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Identification of stable fertile restorer lines for yield and yield components in pigeonpea [*Cajanus cajan* (L.) Millsp)]

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Abstract
In the present investigation, twenty five genotypes involving five cytoplasmic genetic male sterile lines based on A_2 cytoplasm and twenty restorers from diverse source were evaluated at three different locations *viz*. Parbhani (L_1), Badnapur (L_2) and Ambajogai (L_3) during *Kharif* 2020-21. The highly significant differences were observed for male sterile lines and restorers for all the characters studied, however G x E interaction were found significant for all the characters except days to 50% flowering, plant height, pod length and number of seeds per pod indicating its major role in expression of the traits and the performance of the genotypes for seed yield was predicted with great precision across environments. The magnitude of linear component of G x E interaction was greater than non-linear components (pooled deviation) for seed yield and most of the yield components. Female parent BDN 2004-3 A showed average stability for seed yield per plant and most of the important traits *viz.* days to 50% flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, number of pods per plant and protein content. Among male parents (restorers), BDNHR 1, BDNHR 24-1-2 and BDNHR 60-2 exhibited highest seed yield per plant with regression coefficient near to unity and least deviation from regression lines which also exhibited average stability for most of important traits such as number of primary branches per plant, number of secondary branches per plant, number of pods per plant and pod length. Hence, these parents appeared to hold great promise for development of high yielding and widely adaptable pigeonpea hybrids.

Keywords: Pigeonpea, stability, G x E interaction

Introduction
Pigeonpea [*Cajanus cajan* (L.) Millspaugh] is an often cross pollinated crop (20–70%) with diploid (2n = 2x) chromosome number of 22 and genome size of 1C = 858 Mbp. It is a short-lived perennial shrub in which plants may grow for about five years and turn into small trees. It is the sixth most important legume crop, grown predominantly in the tropical and sub-tropical regions of Asia, Africa and Latin America. India is considered as the center of origin of pigeonpea because of its natural genetic variability available in the local germplasm and the presence of its wild relatives. Pigeonpea breeders look forward for widely adapted hybrids responsive to input intensive as well as input deficient agriculture in order to enhance production and productivity of the crop. Multiplication testing of pigeonpea hybrids provide an opportunity to the plant breeders to study the adaptability of hybrids to a particular environment and also the stability of the hybrids over different environments. The information on genotype with environment (G x E) interaction is of major importance to the plant breeders in identifying an improved stable variety, underlines the very success of scientific crop improvement programme and determines the phenotype of an individual which ultimately can be defined as differential phenotypic response of genotypes to environmental changes. By providing suitable environment, the maximum yield potential from a particular hybrid can be realized. Hence, it is necessary to determine the environment which may allow full expression of genes controlling the quantitative traits. The degree of genotype environment interaction involved in the expression of given characters not only helps the plant breeder in planning the future breeding program but also in determining the environment and number of tests to be conducted for evaluation of the prepotency of the breeding material developed. Hence, first objective of commercial exploitation of pigeonpea hybrid was to determine the stability of male sterile lines and restorers over location and over environments. With this background, present investigation was under taken to identity stable male sterile lines and restorers under changing climate situation.

Materials and Methods

The present experimental material comprised of twenty five genotypes involving four cytoplasmic genetic male sterile lines *viz.* BDN 2004-1A, BDN 2004-2A, BDN 2004-3A, BDN 2004-4A and BSMR 736A based on *Cajanus scarabaeoides* (A_2) cytoplasm and twenty restorers from diverse source were evaluated at three different locations *viz.* Parbhani (L_1), Badnapur (L_2) and Ambajogai (L_3) during *Kharif* 2020-21 Among the restorers, fifteen restorers *viz*. BDNHR 1, BDNHR 21-2, BDNHR 22-1-2, BDNHR 24-1-2, BDNHR 41-2, BDNHR 43-1, BDNHR 44-5, BDNHR 46-3, BDNHR 47-2, BDNHR 49-3, BDNHR 52-1, BDNHR 53-4, BDNHR55-2, BDNHR 57-3, BDNHR58-4 were identified and developed from segregating materials of interspecific cross involving *C. scarabaeoides* wild species, however two restorer *viz*. BDNHR 31-1 and BDNHR 60-2 identified and developed from segregating materials of interspecific cross involving *C. albicans* wild species. While three diverse restorers of early maturity groups *viz*. AK 250157, AK 250 159 and AK 250165 were received from Indian Institute of Pulses research, Kanpur. The plot size of two rows each with 4 m row length was followed by spaving of 90 cm between rows 20 cm between plants. The observation were recorded on plot basis for day to 50% flowering and days to maturity, however the observations for remaining nine metric characters *viz.* plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of pods per plant, pod length (cm), number of seeds per pod, 100 seed weight (g), percent pollen fertility (%) were recorded on five randomly selected plants in each replication in each environment. The protein (%) was estimated as per Micro-Kejaldahals method. The stability analysis was carried out by using the stability model proposed by Eberhart and Russell (1966).

