

## HERITABLE GENETIC VARIATION FOR SEED YIELD AND ITS COMPONENT IN SOYBEAN OVER ENVIRONMENTS

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### ABSTRACT

Fifteen genetically diverse genotypes were evaluated at Phanda, Dhar and Silwani in two consequent years to know the real heritable genetic variation for seed yield and its components characters in Soybean. In estimates of heritable genetic variability recorded in pooled analysis over environment were lower in magnitude than their corresponding estimates in individual environment. In pooled analysis plant height, 100-seed weight, pod per plant, seeds per pod and branches per plants exhibited moderate to high estimates of variability. Heritability with moderate to high estimates of genetic advance as percentage of mean. Seed yield per plant, biological yield per plant, harvest index and seeds per pod should low to moderate estimate of heritable genetic variation.

### INTRODUCTION

Soybean is presently one of the most important oilseed crop in the world in term of total production and international trade. The horizontal expansion of this crop was mainly attributed due to the adoption of early maturity and high yielding varieties developed and recommended for cultivation in the recent past. However, the productivity of these varieties considerably differ with change in agro-climates like locations, seasons/years which lead into instability in seed yield. It becomes thus, essential to breed varieties possessing genetic potential for high yield, early maturity and wider adaptability. The understanding of genetic variability provides many avenues for the genetic amelioration of the particular crop. In Soybean, the attempts have been made to assess the extent of genetic variability for seed yield and its determining characters based in their evaluation in a single environmental conditions (Bhatt *et al.*, 1968 and Jagtap and Mehetre, 1994). However, the information on genetic variability for yield and its attributes based on multi-environmental conditions are rarely available in literature.

### MATERIAL AND METHODS

Genetically diverse fifteen genotypes of soybean were tested in randomized complete block

design (RCBD) with three replications at three locations namely Dhar, Phanda and Silwani in two consequent years of 1999-2000 and 2000-2001. Each plot consisted of two rows of 3 meters length with row to row distance of 45 cm. The distance between plants were maintained 10 cm. Fertilizer was applied at the rate 20:60:20 kg. NPK/hectare. Plant protection measures were adopted timely to control the insect-pests. The agronomic practices adapted for better crop growth were common at all the locations in both the years.

### Observations were recorded on:

1. Branches per plant
2. Days to 50% flowering
3. Plant height
4. Days to maturity
5. Pods per plant
6. Seeds per pod
7. 100-seed weight
8. Grain yield per plant
9. Biological yield per plant
10. Harvest index

On ten randomly selected plants from each genotype from each replication. The formula given by Burton (1952) phenotypic and genotypic coefficient of variation, Allard (1960) for heritability and Johnson *et al.*, (1955a) for genetic advance were applied for estimation of genetic parameters.

**RESULTS AND DISCUSSION**

Differences from the genotypes and environment was significant at all the locations in both years. The magnitude of genotypic variability was lower than corresponding phenotypic

variability for all the traits studied in each environment (Table - 1). It also suggests the presence of considerable genotype - environment - interaction in phenotypic expression of all characters as also reported by Jangale *et al.*, (1994) and Mehetre *et al.* (1997) in Soybean.

**Table - 1 : Genetic parameters in Soybean under different environmental conditions**

Characters	Environments	Mean	GCV	PCV	Heritability %	GA	GA% of mean
Days to 50% flowering	E1	42.532	7.240	7.960	82.6	5.760	13.543
	E2	42.224	6.580	6.690	96.8	5.630	13.334
	E3	42.113	5.920	6.150	92.6	4.940	11.730
	E4	44.236	7.240	7.960	82.6	6.000	13.564
	E5	43.910	6.580	6.690	96.8	5.860	13.345
	E6	43.794	5.920	6.150	92.6	5.140	11.737
	Pooled	43.140	3.010	3.760	63.9	2.140	4.954
Days to maturity	E1	100.420	4.390	4.430	98.0	9.010	8.972
	E2	101.068	3.300	3.350	97.0	6.770	6.698
	E3	101.33	3.240	3.290	97.3	6.680	6.592
	E4	103.432	4.390	4.430	98.4	9.280	8.972
	E5	104.102	3.300	3.350	97.0	6.980	6.705
	E6	104.372	3.240	3.290	97.4	6.880	6.592
	Pooled	102.460	1.130	1.260	80.1	2.125	2.074
Plant height	E1	51.050	24.290	25.950	87.6	23.900	46.817
	E2	56.381	19.140	19.650	94.9	21.660	38.417
	E3	51.926	21.350	21.990	94.2	22.170	42.695
	E4	52.528	24.290	25.930	87.6	24.610	46.803
	E5	58.075	19.140	19.650	94.9	22.310	38.416
	E6	51.418	21.350	21.990	94.2	22.830	44.401
	Pooled	53.120	17.120	18.340	87.1	17.481	32.907
100 seed weight	E1	11.938	10.550	11.280	87.6	2.430	20.355
	E2	11.870	9.810	10.480	87.7	2.250	18.955
	E3	11.637	9.780	10.020	95.3	2.290	19.679
	E4	12.058	10.560	11.280	87.6	2.460	20.401
	E5	11.989	9.810	10.470	87.7	2.270	18.934
	E6	11.754	9.780	10.020	95.2	2.310	19.653
	Pooled	11.870	5.240	6.230	70.7	1.077	9.075
Pods per plant	E1	54.110	21.050	26.390	63.6	18.720	34.596
	E2	51.066	20.000	21.730	84.7	19.370	37.931
	E3	50.866	18.510	19.100	94.0	18.800	36.960
	E4	51.406	21.050	26.390	63.6	17.780	24.900
	E5	48.513	20.000	21.730	84.7	18.400	37.928
	E6	48.320	9.780	10.020	95.2	2.310	19.653
	Pooled	50.710	9.570	14.604	42.9	6.545	12.906

