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Estimation of Combining Ability for Yield Traits in Groundnut using Genetic Variance-covariance among Relatives

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ABSTRACT

Background: In standard mating designs, the suitability of a line as a parent is generally assessed by examining its overall genetic effects. However, if the given attributes of a line are due to gene interaction (epistasis), this approach becomes less reliable. As the performance of the line will exceed the sum of alleles, thereby inflating its breeding potential. The current study aimed to partition these genetic effects into additive and non-additive effects and their interaction with the environment for authentic selection of parental line(s) having high additive effects.

Methods: In this study, genetic effects of 40 advanced breeding lines (ABLs) of groundnut developed through pedigree method were partitioned into additive and non-additive effects by incorporating the pedigree information into analysis. These effects and their interactions were further modelled by incorporating variance-covariance structures constructed as Kronecker product across sites.

Result: The merit of 40 ABLs of groundnut was demarcated based on their breeding values. The differential ranking based on both genetic values and additive effects led to conclude that selection for parents should be preferred on breeding values for high genetic gains.

Key words: Additive effect, Breeding value, Combining ability, Mixed model, Multi-environment trials (MET), Non-additive effect.

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INTRODUCTION

In any breeding programme, genetic variability is a pre-requisite for developing new cultivars. This variability can be generated by either mutagenesis or through hybridization of different parents, followed by segregation and recombination. The genetic composition (G) of an individual can be expressed as the sum of the average of additive effects (D) or additive effects plus, a deviation due to non-additive effects, *i.e.*, dominance (H) and epistatic interaction (I) (Falconer and Mackay 1996, Bernardo 2002). Hence, the estimation of additive and non-additive effects of an individual (s) is important for further genetic improvement of the desired trait (s) through hybridization as, the mean genotypic value of its progeny is equal to general mean plus the sum of the breeding values of two parents *i.e.*, general combining ability (GCA) and non-additive effects or epistatic interaction due to specific combination of alleles at different loci known as specific combining ability (SCA) (Bernardo 2002). Thus, to generate new genetic variability in recombinant line (s), the genetic divergence and their magnitude of additive effects (GCA) vis-à-vis non-additive effects (SCA) among candidature parent(s) are of utmost importance.

In the classical breeding programs, selection for the suitable parental line (s) is made through standard mating designs, example *via* diallel cross or top cross which partitions the genetic effect of a line into additive and non-additive effects. These additive and non-additive effects are referred to as general and specific combining ability respectively, in these mating designs in plant breeding programs. However, such designs are associated with certain disadvantages like i) Evaluation of the lesser number of parental lines, ii) Assumptions associated with these designs like the absence of epistasis, absence of multiple allelism, random mating, *etc*. are seldom met, iii) In advanced generations of self-pollinating crops dominance deviation diminishes and only additive × additive interaction is fixed in elite genotypes. Thus, these designs cannot be used for estimating the real magnitude of additive effects vis-à-vis epistatic interaction for the desired trait(s).