Results and Discussion

The information on genotype x environment interactions has a crucial importance to the plant breeder in identifying stable variety/ hybrid that interact less with the environment and determining differential phenotypic response of genotypes to environmental changes. The degree of genotype environment interaction involved in the expression of a given characters in a particular genotype not only useful to plant breeder in planning future breeding programme, but also in determining the number of tests to be conducted for evaluation of the prepotency of the variety or hybrid across different environments.

The mean data over two replications for the parents and hybrids from the three locations were subjected to pooled stability analysis. The analysis of variance revealed that the mean sum of square due to genotypes (G) were found to be significant for all the characters and mean sum of square due to locations were significant for all the characters when tested against mean sum of square due to G x E interaction. The mean sum of square due to genotype x environment interaction when compared against MSS due to pooled error, it was found that G x E interaction were significant for all the characters except days to 50% flowering, plant height, pod length and number of seeds per pod indicating its major role in expression of the traits and the performance of the genotypes for seed yield was predicted with great precision across environments. These significant outcomes were revealed earlier by Meena *et al.* (2017) [3] for the variance due to genotype x environment which was found significant for all the characters except days to 50% flowering and number of seeds/pod.

Further, partitioning of variance due to G x E into its components revealed that Environment + (Genotype + Environment) was significant for days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, 100 seed weight, pollen fertility per cent and seed yield per plant. Similarly, it was noticed that variance due to environments (Linear) was significant for all of the traits except number of primary branches per plant, number of secondary branches per plant, while significant variance due to genotype x environment (Linear) were observed for plant height, number of primary branches per plant, 100 seed weight, pollen fertility per cent and seed yield per plant. The magnitude of linear component of G x E interaction was greater than non-linear components (pooled deviation) for seed yield and most of the yield components. Non linear portion of variance due to pooled deviation was significant for all the traits except number of secondary branches per plant suggesting response of genotypes differentially to variation in environmental changes. When compared these results with earlier findings of Ramesh *et al*. (2017) [5] who recorded the variance due to pooled deviation was highly significant for all the traits except for primary branches and number of seeds per pod which reflected considerable variability in the material.

The low mean value than population mean (117.10) and non-significant values of regression coefficient (bi<1) and deviation from regression line (S2di <0) were desirable for days to 50% flowering. The estimates of stability parameters for days to 50% flowering revealed that female parents BDN 2004-3A required minimum number of days to 50% flowering (109.83 days) with regression coefficient around unity (1.02) and least deviation from regression lines (0.14) showing stable performance for earliness across the three environments. Similarly, male parents BDNHR 21-2 required minimum number of days to 50% flowering (102.00 days) with regression coefficient around unity (1.02) and least deviation from regression lines (0.69) showing stable performance for earliness followed by male parents BDNHR 22-1-2 (Mean = 105.17 days, bi = 0.84, S^2di = 1.08) and AK 250157 (Mean = 107.83 days, bi = 1.48, S^2di = 1.23). These results confirmed the observation of Jyoti *et al.* (2019) [1] that depicted average stability for days to maturity in the genotypes KRG 155 and AGL 1603-2 with the regression value about unity and least regression coefficient.

