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# BLUP Estimation and Genotype Stability in *Arachis hypogaea* L. Variety Testing using Mixed Model Equations

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## ABSTRACT

**Background:** One of the major goals of plant breeding is the selection of high yielding superior cultivars having wide or specific adaptation. However, there is a fluctuation in the annual production due to the sensitive behaviour of the genotypes under different environmental conditions referred to as Genotype by Environment Interaction (GEI). The current study aimed to study the contribution of GEI for the adaptation of groundnut lines for spring and/or *kharif* season.

**Methods:** To assess the contribution of GEI, Multi-Environment Trials (METs) were conducted for 40 confectionery purpose groundnut genotypes at $F_9$ generation along with checks, across three locations for two seasons (spring and *kharif*). The contribution of environmental effects, genotypic values and genotype × environment interaction values were obtained from genotypic variance-covariance matrix $Gi = \Sigma_9 \otimes A$ using mixed models (MM) in Best linear unbiased predictions (BLUPs). The pooled data was first partitioned into fixed effects of sites across the seasons and BLUP genotypic values (G*gge*). The BLUP genotypic values are further partitioned into genetic value (G*g*) and their interaction with the environment (G*ge*) for the adaptability of genotypes across seasons.

**Result:** The results of MET revealed the presence of significant crossover interaction. The demarcation of advance breeding lines for adaptability across the environment as well as for season specific adaptation was done for variety testing. Genotypes having moderate to high G*ge* values along with high G*g* values in spring than *kharif*, owing to their better performance during the spring season. CGL-11, CGL-23 and CGL-04 were the highest yielding genotypes, with quite high G*ge* values. This is due to the more favourable environmental conditions interacting positively with genotypes during the spring. Thus, the high G*g* value(s) of genotype(s) alone is not a capable factor for commercialization as G*ge* value is the deciding factor for the adaptability for the targeted season.


**Key words:** BLUPs, Genetic effect, Genotypic value, Groundnut, Mixed model.

## INTRODUCTION

Domesticated groundnut (*Arachis hypogaea* L.) is an important self-pollinating, tropical legume mainly grown for oil production in more than 100 countries. Asia is the major groundnut producing region with China being the major contributor (17.39 million tons) followed by India (6.6 million tons) (FAOSTAT, 2018). However, there is a fluctuation in the annual production due to the sensitive behaviour of the genotypes to different environmental conditions (Mekontchou *et al*., 2006), referred as Genotype by Environment Interaction (GEI). Since, in plant breeding, high yield is a major goal, it is important to select superior cultivars having wide or specific adaptation, which can be tested by its degree of interaction with different environments (Hardwick *et al*., 1972; Finlay and Wilkinson, 1963). For this, Multi-Environment Trials (METs) can be used, which provide an estimate of the overall stability and adaptability of the genotype(s), along with GEI. The statistical models developed earlier, for studying GEI were based on the two-way fixed-effects or random-effects models (Cornelius *et al*., 1996; Cornelius and Crossa, 1999) assuming sites to be independent considering the pairwise covariances between sites be zero and variances within sites, be equal (Crossa *et al*., 2001; Cornelius *et al*., 2001). These models further assume the spatial independence of individual field plot errors in each site and the genotypes to be unrelated. However, these assumptions are not realistic as related genotypes *i.e.,* full-sibs, half-sibs, sister lines tend to be more alike than unrelated genotypes. As a result, more complex and informative mixed linear models have been proposed for efficient data analysis. Linear model underlying Best Linear Unbiased Predictors (BLUP) and best linear unbiased estimates (BLUE) is called mixed model because it includes both fixed and random effects. The various advantages associated with these models involve efficient handling of unbalanced or incomplete data, *i.e*., not all lines or genotypes are tested in all environments, ability to assume some effects for example, variety and/or environment to be random than as fixed effect (Smith *et al.,* 2005).

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The general linear mixed model can easily accommodate covariances among observations. The mixed model handles correlated data by incorporating random effects and estimating their associated variance components to model variability over and above the residual error (Wolfinger and Tobias, 1998). Mixed models assume some effects to have arisen from the distribution of random-effects, implying the presence of a broad population of genetic effects and the samples being the realized values from that population, which can be predicted by BLUPs (Henderson, 1975). The analysis of metric data based on mixed linear model can be of the form.

$$y = X\beta + Z\mu + e$$

Where,

y = Vector of observations.

β and μ = Vectors of fixed and random effects, respectively.

X and Z = Associated design matrices.

e = Residual vector.

The random effects are assumed to have a distribution as u ~ *MNV* (0, G) and e ~ *MNV* (0, R) with *MNV* as multivariate normal distribution with mean vector μ and variance co-variance matrix V (Piepho *et al*., 2008). For variety testing and development of new varieties genotype effects are often considered as fixed effects thus becoming a part of β in the mixed model. But, when genotypes are considered to be random effects, the genotypic effects become a part of u and thus, estimated by BLUP. Smith *et al*. (2005) argued that genotype effects should be specified as random in a statistical mixed model because this: (1) minimizes selection errors when identifying the best genotypes, (2) provides more realistic estimates of genotype performance (predictions of genetic gain) and (3) allows a valid analysis of data combined across stages/generations of selection. The choice to classify variety effects as fixed or random depends upon the aim and the properties of the two estimation procedures *i.e*., empirical best linear unbiased prediction (E-BLUP) for random effects and best linear unbiased estimates (E-BLUE) for fixed effects considered for the analysis (Smith *et al.,* 2005). If the analysis aims to identify the best variety out of those under consideration, then, the variety effect should be considered random, implying the use of BLUPs during the early stages of the selection program. However, the same can be considered as a fixed effect at later stages of selection or, if the aim is to determine the difference between specific pair of varieties, as BLUP of a specific difference is biased and hence will be inappropriate to use (Federer 1997; Smith *et al.,* 2005). When, genotypic main effects are taken as random the mixed model can be defined as:

$$\mu_{ij} = \mu + G_i + E_j + \varepsilon_{ij}$$

$$G_i \sim N(0, \sigma^2_G) \text{ and } \varepsilon_{ij} \sim N(0, \sigma^2_\varepsilon)$$

