selected based on the Smith-Hazel index in the $F_{2:4}$ generation

Variables	Xo	Xs	SD	SG	Selected genotypes
PHT	41.0	45.1	4.08	1.57	VN91, VN96, VN140, VN123, VN42, VN124, VN179, VN109, VN189, VN223, VN204, VN111, VN196, VN103, VN152, VN141, VN12, VN126, VN181, VN18, VN101, VN47, X64, VN112, VN46, VN116, VN113, VN85, VN40, VN156, VN254, VN64, VN191, VN170 and VN187
BRN	4.47	4.54	0.07	0.01	
NOD	10.3	10.5	0.17	0.02	
POD	43.1	46.1	3.01	0.83	
HSW	13.0	13.2	0.20	0.05	
YLD	83.7	103.0	19.0	6.81	

yield (6.81), followed by plant height (1.57), while no or little gain was noted in the case of hundred seed weight, no of nodes, no of pods and no of branches. Details of $F_{2:4}$ progenies selected through SH are given in Table 8. Overall, in $F_{2:4}$ generation, 20 progenies viz., VN18, VN40, VN42, VN85, VN91, VN96, VN103, VN109, VN111, VN113, VN123, VN124, VN126, VN140, VN141, VN152, VN170, VN179, VN189 and VN196 were found common in all the three indices used. Furthermore, two progenies- VN96 and VN 170 are found to be promising across both generations, and based on all three indices (Table 9, Figs. 1 and 2).

Table 9. The salient features of superior progenies selected based on the MGIDI and FAI-BLUP index during $F_{2:3}$ and $F_{2:4}$ generations

Progenies	Generation	PHT	POD	YLD/plot (g)	BRN	NOD	HSW (g)
VN96	F_3	54.9	68.38	155.4	6.7	11.6	14.3
	F_4	51.3	61.37	203.5	5.0	12.0	14.6
VN170	F_3	47.31	51.98	106.8	4.8	10.6	12.71
	F_4	44.17	47.08	95.75	4.5	10.5	13.19
JS 20-98	Parents	48.6	55.6	86.0	6.2	11.1	14.4
JS 20-34		29.1	27.2	65.60	2.8	8.7	12.0
JS 95-60		35.2	28.8	148.2	2.9	8.7	12.5
EC 457254		33.3	23.9	15.7	3.9	8.8	10.7

Fig. 1. Comparison of selected progenies and parents for No of branches (BRN), No of nodes (NOD) and hundred seed weight (g) (HSW)

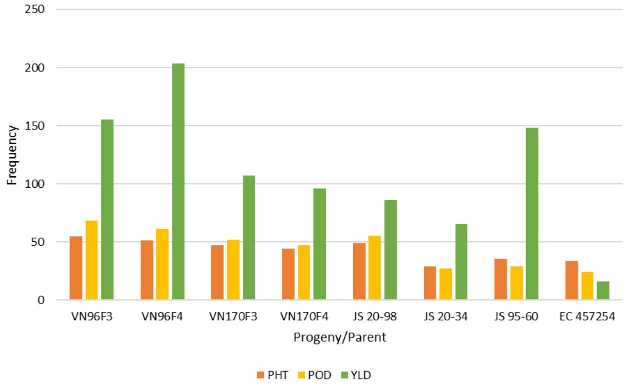

Fig. 2, Comparison of selected progenies and parents for plant height (cm) (PHT), No of pods (POD) and grain yield (g/plot) (YLD)