The mean value less than population mean (168.30) and non-significant values of regression coefficient (bi<1) and deviation from regression line (S2di <0) were desirable for days to maturity. The estimates of stability parameters for days to maturity revealed that female parents BDN 2004-3A required minimum number of days to maturity (1157.33 days) with regression coefficient around unity (1.12) and least deviation from regression lines (1.88) showing stable performance for early maturity across the environments. Likewise, male parents AK 250157 (Mean = 149.33 days, bi = 1.08, S^2di = 0.63) and BDNHR 22-1-2 (Mean = 146.83 days, bi = 1.31, S^2di = 2.71) required minimum number of days to maturity with regression coefficient around unity and least deviation from regression lines revealing the stable performance for early maturity. However, male parent BDNHR 21-2 (Mean = 144.00 days, bi = 1.69, S^2di = -2.97) and AK 250165 (Mean = 151.00 days, bi = 1.68, S^2di = 3.97) had regression coefficient more than unity and least deviation

from regression lines depicting its suitability to favourable environments with below average stability. Ramesh *et al.* (2017) [5] reported similar results for pigeonpea genotype JSA 59 and Pusa 2001 having stable performance for days to maturity across the environments with good stability under irrigated condition.

The female parent BSMR 736A recorded plant height more than population mean (212.30 cm), value of regression near to unity (0.89) with minimum deviation from regression line (1.88) suggesting stable performance for plant height over all the environments. Among the male parents, BDNHR 60-2 plant height more than population mean (212.30 cm), value of regression near to unity (0.89) with minimum deviation from regression line (1.88) found to be stable across environments, whereas the male parents BDNHR 44-5 (Mean = 239.85 cm, bi = 0.47, S^2di =-2.98) and BDNHR 31-1 (Mean = 207.30 cm, bi = 0.82, S^2di = 8.05) showed high mean value with regression coefficient less than unity and less deviation from regression line revealing the suitability of these hybrids for poor environments with above average stability. Further, it was observed that female parent BDN 2004-3A (Mean = 11.57, bi = 1.18, S^2di = 0.02) and male parents BDNHR 60-2 (Mean = 15.90, bi = 1.39, S^2di = 1.11) and BDNHR 1 (mean = 15.13, bi = 1.16, S^2di = 0.71) for number of primary branches per plant and female parent BSMR 736A (Mean = 29.03, bi = 1.49, S^2di = -0.39) and male parents BDNHR 60-2 (Mean = 27.40, bi = 1.05, S^2di = 1.40), BDNHR 24-1-2 (Mean = 22.43, bi = 1.25, S^2di = 0.82), BDNHR 1 (Mean = 23.72, bi = 1.48, S^2di = 2.00) for number of secondary branches per plant recorded high mean among female and male parents, respectively with regression coefficient around unity and minimum deviation from regression lines indicating stable performance of these parents across the three environments for number of primary and secondary branches per plant in pigeonpea. These results confirmed the findings of Jyoti *et al.* (2019) [1] who revealed stable performance for plant height, number of primary and secondary branches per plant in the genotypes ICPL 332, KRG 33, GRG 617 and GRG 622, however genotype GRG 221 showed the regression value more than unity indicating its suitability to favourable environments and genotypes GRG 177, ICPL 15014 and GRG 2013 manifested the regression value less than unity indicating its suitability to unfavorable environments in pigeonpea

Stability analysis of parents for number of pods per plant evinced that female parent BDN 2004-3A (Mean = 250.50, bi = 1.26, S^2di = 26.40) and male parents BDNHR 1 (Mean = 209.12, bi = 0.95, S^2di = 37.81), BDNHR 24-1-2 (Mean = 250.02, bi = 0.92, S^2di = 78.12), BDNHR 60-2 (Mean = 230.33, bi = 1.10, S^2di = 29.60) exhibited high mean among female and male parents, regression coefficient around unity and minimum deviation from regression lines showing their stable performance across the three environments for number of pods per plant in pigeonpea. Similar findings were in harmony with Sreelakshmi *et al.* (2010) [8] who noticed higher number of pods per plant with stable performance over average environmental conditions in pigeonpea genotypes ICPL 20042, ICPL 20062, ICPL 87089 and ICPX 77303.