Hybridization in groundnut is very difficult and the success rate is very low, hence, sufficient population size cannot be achieved for proper testing of GCA and SCA across the years or locations in diallel or line × tester fashion of mating of the parent(s). Further, being cleistogamous, advanced generations are purely composed of additive effects and additive ´ additive gene interactions (epitasis). Since, the models diallel and line ´ tester assess suitability of line as a parent based on the overall genetic effect. However, if the given attributes of line are due to the result of interaction between genes (epistasis), then this approach is not ideal as, the performance of the line is more than sum of alleles, leading to an inflated breeding potential for it (Oakey *et al*., 2006).Thus, the real worth of a genotype(s) as a donor for the further genetic improvement of the desired trait(s) cannot be assessed with precision. But, Oakey *et al.,* (2006) resolved these limitations by partitioning the total genetic effect 'g' of lines into additive 'a' and non-additive 'i' effects by modelling genetic variance-covariance of genotypes in mixed model equation (MME) by incorporating coefficient of parentage (COP) *i.e*., additive relationship matrix (A) for genetic effects and Ã matrix for epistatic effects of BLUP analysis, where, Ã is constructed as (A#A)= Ã (where # is the element-wise multiplication operator) (Falconer and Mackay 1996). This was useful for the identification of lines with high additive effects and overall high production. Crossa *et al.,* (2006) predicted the breeding values of lines using the additive genetic covariances of relatives, which is the additive relationship matrix A, multiplied by additive genetic variance. Further, the BLUPs of breeding values were obtained using genetic variance-covariance structures constructed as Kronecker product of a structured matrix of genetic variances and covariances for sites and, a matrix of genetic relationship between strains, A. This, was found to efficiently model the genotypic main effects and GE and a low standard error of the BLUPs of breeding values were obtained. But the study did not consider covariances between relatives due to epistatic genetic effects. To overcome this, Burgueño *et al.,* (2007) further extended the factor analytic model proposed by Crossa *et al.,* (2006) to partition GEI into additive × environment interaction and additive × additive × environment interaction in wheat for the identification of lines having high additive effects. This was achieved with the incorporation of variance-covariance structures constructed as Kronecker product of a FA model, across sites and additive (A) and additive × additive relationship between lines. The results obtained showed the efficacy of the model for the identification of lines having high additive effects to be used as parents in crossing program as well as have overall high production. In the present investigation, the model given by Burgueño *et al.,* (2007) for the partitioning of genetic effects into additive (GCA) and non-additive (SCA) effects and their interaction with the environment will be used for the identification of lines having high additive effects, which can be used as parents in crossing programme for germplasm improvement in groundnut.

MATERIALS AND METHODS

In present study a set of 40 advanced breeding lines (ABL) at F_9 generation developed through pedigree breeding methos, comprising full sibs and half -sibs were used (Table 1). The lines were sown at three locations *viz*., Farm area of Oilseeds section, Department of Plant Breeding and Genetics, Punjab Agricultural University, Ludhiana, Regional Research Station, Kapurthala, Krishi Vigyan Kendra, Kheri during spring (first fortnight of March 2019) and *kharif* (mid May 2019). The test genotypes were planted in the alpha lattice design with three replications each. A plot of three rows of three-meter-length were sown for each genotype with row-to-row and plant-to-plant spacing of 30 cm and 15 cm, respectively in each replication at each location. Table 2 represents mean yield of these genotypes at given locations during respective seasons.

The data for yield was recorded for each ABL and was analyzed for the estimation of genetic variance-covariance for environment using the model developed by Oakey *et al.* (2006) and Burgueño *et al.* (2007) in Microsoft excel 2017. Information from relatives through COP *i.e*., $2[f\,ii']$ among half and full-sib lines was estimated as:

$$fxy\ (FS) = \frac{1}{4}\left[\frac{1}{2}(1+F_A) + 2\,f_{AB} + \frac{1}{2}(1+F_B)\right] \text{ for full sibs}$$

$$fxy\ (HS) = \frac{1}{4}\left[\frac{1}{4}(1+F_A) + 2\,f_{AB} + \frac{1}{4}(1+F_B)\right] \text{ for half sibs}$$

Where,

Individual X and Y are full sibs (FS) or half sibs (HS) if they both have same parents A and B or have one common parent.

The variance-covariance matrix of additive genetic effect was obtained from COP multiplied by the population additive genetic variance, σ^2_a. Mixed model equations (MME) combining the genetic main effects and genetic × environment interaction effects for fitting the data from g genotypes, (i=1,2,... ...,g), s site (j=1,2,... ...,s) and r replicated (in each site) using the Ã and A matrices (both of dimensions g × g) can be written as:

$$Y = Xb + Z_r r + Z_{g1}(a_1 + i_1) + Z_{ge}(ae + ie) + E$$

Where,

X, Z_r, Z_g and Z_{ge} are the design matrices for fixed effects of sites, random effects of replicates within sites, genotype(s) ge, respectively. Vector b denotes the fixed effects of sites and vectors. r, a, i, ie and E contain random effects of replicates within sites, additive, additive × additive, additive × environment interaction, additive × additive × environment interaction and residuals respectively and are assumed to be random and normally distributed with zero mean vectors and variance-covariance matrices R, G_a, G_i, G_{ae}, G_{ie} and N, respectively, such that:

$$\begin{bmatrix} r \\ a \\ i \\ ae \\ ie \\ E \end{bmatrix} \sim N \left(\begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix} \begin{matrix} R & 0 & 0 & 0 & 0 & 0 \\ 0 & G_a & 0 & 0 & 0 & 0 \\ 0 & 0 & G_i & 0 & 0 & 0 \\ 0 & 0 & 0 & G_{ae} & 0 & 0 \\ 0 & 0 & 0 & 0 & G_{ie} & 0 \\ 0 & 0 & 0 & 0 & 0 & E \end{matrix} \right]\right)$$

Variance-covariance matrices R and N are assumed to have a simple variance component structure, as defined for MME.