Discussion

Plant breeding programs aiming for improvement in grain yield and attributing traits employ several segregating populations derived from diverse crosses (Bernardo 2014; De Resende et al. 2016; Pereira et al. 2017; Pires et al. 2014; Shivakumar et al. 2019). An ideotype-based breeding program focuses on multiple traits simultaneously and it differs from other multivariate approaches such as the Smith-Hazel index. In soybean, Nested association mapping RILs, MAGIC RILs, and several advanced breeding lines were evaluated and a few promising lines have been identified for grain yield, early maturity, charcoal rot and yellow mosaic disease resistance by using different indices (Shivakumar et al. 2023, 2021, 2024). In the present study genotype to error variance ratio indicated that the traits under consideration showed greater expression of the environmental component to the detriment of the genetic makeup. It means lower gains with selection through these traits due to moderate or low estimates of heritability. Many of the studies revealed more influence of the environmental effect on the traits governed by several genes (Falconer 1987; Souza et al. 2017). The assessment of experimental precision was conducted by analysing the estimates of selective accuracy; it serves as an indicator of the effectiveness of methodologies employed for predicting genetic values. Selective accuracy, closely linked to the accuracy of selection, quantifies the correlation between the predicted genetic values and the actual genetic values of individuals, as described by Pimentel et al. (2014). In the current study accuracy estimate was highest for plant height, followed by pods per plant and grain yield. Resende et al. (2014) reported that moderate to high accuracy values help in identifying superior individuals. Further, the accuracy above 0.9 is only possible for traits with high heritability, like disease resistance, and values greater than 0.70 are sufficient to provide a more accurate inference about the genetic value of progenies (Resende et al, 2014; Volpato et al., 2018; Rocha et al., 2018). Ambrosio et al. (2024) reported that it is possible to verify that the common genotypes that were selected by all indices show broad adaptation, may present good performance in different environments. The three index, viz., MGIDI, FAI-BLUP and SH, identified VN96 and VN 170 as ideal and these progenies need to be tested in a larger plot size for comparison with check varieties for grain yield and yield component traits. The progeny selection and performance are dependent on the number of traits, the number of genotypes analyzed and the degree of correlation between traits. In the present study, selection differentials for the number of branches per plant, number of nodes per plant and 100 seed weight were low. The low genetic gains may be due to the fact that simultaneous selection for several traits reduces the genetic gain per trait individually (Zetouni et al. 2017). Further, in each case, genetic gain for grain yield was highest in the case of the SH index, indicating its potentiality in selecting progenies for yield per se. Overall, all MGIDI, FAI BLUP and SH index provided gains and were found effective in selecting genotypes close to the ideotype with all the desirable traits like more number of pods per plant, more 100-seed weight and higher grain yield per plot. Earlier studies reported that 71.7% of success was achieved by using MGIDI in selecting superior genotypes (Olivoto and Nardino 2021). Thus, several studies have reported the efficiency of multivariate selection in the identification of drought and salinity-resistant soybean genotypes (Zuffo et al. 2020), the development of bread wheat ideotypes tailored for early sowing conditions (Farhad et al. 2022), the selection of millet strains with resistance against shoot fly infestations (Padmaja et al. 2022), and the breeding of chickpea genotypes with enhanced drought tolerance (Yan et al. 2019).

The three populations evaluated in this study involve four parents: JS 20-98, JS 9560, JS 20-34, and EC 457254. The JS 95-60 was used as a common parent in all three crosses. Variety, JS 20-98 used as a parent in the study possesses charcoal rot and YMD resistance, whereas EC457254 is resistant to anthracnose disease. Out of three crosses evaluated, one cross, JS 20-98 x JS 95-60, was found promising for yield and yield attributing traits compared to the other two crosses, EC 457254 × JS 95-60 and JS 20-34 × JS 95-60. The progenies' mean differs from the best check for the traits evaluated in F_3 and F_4 generations. The findings suggested the high potential of these progenies for the extraction of lines that simultaneously present favourable phenotypes for the target traits genetic breeding.

Authors' contribution

Conceptualization of research (SM, VN); Designing of the experiments (SM, VN); Contribution of experimental materials (VN, SM); Execution of field/lab experiments and data collection (SM, VN, SN, PM, GK); Analysis of data and interpretation (VN, SM); Preparation of the manuscript (SM, VN, SG, KHS).

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