In the present study, female parent BDN 2004-2A was long poded recording highest mean value (7.48 cm) with regression value near to unity (1.43) and least deviation from regression line (0.03) and had maximum stability for pod length across environments. Similarly, female parent BDN 2004-2A had highest number of seeds (5.73) with regression value near about unity (1.20) and minimal deviation from regression line (0.02) showed most stable female parent across the environments. Among twenty male parents evaluated for stability, BDNHR 58-4 (Mean = 5.87 cm, bi = 1.19, S^2di = 0.09), BDNHR 24-1-2 (Mean = 5.42 cm, bi = 0.92, S^2di =-0.06), BDNHR 60-2 (Mean = 5.32 cm, bi = 1.32, S^2di =-0.23), BDNHR 1 (Mean = 5.28 cm, bi = 1.14, S^2di =-0.15) recorded high mean performance over population mean, regression coefficient around unity and minimum deviation from regression lines depicting stability of parents across tested all three environments. None of the male parents recorded high mean value in combination with unit regression coefficient and least deviation from regression line for number of seed per pod. These findings were in consonance with those of Ramesh *et al*. (2017) [5] revealed that genotypes such as RVK-285, AKT-9913, JKM-189 and ICP-13579 were consistent and high yielding compared to local check for irrigated conditions found to be a stable for pod length and number of seeds per pod in pigeonpea.

However, the female parent BDN 2004-2A was bold seeded observing highest mean value (14.85 g) with regression value near to unity (0.93) and minimal deviation from regression line (0.02) showed most stable and wider adaptable for 100 seed weight across the environments. Out of the twenty male parents evaluated for stability, extra bold seeds were observed in male parents BDNHR 58-4 (12.52 g) and BDNHR 44-5 (12.25 g) with regression value near about unity and minimal deviation from regression lines depicting their stable performance for 100 seed weight over environments. Similar findings in accordance with observations of Reddy *et al.* (2011) for genotype LRG 41 showing most stable performance for 100-seed weight as well as for seed yield Further, similar observation was obtained by Kumara *et al.* (2016) and recorded most stable genotype GRG 825 for test weight as well as for seed yield in pigeonpea.

In the present study, maintainer lines of female parents BDN 2004-3A and BSMR 736 A had 100% pollen fertility, while that of BDN 2004-1 A had high mean value (98.75%), regression coefficient about unity (1.15), least deviation from regression line (-5.73). However, male parents BDNHR 1; BDNHR 60-2 (Mean = 99.58%, bi = -0.22, S^2di = -7.37) and BDNHR 24-1-2; BDNHR 44-5 (Mean = 99.17%, bi = -0.45, S^2di = -4.30) had above average stability and suitable for poor environments. Further, the female parent BDN 2004-3A recorded highest protein per cent (20.83%) with regression value near about unity (1.06) and minimal deviation from regression line (-0.16) and showed most stable parent for protein per cent across the environments. Among the twenty male parents, the maximum protein per cent was observed in male parents BDNHR 1 (Mean = 21.23%, bi = 1.07, S^2di = 0.32), BDNHR 53-4 (Mean = 21.33%, bi = 0.93, S^2di = -0.31), AK 250157 (Mean = 21.25%, bi =1.06, S^2di = 0.37) and BDNHR 58-4 ((Mean = 20.82%, bi = 0.92, S^2di = -0.23)) with regression value near about unity and minimal deviation from regression lines depicting their stable performance for protein per cent over environments.

Stability analysis of parents for seed yield per plant revealed that female parent BDN 2004-3A (Mean = 68.80 g, bi = 1.04, S^2di = 3.91) and male parents BDNHR 1 (Mean = 63.40 g, bi = 1.02, S^2di = 3.74), BDNHR 24-1-2 (Mean = 66.33 g, bi = 1.09, S^2di = 4.43), BDNHR 60-2 (Mean = 69.50 g, bi = 1.16, S^2di = 5.30) recorded high mean among female and male parents, respectively with regression coefficient around unity and minimum deviation from regression lines indicating

theses parents showed stable performance for seed yield per plant across the three environments.

The male sterile line BDN 2004-3A had stability for seed yield per plant as well as for earliness, plant height, branches per plant, number of pods per plant and protein content, however another male sterile line BSMR 736A was stable for primary and secondary branches per plant, number of pods per plant, seed yield per plant. These results were in conformity with Pandat *et al.* (2015) [4] who noticed that CMS lines based on A2 and A4 cytoplasms can be effectively exploited in hybrid development programme as these were stable for maintaining their sterility under varying environmental conditions. All the CMS lines were significantly early in flowering and maturity, short plant stature and stable for primary branches, secondary branches, number of pods, seed yield in pigeonpea. These results confirmed the findings of Singh *et al.* (2016) [7] who recorded nine stable and high yielding genotypes exhibiting stable performance under the rainfed environmental conditions for more than one traits studied and also under more than one year. Similarly, the genotypes GRG 177, KRG 224 and GRG 811 exhibited high mean performance but higher regression value (bi>1) and significant deviation (S2di= 0) value indicating adapted for high performance environments showed that these genotypes were sensitive to environments and give maximum yield when inputs are not limited.