Assuming independence between vectors a and i, partitioning of total genetic effect g has normal distribution with mean zero and variance-covariance Gg= Ga + Gi, where the variance-covariance matrix of the additive, (G_a) and additive × additive main effects, (G_i), are modelled as $G_g = \sigma^2_a$

A, and Gi= σ_{aa}^{2} $\tilde{A}$. The unstructured variance-covariances are transformed to heterogeneity of within environment genetic variance (CSH model), in which case Σ_{g1} or Σ_{ge} has structure:

$$\{diag\ (\sigma_{aj})\ [(1-\rho)\ I_s + \rho j_s]\ (\sigma_{aj})\} \otimes A$$

$$\begin{bmatrix} \sigma^2_{ae1} & \rho_{12}\sigma_{ae1}\sigma_{ae2} & \cdot & \cdot & \cdot & \rho_{1s}\sigma_{ae1}\sigma_{aes} \\ \rho_{12}\sigma_{ae2}\sigma_{ae1} & \sigma^2_{ae1} & \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot & \cdot & \cdot \\ \rho_{1s}\sigma_{aes}\sigma_{ae1} & \cdot & \cdot & \cdot & \cdot & \sigma^2_{aes} \end{bmatrix} \otimes A$$

Similarly, other matrices $Z_{ge}ie$, $Z_{g}i$ and $Z_{g}e$ were also obtained.

The solution for the vector of fixed site effects, $\widehat{b}$ and vector of random effects of replicates within sites $\widehat{r}$; additive $\widehat{a}$; additive × additive $\widehat{i}$; additive × environment (G*ae*) $\widehat{ae}$ and additive × additive × environment (G*ie*) interaction $\widehat{ie}$ were obtained following Henderson (1975).

$$\begin{bmatrix} \beta \\ r \\ a_1 \\ i_1 \\ ae \\ ie \\ E \end{bmatrix} = \begin{bmatrix} X'R^{-1}X & X'R^{-1}Z_r r & X'R^{-1}Z_{a1}a & X'R^{-1}Z_{i1}i & X'R^{-1}Z_{ae}ae & X'R^{-1}Z_{ie}i & X'R^{-1}Z_e E \\ Z_r r'R^{-1}X & Z_r r'R^{-1}Z_r r & Z_r r'R^{-1}Z_{a1}a & Z_r r'R^{-1}Z_{i1}i & Z_r r'R^{-1}Z_{ae}ae & Z_r r'R^{-1}Z_{ie}i & Z_r r'R^{-1}Z_e E \\ Z_{a1}a'R^{-1}X & Z_{a1}a'R^{-1}Z_r r & Z_{a1}a'R^{-1}Z_{a1}a & Z_{a1}a'R^{-1}Z_{i1}i & Z_{a1}a'R^{-1}Z_{ae}ae & Z_{a1}a'R^{-1}Z_{ie}i & Z_{a1}a'R^{-1}Z_e E \\ Z_{i1}i'R^{-1}X & Z_{i1}i'R^{-1}Z_r r & Z_{i1}i'R^{-1}Z_{a1}a & Z_{i1}i'R^{-1}Z_{i1}i & Z_{i1}i'R^{-1}Z_{ae}ae & Z_{i1}i'R^{-1}Z_{ie}i & Z_{i1}i'R^{-1}Z_e E \\ Z_{ae}ae'R^{-1}X & Z_{ae}ae'R^{-1}Z_r r & Z_{ae}ae'R^{-1}Z_{a1}a & Z_{ae}ae'R^{-1}Z_{i1}i & Z_{ae}ae'R^{-1}Z_{ae}ae & Z_{ae}ae'R^{-1}Z_{ie}i & Z_{ae}ae'R^{-1}Z_e E \\ Z_{ie}i'R^{-1}X & Z_{ie}i'R^{-1}Z_r r & Z_{ie}i'R^{-1}Z_{a1}a & Z_{ie}i'R^{-1}Z_{i1}i & Z_{ie}i'R^{-1}Z_{ae}ae & Z_{ie}i'R^{-1}Z_{ie}i & Z_{ie}i'R^{-1}Z_e E \\ Z_e E'R^{-1}X & Z_e E'R^{-1}Z_r r & Z_e E'R^{-1}Z_{a1}a & Z_e E'R^{-1}Z_{i1}i & Z_e E'R^{-1}Z_{ae}ae & Z_e E'R^{-1}Z_{ie}i & Z_e E'R^{-1}Z_e E \end{bmatrix}^{-1} + \begin{bmatrix} X'R^{-1}y \\ Z_r r'R^{-1}y \\ Z_{a1}a'R^{-1}y \\ Z_{i1}i'R^{-1}y \\ Z_{ae}ae'R^{-1}y \\ Z_{ie}i'R^{-1}y \\ Z_e E'R^{-1}y \end{bmatrix}$$