Seeds per pod	E1	2.371	15.860	20.810	58.1	0.590	24.880
	E2	2.467	15.630	17.550	79.3	0.710	28.780
	E3	2.502	12.420	14.780	70.5	0.540	21.583
	E4	2.348	15.870	20.800	58.2	0.590	25.128
	E5	2.444	15.600	17.510	79.4	0.700	28.642
	E6	2.478	12.390	14.760	70.5	0.530	21.388
	Pooled	2.440	7.220	12.360	34.4	0.213	8.712
Branches per plant	E1	4.329	17.650	18.680	89.3	1.480	34.188
	E2	4.243	16.280	17.620	85.4	1.320	31.110
	E3	4.358	15.560	16.510	88.7	1.320	30.289
	E4	4.152	17.660	18.680	98.3	1.500	36.127
	E5	4.286	16.290	17.620	85.4	1.330	31.031
	E6	4.400	12.390	14.760	70.5	0.530	21.388
	Pooled	4.330	8.915	10.800	68.0	0.656	15.139
Biological yield per plant	E1	35.009	5.000	8.020	39.9	2.250	6.427
	E2	31.042	13.520	15.420	76.9	7.580	24.419
	E3	34.645	4.580	7.300	39.3	2.050	5.917
	E4	35.359	5.010	8.020	38.9	2.280	6.448
	E5	31.352	13.520	15.520	76.9	7.650	24.400
	E6	34.991	4.520	7.300	39.3	2.070	5.916
	Pooled	33.750	2.515	6.860	13.4	2.035	5.994
Harvest index	E1	33.869	5.860	9.050	42.0	2.650	7.824
	E2	42.456	18.680	22.610	68.3	12.920	30.432
	E3	37.146	6.950	9.260	56.3	3.990	10.741
	E4	33.847	5.740	9.080	39.9	2.530	7.475
	E5	40.869	19.080	22.490	72.0	13.640	33.375
	E6	37.148	6.950	9.200	57.2	4.020	10.822
	Pooled	37.250	2.535	9.620	55.9	0.509	1.360
Seed yield per plant	E1	11.812	8.810	8.840	85.6	1.840	15.577
	E2	12.360	8.040	8.650	86.5	1.900	15.440
	E3	12.812	6.410	6.760	90.5	1.610	12.566
	E4	11.930	8.180	8.840	85.6	1.860	15.591
	E5	12.430	8.040	8.650	86.5	1.920	15.447
	E6	12.941	6.420	6.760	90.1	1.620	12.518
	Pooled	12.370	1.328	3.199	17.2	0.140	1.132

The estimates of heritable genetic variability recorded in pooled analysis over environments were lower in magnitude than their corresponding estimates in individual environments. The presence of genotypes-environment interaction in the estimate of genetic variability may be the reason for lower estimates of heritable genetic variation in pooled analysis (Johnson *et al.*, 1955). Thus, genetic parameters obtained in pooled analysis showed the real estimates after deleting genotype-

environment interaction in pooled analysis, seed yield and its determining characters showed low to moderate estimates of GCV and PCV. None of the characters exhibited. In pooled analysis, seed yield and its determining characters showed low to moderate estimates of GCV and PCV. None of the characters exhibited higher estimate of genotypic coefficient of variability in pooled analysis. It may be due to presence of genotype-environment interaction and testing of limited

number of genotypes in the present study. However, most of the characters showed moderate to high estimates of heritability in pooled analysis indicating that selection based on the phenotypic performance would be effective. Days to 50% flowering, days to maturity, plant height, 100 seed weight and branches per plant, harvest index and seed yield exhibited low to moderate estimates. Genetic advance as percentage of mean was recorded moderate to high for plant height, 100 seed weight, pods per plant, branches per plant and seed per pod in pooled analysis. The relative comparison of heritability and genetic advance as percentage of mean revealed that plant height, 100 seed weight, pods per plant, seed per pod and branches per plant showed moderate to high estimates of heritability coupled with moderate to high estimates of genetic advance as percentage of mean. It indicates the contribution of additive genes in the phenotypic expression of these characters (Panse and Sukhatame, 1967). On the

other hand, seed yield per plant, biological yield per plant, harvest index and seeds per pod exhibited low to moderately estimates of both heritability and genetic advance, revealing the existence of non-additive genes in governing the inheritance of these characters. Non-additive genes in governing the inheritance of these characters is also reported by Rao *et al.* (1981), Mehetere *et al.* (1997) and Jangale *et al.*, (1994). However, direct selection in form of selection indices based on genetic merits these genetic merits characters would be effective for improvement in seed yield in Soybean. It can be completed for the present study that plant height, 100 seed weight for pods per plant, seeds per pod and branches per plant can be included by conventional breeding method while, seed yield per plant, biological yield per plant, harvest index, governed by non-additive genes can be improved by breeding methods such as recurrent selection, bi-parental matting which can utilize non-additive variables in Soybean.

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