From the present study, it was concluded that the female parents, BDN 2004-3A showed average stability for seed yield per plant and most of the important traits *viz.* days to 50% flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, number of pods per plant and protein content and this female parent was earlier to flower and mature and can be utilized for breeding early duration stable pigeonpea hybrids. Among male parents (restorers), BDNHR 1, BDNHR 24-1-2 and BDNHR 60-2 exhibited highest seed yield per plant with regression coefficient near to unity and least deviation from regression lines which also exhibited average stability for most of important traits such as number of primary branches per plant, number of secondary branches per plant, number of pods per plant and pod length.

Hence, these male parents appear to hold great promise for development of high yielding pigeonpea hybrids. Further, it was suggested to verify the performance of these male sterile line and restorer lines over the season and over the location for the development of more heterotic, widely adaptable and stable high yielding hybrids for commercial exploitation in pigeonpea.

Table 1: Analysis of variance for phenotypic stability of yield and yield contributing characters in pigeonpea

Source	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches/ plant	No. of secondary branches/ plant	No. of pods/ plant
Rep. within Env.	5.52	5.77	235.69	2.33	13.48	259.22
Genotypes	195.57**	564.32 **	1272.13 **	60.05 **	207.43 **	14081.61 **
Environments	640.54 **	617.29 **	7947.76 **	1.07	4.07	5534.99 **
Geno. x Env.	8.14	37.28**	175.18	2.20 *	9.84**	408.47 **
Env. + (Geno. x Env.)	13.12 **	110.79**	236.38**	2.19 *	10.82**	448.84 **
Environments (Lin.)	1281.07 **	1234.59 **	15895.52 **	2.14	8.14	11069.98 **
Geno. x Env. (Lin.)	7.59	19.86	213.18 **	2.81**	6.43	437.64**
Pooled deviation	8.62 **	24.44 **	136.10 *	1.59 *	5.22	176.32*
Pooled error	2.86	3.64	98.37	1.25	5.28	41.29
Total	73.61	208.46	235.69	21.38	72.67	4969.18

Table 1: Continue….

Source	Pod length (cm)	No. of Seeds/ pod	100-Seed weight (g)	Pollen fertility (%)	Protein (%)	Seed yield/ plant (g)
Rep. within Env.	0.09	0.13	0.64	14.70	0.71	41.87
Genotypes	1.37 **	0.86 **	9.28**	318.68 **	7.77 **	1962.63**
Environments	0.35	0.45 **	38.56 **	22.17	21.77 **	312.55**
Geno. x Env.	0.11	0.08	0.53 *	24.74 *	0.66	243.76**
Env. + (Geno. x Env.)	0.11	0.08	0.82 **	24.72 *	0.83	445.87**
Environments (Lin.)	0.69 *	0.910**	77.11 **	44.35	43.53 **	625.11**
Geno. x Env. (Lin.)	0.10	0.073	0.65 **	2 30.40 *	0.64	230.06**
Pooled deviation	12.06 **	112.22 **	136.10 *	5.13 **	21.01 ***	57.00 **
Pooled error	2.88	3.64	98.37	1.255	5.49	24.76
Total	5.24	5.77	235.69	2.44	16.81	681.43

Table 2: Stability parameters in respect of different quantitative traits in Pigeonpea

Sr. No.	Genotypes	Days to 50% flowering			Days to maturity			Plant height (cm)		
		Mean	Bi	S^2di	Mean	bi	S^2di	Mean	bi	S^2di
Male Sterile Lines										
1	BDN 2004-1A	125.50	0.50	19.08**	174.67	1.03	-2.87	178.00	-0.19	162.43
2	BDN 2004-2A	117.00	1.02	0.69	168.67	2.25	-2.42	204.20	0.05	18.02
3	BDN 2004-3A	109.83	1.01	0.14	157.33	1.12	1.88	185.38	0.92	-2.67
4	BDN 2004-4A	122.17	0.85	-2.04	174.67	0.37	1.18	178.87	1.13	-95.67
5	BSMR 736A	125.17	1.14	0.21	179.00	0.49	2.04	206.90	0.89	0.97
Restorers										
1	BDNHR 1	118.00	0.91	1.99	171.00	1.55	5.04	169.53	0.93	5.81
2	BDNHR 21-2	102.00	1.02	0.69	144.00	1.69	-2.97	168.08	0.26	-59.89
3	BDNHR 22-1-2	105.17	0.84	1.08	146.83	1.31	2.71	167.18	0.26	63.68