The genetic gain-based heritability (narrow sense) for individual genotypes was estimated as per method given by Oakey *et al.,* (2006).

RESULTS AND DISCUSSION

Combining ability refers to the relative ability of a genotype to transfer the desirable performance to its crosses. It is one of the powerful tools available to estimate the combining ability effects and in the selection of desirable parents and crosses for exploiting heterosis (Sarker *et al.* 2002; Muhammad *et al.* 2007). Since, the potential for being a good donor is primarily attributed by additive effects or breeding value, it is important to separate these effects from epistatic genetic effects. The partitioning of genotypic values

Table 1: List of advanced breeding lines (ABL) used for evaluating breeding values to be used as parents in crossing program.

ABL	Pedigree
CGL-01	(M-522 × M-13)-F_1-F_2-1-2-3-1-B
CGL-02	(M-522 × M-13)-F_1-F_2-1-2-5-2-B
CGL-03	(M-522 × M-13)-F_1-F_2-6-4-3-1-B
CGL-04	(M-522 × M-13)-F_1-F_2-7-4-3-2-B
CGL-07	(M-522 × BAU-13)-F_1-F_2-1-1-3-2-B
CGL-08	(M-522 × BAU-13)-F_1-F_2-1-8-6-2-B
CGL-11	(M-522 × BAU-13)-F_1-F_2-11-4-3-2-B
CGL-13	(M-522 × BAU-13)-F_1-F_2-15-1-8-7-B
CGL-14	Mutant of M-522-M_2-2-3-B
CGL-20	Mutant of M-522-M_2-2-10-B
CGL-22	Mutant of M-522-M_2-8-4-1-B
CGL-23	Mutant of M-522-M_2-9-3-B
CGL-27	(PBS-29078 × ICGV-00440)-F_7-1-B
CGL-29	(PBS-29078 × ICGV-00440)-F_7-9-B
CGL-33	(ICGV-97079 × *GG*-20)-F_6-1-1-B
CGL-35	(ICGV-97079 × *GG*-20)-F_6-1-6-B
CGL-36	(ICGV-97079 × *GG*-20)-F_6-1-2-B
CGL-37	(ICGV-97079 × *GG*-2)-F_6-1-6-B
CGL-39	(ICGV-97079 × *GG*-2)-F_6-2-1-B
CGL-40	(ICGV-97079 × *GG*-2)-F_6-2-7-B
CGL-46	(TG-40 × ICGV-97079)-F_6-1-1-B
CGL-48	(ICGV-97097 × DH-3-30)-F_5-2-2-1-B
CGL-49	(ICGV-97097 × DH-3-30) -F_5-2-2-8-B
CGL-50	(ICGV-97097 × DH-3-30) -F_5-4-1-2-B
CGL-53	(ICGV-97097 × DH-3-30)-F_5-12-1-13-B
CGL-58	(ICGV-97079 × MH-4)-F_5-1-1-4-B
CGL-61	(ICGV-97079 × MH-4)-F_5-1-1-4-B
CGL-62	(ICGV97079 × MH-4)-F_5-1-4-4-B
CGL-63	(ICGV97079 × MH-4)-F_5-7-2-3-B
M-13	Selection from 'NC-13'
M-522	PG-1 × F334-AB-14
GJG (HPS-1)	JSP-21 × VG-5
J-87	-
Raj mig-3	-
Mallika	(ICGV-88386 × ASHFORD) × ICGV-95172-F_2-B1-B1-B3-B1
SG-99	ICGV-86829 × ICGV-87160 {ICG(FDRS)-10}
TG-37A	TG-25 × TG-26
M-548	M-37 × Blanco Puro White
TAG-24	Selection from TGS-2 (TG-18A × M-13) × TGE-1 (Tall mutant × TG-9)
Gangapuri	Selection from local strain