4	BDNHR 24-1-2	113.33	0.82	0.74	168.83	0.85	3.61	190.83	-0.35	7.34
5	BDNHR 31-1	123.33	0.46	0.16	181.83	0.74	15.69	207.30	0.82	8.05
6	BDNHR 41-2	120.83	0.62	16.46**	178.67	-2.03	-3.21	186.18	1.46	-93.73
7	BDNHR 43-1	130.33	-0.79	25.53**	187.33	-1.44	4.42	220.20	-1.28	-96.99
8	BDNHR 44-5	109.67	-0.61	-1.41	160.33	0.28	18.76*	239.85	0.47	-2.98
9	BDNHR 46-3	134.50	1.38	-0.65	189.50	0.88	40.26**	229.65	-0.56	213.45
10	BDNHR 47-2	124.33	0.53	2.95	184.67	0.61	7.85	196.73	1.18	331.68*
11	BDNHR 49-3	132.50	1.38	-0.65	182.83	1.81	-3.24	223.62	-1.04	343.49
12	BDNHR 52-1	133.33	-0.27	5.54	190.00	-2.18	37.48**	191.12	0.72	-71.17
13	BDNHR 53-4	120.00	-0.44	-0.34	173.17	-1.25	-3.66	210.95	-0.34	-61.16
14	BDNHR 55-2	121.50	0.73	-1.71	175.33	0.39	11.01*	192.95	0.28	-60.72
15	BDNHR 57-3	114.50	1.02	-2.88	164.00	-1.84	99.97**	178.67	0.32	-75.02
16	BDNHR 58-4	124.83	1.34	-2.70	185.17	3.51	-3.22	202.60	-0.50	-76.46
17	BDNHR 60-2	122.50	0.91	1.03	169.50	-0.98	2.17	225.17	0.97	0.27
18	AK 250157	107.83	1.48	1.23	149.33	1.08	0.63	155.08	0.95	-25.53
19	AK 250159	109.17	0.63	-2.22	155.50	3.55	1.15	149.98	0.78	65.39
20	AK 250165	110.00	1.16	7.54	151.00	1.68	3.97	157.80	0.25	8.06

Table 2: Continue….

Sr. No.	Genotypes	No. of primary branches/plant			No. of secondary branches/plant			Number of pods /plant		
		Mean	Bi	S^2di	Mean	Bi	S^2di	Mean	bi	S^2di
Male Sterile Lines										
1	BDN 2004-1A	10.48	18.28	-0.02	21.15	11.36	0.28	164.27	0.87	-103.34
2	BDN 2004-2A	8.32	-10.76	-1.17	17.48	5.95	-4.66	174.97	1.91	678.83*
3	BDN 2004-3A	11.57	1.18	0.02	26.30	1.77	0.91	250.50	1.26	26.40
4	BDN 2004-4A	10.50	14.21*	-1.26	21.23	-11.60	-4.99	156.63	-2.87**	-142.19
5	BSMR 736A	14.18	1.67	2.41	29.03	1.49	-0.39	197.63	1.50	30.41
Restorers										
1	BDNHR 1	15.13	1.16	0.71	23.72	1.48	2.00	209.12	0.95	37.81
2	BDNHR 21-2	5.48	-11.00	-0.29	11.30	6.01	-5.33	116.97	-2.41	136.44
3	BDNHR 22-1-2	6.37	-4.38	-0.61	11.17	0.14	-0.34	134.60	-1.88**	-142.09
4	BDNHR 24-1-2	14.50	1.86	1.12	23.43	1.25	0.82	250.02	0.92	78.12
5	BDNHR 31-1	14.82	32.60	-0.29	22.95	11.22	-3.93	218.50	2.31	-104.95
6	BDNHR 41-2	12.88	-3.28	0.31	18.95	-1.41	0.44	148.65	0.91	6.97
7	BDNHR 43-1	12.70	-8.12	1.02	18.07	-9.95	-3.36	138.68	-1.06	-131.22
8	BDNHR 44-5	12.75	-4.07	-1.22	17.52	-9.54	-4.31	173.63	-1.20	49.58
9	BDNHR 46-3	13.42	17.73	1.65	19.12	0.28	-4.23	151.82	0.21	22.97
10	BDNHR 47-2	13.78	2.11	0.03	22.70	4.00	1.66	276.57	2.17	87.33
11	BDNHR 49-3	14.23	11.07	-0.61	21.17	10.03	-5.31	153.30	1.25	-135.75
12	BDNHR 52-1	9.75	7.64	-1.12	15.12	-1.61	-3.68	141.47	5.78**	-142.21
13	BDNHR 53-4	13.92	3.92	2.96	22.45	-11.26	-4.78	244.53	1.79	-132.91
14	BDNHR 55-2	12.93	0.89	6.66*	21.57	-10.02	-4.89	188.28	0.21	376.02
15	BDNHR 57-3	12.32	0.97	1.77	20.63	3.94	-1.82	174.62	3.30	-49.73
16	BDNHR 58-4	9.70	1.99	-0.79	14.63	1.43	1.95	133.90	1.87	115.68
17	BDNHR 60-2	15.90	1.39	1.11	27.40	1.05	1.40	230.33	1.10	29.60
18	AK 250157	4.87	-16.84	-1.11	10.33	2.40	-2.71	121.57	0.77	487.29
19	AK 250159	5.20	-11.71	-0.93	10.15	-5.10	-3.83	131.48	1.29	940.16
20	AK 250165	6.73	-23.39	-1.20	11.47	-3.42	-4.81	120.02	1.27	-120.27

Table 2: Continue….

Sr. No.	Genotypes	Pod length (cm)			No. of seeds/pod			100 seed weight (g)		
		Mean	bi	S^2di	Mean	bi	S^2di	Mean	bi	S^2di
Lines										
1	BDN 2004-1A	5.27	1.29	-0.08	4.27	3.34	-0.04	10.42	-0.23	-0.12
2	BDN 2004-2A	7.48	1.43	0.03	5.73	1.20	-0.01	14.85	0.93	0.02
3	BDN 2004-3A	5.68	-0.69	0.13	4.20	2.50	-0.04	10.95	-0.83	-0.82
4	BDN 2004-4A	4.07	-4.97	-0.13	3.38	-2.97	0.17**	10.43	0.32	-0.36
5	BSMR 736A	5.32	-4.08	-0.04	4.07	0.83	-0.04	10.12	-0.51	0.87
Testers										
1	BDNHR 1	5.28	1.14	0.15	4.07	0.82	-0.01	11.08	0.69	-0.10
2	BDNHR 21-2	4.83	-5.47	0.03	3.62	-1.24	-0.04	8.88	0.45	-0.21
3	BDNHR 22-1-2	5.00	0.07	0.03	3.87	0.45	0.07	9.08	0.26	1.55*
4	BDNHR 24-1-2	5.42	0.92	-0.06	4.27	-1.70	0.06	11.30	0.77	-0.29
5	BDNHR 31-1	5.57	0.55	-0.08	4.33	-1.66	-0.04	11.13	0.83	-0.33
6	BDNHR 41-2	5.17	-5.72	0.03	4.33	-0.84	0.05	9.13	1.18	-0.09
7	BDNHR 43-1	5.67	-4.98	-0.05	4.30	2.53	0.01	9.23	-0.55	0.22
8	BDNHR 44-5	5.27	0.18	0.09	4.37	-2.54	0.05	12.25	0.92	0.37