Table 1: Continue...

Table 1: Continue...

Table 2: Mean pod yield of 40 confectionery groundnut lines across seasons: Spring and *Kharif* at locations: Ludhiana, Kheri and Kapurthala.

Genotype	Spring			Mean		*Kharif*			Mean		Overall phenotypic mean	
	Ludhiana	Kheri	Kapurthala			Ludhiana	Kheri	Kapurthala				
CGL-01	3655	3973	2702	3443	**16**	2566	2551	2057	2391	**18**	2917	**15**
CGL-02	2724	2922	3625	3090	**20**	2136	2482	2211	2276	**22**	2683	**21**
CGL-03	2869	3002	3058	2976	**22**	1987	1975	2656	2206	**24**	2591	**23**
CGL-04	3731	4154	3701	3862	**8**	2919	2902	2879	2900	**7**	3381	**6**
CGL-07	3331	3258	3304	3298	**18**	2580	2565	2352	2499	**15**	2898	**17**
CGL-08	2901	3576	2879	3119	**19**	2253	2240	2326	2273	**23**	2696	**20**
CGL-11	4359	4790	4324	4491	**2**	3103	3289	3022	3138	**5**	3814	**3**
CGL-13	2860	3400	2842	3034	**21**	2341	2331	2400	2357	**20**	2696	**19**
CGL-14	3572	3793	3553	3639	**11**	2768	2544	2820	2711	**12**	3175	**14**
CGL-20	3280	3501	3258	3346	**17**	2196	2185	1763	2048	**26**	2697	**18**
CGL-22	4244	4495	4134	4291	**4**	3423	3482	3516	3474	**1**	3882	**2**
CGL-23	4231	4850	4446	4509	**1**	3403	3084	3522	3336	**2**	3923	**1**
CGL-27	2751	2966	2567	2761	**26**	2435	2212	2446	2364	**19**	2563	**25**
CGL-29	2314	2773	2296	2461	**32**	1516	1507	1500	1508	**36**	1984	**32**
CGL-33	2695	2946	2673	2771	**25**	2378	2364	2461	2401	**17**	2586	**24**
CGL-35	3547	3822	3518	3629	**15**	3024	3006	3130	3053	**6**	3341	**8**
CGL-36	2494	2495	2475	2488	**30**	2077	2066	2048	2064	**25**	2276	**27**
CGL-37	3630	3952	3598	3727	**9**	2811	2645	2921	2792	**10**	3259	**12**
CGL-39	2622	2829	2253	2568	**29**	1724	1712	1895	1777	**29**	2173	**30**
CGL-40	2096	2371	2075	2181	**37**	1543	1531	1617	1563	**33**	1872	**36**
CGL-46	1785	1914	1771	1823	**39**	1264	1257	1310	1277	**39**	1550	**39**
CGL-48	2331	2590	2307	2409	**33**	1330	1318	1888	1512	**35**	1961	**34**
CGL-49	3677	4333	3647	3886	**7**	2717	2834	2812	2788	**11**	3337	**10**
CGL-50	4292	4028	4258	4193	**5**	2587	2572	2678	2612	**14**	3402	**5**
CGL-53	2853	3101	2830	2928	**24**	2405	2391	2489	2428	**16**	2678	**22**
CGL-58	2276	2522	2258	2352	**34**	1519	1509	1572	1533	**34**	1942	**35**
CGL-61	2679	3497	2658	2945	**23**	1985	1973	2054	2004	**27**	2474	**26**
CGL-62	2564	2798	2543	2635	**28**	1840	1829	1527	1732	**30**	2184	**29**
CGL-63	1638	1912	1802	1784	**40**	1243	1236	1287	1255	**40**	1520	**40**
M-13	2034	2257	2369	2220	**36**	1386	1688	1435	1503	**37**	1861	**37**
M -522	2175	2271	2531	2326	**35**	1623	1303	1979	1635	**31**	1980	**33**
GJG(HPS-1)	2591	2681	2717	2663	**27**	1389	1685	1828	1634	**32**	2148	**31**
J-87	4332	4641	4295	4423	**3**	3165	3143	3289	3199	**3**	3811	**4**
Raj-Mig 3	2403	2612	2384	2466	**31**	2046	2033	1757	1945	**28**	2206	**28**
Mallika	3593	3667	3340	3533	**13**	2975	3259	3190	3141	**4**	3337	**9**
SG-99	3971	4317	3865	4051	**6**	2612	2597	2704	2637	**13**	3344	**7**
TG-37A	3655	3860	3637	3717	**10**	2712	3151	2760	2874	**8**	3296	**11**
M-548	3433	3679	3406	3506	**14**	3073	2308	3181	2854	**9**	3180	**13**
TAG-24	3403	3706	3376	3495	**15**	2309	2295	2389	2331	**21**	2913	**16**
Gangapuri	2038	1997	2024	2020	**38**	1456	1440	1136	1344	**38**	1682	**38**
Mean	3041	3306	3033	3127	2270	2262	2320	2284				