9	BDNHR 46-3	5.35	-7.92	0.96**	4.27	5.90	0.23	9.42	-0.37	0.50
10	BDNHR 47-2	4.73	2.59	-0.07	3.85	0.43	-0.02	9.68	0.91	-0.35
11	BDNHR 49-3	4.85	4.63	-0.04	4.05	-0.43	-0.02	10.68	-0.41	-0.33
12	BDNHR 52-1	4.83	6.47	-0.01	3.72	-2.11	0.02	11.82	0.27	-0.34
13	BDNHR 53-4	4.85	6.57	-0.07	4.15	-3.77	-0.02	9.32	1.05	-0.33
14	BDNHR 55-2	4.75	2.09	-0.04	3.95	-2.92	-0.05	11.40	-0.46	0.83
15	BDNHR 57-3	5.07	-1.69	-0.01	4.13	-2.53	0.03	10.62	1.50	-0.33
16	BDNHR 58-4	5.87	1.19	0.09	4.63	-2.53	0.03	12.52	0.88	0.10
17	BDNHR 60-2	5.32	1.32	0.23	4.28	-0.45	0.07	11.38	0.91	0.30
18	AK 250157	3.98	-0.54	0.07	3.17	3.29	0.28	7.78	1.54	0.23
19	AK 250159	4.08	0.05	0.17	3.12	2.08	-0.03	8.03	0.77	-0.16
20	AK 250165	3.83	0.05	0.17	3.10	4.19	-0.04	8.97	2.28	0.64

Table 2: Continue…

Sr. No.	Genotypes	Percent pollen fertility (%)			Protein (%)			Seed yield/ plant (g)		
		Mean	bi	S^2di	Mean	Bi	S^2di	Mean	bi	S^2di
Male Sterile Lines										
1	BDN 2004-1A	98.75	1.15	-5.73	19..10	-1.31	-0.34	47.13	4.12	-22.23
2	BDN 2004-2A	91.25	8.42	7.47	19.60	-1.31	2.04*	52.60	4.03	-23.71
3	BDN 2004-3A	100.00	0.00**	-8.40	20.83	1.06	-0.16	68.80	1.04	3.91
4	BDN 2004-4A	90.42	-3.89	-0.14	17.40	1.70	-0.03	31.37	0.87	-11.21
5	BSMR 736A	100.00	0.00**	-8.40	18.00	-0.25	0.57	58.43	1.84	-6.00
Restorers										
1	BDNHR 1	99.58	-0.22	-7.37	21.23	1.07	0.32	63.40	1.02	3.74
2	BDNHR 21-2	87.92	8.64	16.56	18.90	1.70	-0.03	26.06	-0.05	-20.41
3	BDNHR 22-1-2	91.67	5.01	-3.61	18.87	1.64	-0.33	25.60	-0.12	71.16
4	BDNHR 24-1-2	99.17	-0.45	-4.30	18.13	-2.16	0.89	66.33	1.09	4.43
5	BDNHR 31-1	98.75	2.97	-8.34	18.93	1.60	-0.38	63.77	7.20	-3.53
6	BDNHR 41-2	91.67	-5.04	11.90	17.75	0.55	-0.39	41.67	5.54	-14.18
7	BDNHR 43-1	96.25	5.93	-8.19	19.80	1.30	-0.39	37.37	0.72	-21.94
8	BDNHR 44-5	99.17	-0.45	-4.30	19.80	-1.35	0.04	48.13	0.66	-16.01
9	BDNHR 46-3	85.83	-0.89	7.99	18.85	1.90	-0.17	39.13	-1.20	-12.68
10	BDNHR 47-2	95.00	2.49	11.32	17.37	0.17	-0.08	68.17	4.13	-20.73
11	BDNHR 49-3	86.25	-9.57	-2.87	18.28	-0.64	0.12	41.70	-0.36	7.83
12	BDNHR 52-1	93.33	7.72	49.97**	19.15	2.11	-0.20	29.90	2.40	-17.17
13	BDNHR 53-4	95.42	3.19	-7.78	21.33	0.93	-0.31	52.40	1.92	59.39
14	BDNHR 55-2	95.00	0.00**	-8.40	18.80	0.70	-0.37	45.13	2.11	-19.63
15	BDNHR 57-3	93.33	8.68	-5.51	17.43	0.70	-0.15	44.40	2.73	10.69
16	BDNHR 58-4	97.50	-5.93	-8.19	20.82	0.92	-0.23	29.13	1.28	-0.14
17	BDNHR 60-2	99.58	-0.22	-7.37	17.73	-0.11	-0.38	69.50	1.16	5.30
18	AK 250157	95.00	-4.11	-4.93	21.25	-1.06	0.37	29.17	1.07	24.62
19	AK 250159	94.17	4.34	-7.68	19.75	1.62	-0.39	32.77	2.02	51.56
20	AK 250165	93.75	1.15	-5.73	18.63	1.06	-0.34	32.83	0.17	28.95

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