*Values in the bold represent ranking of genotypes with respect to phenotypic values.

into its components *i.e.*, additive, additive × additive and their interaction with environment calculated as per the model given by Burgueño *et al.* (2007) are depicted in Table 3. Groundnut being a self-pollinated crop, so here the non-additive effects i.e., G*i* and G*ie* reflect epistatic interactions, as inbreeding largely eliminated dominance effects (Oakey *et al.* 2006). From Table 3, line Mallika has low genotypic value but shows highest G*a* value. Similarly, line CGL-27 has quite low genotypic value, but the second highest G*a* value, vice-versa is the case with line CGL-23. These results,

Table 3: Additive and epistatic effects of 40 confectionery purpose groundnut genotypes for pod yield.

Genotype	BLUP genotypic values		Ga		Gae	G*i*	G*ie*	H^2	h^2	GA
CGL-01	2894	**17**	-299.01	**23**	810.25	-27.52	191.13	94.11	60.32	436.96
CGL-02	2659	**22**	-147.51	**19**	489.29	-209.68	307.65	93.94	63.58	471.43
CGL-03	2583	**24**	-146.01	**18**	189.39	-89.21	409.71	94.71	64.13	471.77
CGL-04	3435	**5**	-204.26	**22**	-762.53	982.14	1200.90	95.11	62.11	458.52
CGL-07	2898	**16**	111.24	**10**	79.59	113.31	374.86	94.51	57.65	530.32
CGL-08	2684	**21**	-50.09	**13**	262.28	-163.96	416.18	95.67	68.47	493.60
CGL-11	3825	**3**	186.07	**7**	-195.88	61.24	1554.78	92.83	44.97	547.34
CGL-13	2686	**20**	-100.71	**16**	162.12	105.46	299.86	96.26	71.61	482.08
CGL-14	3196	**10**	-32.84	**12**	-211.44	471.84	749.01	95.35	64.89	497.53
CGL-20	2687	**19**	116.64	**9**	413.50	-786.22	724.05	94.26	55.34	531.55
CGL-22	3869	**2**	129.13	**8**	216.92	979.21	324.76	95.53	59.27	534.39
CGL-23	3926	**1**	60.97	**11**	37.42	656.86	951.69	95.06	61.46	518.88
CGL-27	2316	**27**	616.86	**2**	745.87	-1281.25	15.21	99.03	89.84	645.38
CGL-29	2070	**32**	-632.14	**29**	-1264.25	173.33	1573.61	97.03	76.64	361.15
CGL-33	2554	**25**	-171.59	**21**	122.37	297.84	86.38	99.30	92.53	465.95
CGL-35	3154	**13**	-406.58	**25**	1037.77	341.61	-37.98	99.06	90.36	412.48
CGL-36	2598	**23**	257.08	**4**	-439.45	475.72	85.73	99.82	97.15	563.50
CGL-37	3187	**11**	-1058.00	**36**	1155.39	1030.02	-159.50	97.03	77.09	264.23
CGL-39	2192	**29**	-1079.23	**37**	-121.48	688.59	485.35	96.87	75.73	259.40
CGL-40	1979	**34**	-763.68	**31**	-674.22	713.18	484.16	97.19	78.87	331.21
CGL-46	1611	**35**	-857.21	**32**	-237.87	245.42	241.37	97.25	79.78	309.93
CGL-48	1960	**40**	-903.16	**33**	111.74	-42.98	574.88	95.93	69.32	299.47
CGL-49	3347	**7**	-943.51	**34**	-109.68	1093.96	1086.74	95.60	67.53	290.29
CGL-50	3391	**6**	-1317.05	**40**	608.96	1198.96	681.44	95.41	66.13	205.28
CGL-53	2708	**18**	-345.19	**24**	-87.75	719.50	202.34	97.52	78.34	426.45
CGL-58	1958	**36**	-1052.94	**35**	-94.19	372.80	513.10	94.64	77.64	265.38
CGL-61	2445	**26**	-1255.87	**39**	665.85	589.63	225.90	96.56	75.21	219.20
CGL-62	2171	**30**	-1171.78	**38**	280.11	425.18	418.24	96.96	77.21	238.34
CGL-63	1623	**39**	-655.83	**30**	-444.92	217.31	286.88	96.99	77.83	355.75
M-13	1889	**37**	-454.62	**27**	-181.25	-130.23	436.45	97.03	78.59	401.54
M-522	1985	**33**	-56.33	**14**	27.71	-619.75	414.59	93.98	59.95	492.18
GJG(HPS-1)	2158	**31**	-446.16	**26**	-74.25	-360.08	819.56	97.07	77.20	403.47
J-87	3807	**4**	244.43	**5**	219.99	279.89	843.59	96.66	74.93	560.63
Raj-Mig 3	2218	**28**	-159.98	**20**	-8.90	-36.33	204.36	97.77	82.60	468.59
Mallika	3123	**14**	1276.80	**1**	611.64	-1014.48	30.36	99.12	88.36	795.56
SG-99	3346	**8**	-115.33	**17**	94.56	-172.59	1319.79	96.48	73.00	478.75
TG-37A	3287	**9**	281.29	**3**	199.65	164.70	422.65	97.19	78.99	569.01
M-548	3172	**12**	240.11	**6**	180.16	130.79	402.23	96.91	79.35	559.64
TAG-24	2905	**15**	-59.99	**15**	285.39	-203.23	664.21	96.61	74.10	491.35
Gangapuri	1721	**38**	-486.66	**28**	-138.22	-112.72	239.01	98.07	82.49	394.25
Mean	2705.40		-296.32		99.04	181.96	501.63	96.41	73.26	437.57
Overall fixed environmental effects						2219.11				

*Values in the bold represent ranking of genotypes with respect to BLUP genotypic values and additive effects, Ga: Additive effects, Gae: Additive × environment interaction, Gi: Epistatic effects and Gie: epistasis × environment interaction.

hence, indicate lines having high breeding values does not have high commercial value (Burgueño *et al.* 2007). Secondly, although lines Mallika and CGL-27 show high G*a* value but also show moderate to high G*ae* values. Hence, subdivision of environments is needed for exploiting this interaction of these lines in specific environments to maximize the overall genetic gains. These observations are in agreement with the findings of Burgueño *et al.* (2007). Lines CGL-36 and CGL-11 although have low G*a* value than Mallika and GL-27 but show negative value for G*ae* (Table 3). Here, cross can be attempted between lines with overall high genetic effects, for example CGL-11 having both overall high genotypic value and G*a* with negative G*ae* (Table 3) and CGL-36 with overall high additive effects and negative G*ae*, *i.e.*, crossing good × good to maximize overall genetic gains (Burgueño *et al.* 2007).

CONCLUSION

Overall high genetic value of a line may not be an indicator of its breeding potential, as genetic value is contributed by both additive and non-additive effects. Hence, partitioning of these effects into its components and their interaction with environment is necessary to assess reliable potential of lines for their suitability as parents.

Conflict of interest: None.

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