The model has two variance components, one corresponding to the random genotypic main effects ($\sigma^2_G$) and the other *i.e*., $\sigma^2_\varepsilon$ corresponding to the residual, that involves true GEI and error (Malosetti *et al*., 2013).

In plant breeding, a breeder as to make selection among a large set of candidate genotypes and thus, it is important to make phenotypic selection based on the estimated genotypic values for varietal testing and commercialization (Piepho *et al*., 2008). BLUPs can serve as a great tool to select the best individuals as it maximizes the correlation of true genotypic values and the predicted genotypic values (Searle *et al*., 1992). Hence, in the present investigation, the phenotypic values are partitioned into genetic value (G*g*) and their interaction with environments (G*ge*) using mixed model equations (MME) in BLUPs as suggested by Crossa *et al.* (2006) including co-ancestry of parents (COP) to elucidate precise estimates of genetic values vis-à-vis their environmental interactions.

## MATERIALS AND METHODS

Experimental material: Due to high marketing avenues and mounting demand of table purpose groundnut, Punjab Agricultural University, Ludhiana geared up research programme to breed for confectionery groundnut since 2011-12. Under this program, advanced breeding material was generated through pedigree breeding method using the parental lines developed by The International Crops Research Institute for the Semi-Arid Tropics, Patancheru, India (ICGV series), Bhaba Atomic Research Centre (BARC), Trombay (TG-lines) and various state agricultural universities such as GJG- and GG-lines from Junagadh Agricultural University (JAU), Junagadh, DH-lines from University of Agricultural Sciences (UAS) Dharwad. From this material, a set of 40 advanced breeding lines (ABL) at $F_9$ generation, comprising full sibs (having the same male and female parents) and half sibs (individuals that have one parent in common) were used in the present study (Table 1).

### Experimental design

Three released varieties J-87, SG-99 and TG-37A were used along these test lines as checks. 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. The lines were grown across three locations in Punjab state of India *viz*., Ludhiana, Kheri and Kapurthala for two seasons spring (mid-March to June) and *kharif* (first fortnight of July to October). The *kharif* season (main crop season) accounts for about 80% of the total groundnut production (Vijaya, 2007). Monsoon variations cause major fluctuations in groundnut production in India. Groundnut is grown in different cropping systems like sequential, multiple and intercropping (Basu and Ghosh, 1995). If irrigation facilities are available and fits in cropping pattern, groundnut can be grown during January to May as a spring or summer crop as well. Spring cultivation of groundnut is taken in the states of Uttar Pradesh, Punjab and West Bengal *etc.* (March to May). The two seasons vary in their weather parameters such as temperature, humidity and

rainfall (Table 2a,b). Abiotic stresses such as variation in rainfall (Sindagi and Reddi, 1972) are prevalent during spring season. While, biotic stresses are such as disease incidences are prevalent during *kharif* season giving differential response of genotypes with diverse genetic background.

### Statistical analysis

The variance-covariance matrix of additive genetic effect was obtained from COP multiplied by the population additive genetic variance, $\sigma_a^2$. Genotypic values and genotypic × environment interaction was obtained from genotypic variance-covariance matrix $Gi = \Sigma_g \otimes A$ using mixed models (MM) in BLUPs as suggested by Crossa *et al*. (2006) *i.e*.,

$$Gi = \Sigma_g \otimes A = \begin{bmatrix} \sigma^2_{a_1} & \rho_{12}\sigma_{a_1}\sigma_{a_2} & \cdots & \rho_{1s}\sigma_{a_1}\sigma_{a_s} \\ \rho_{12}\sigma_{a_1}\sigma_{a_2} & \sigma^2_{a_2} & \cdots & \cdot \\ \cdot & \cdot & \cdots & \cdot \\ \cdot & \cdot & \cdots & \cdot \\ \cdot & \cdot & \cdots & \cdot \\ \rho_{1s}\sigma_{a_s}\sigma_{a_1} & \cdot & \cdots & \sigma^2_{a_s} \end{bmatrix} \otimes A$$

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

$$R = \Sigma_r \otimes I_r = I_r = \begin{bmatrix} \sigma^2_{r_1} & 0 & \cdots & 0 \\ 0 & \sigma^2_{r_2} & \cdots & \cdot \\ \cdot & \cdot & \cdots & \cdot \\ \cdot & \cdot & \cdots & \cdot \\ \cdot & \cdot & \cdots & \cdot \\ 0 & \cdot & \cdots & \sigma^2_{r_s} \end{bmatrix} \otimes I_r \text{, and}$$

$$E = \Sigma_e \otimes I_{rg} = \begin{bmatrix} \sigma^2_{e_1} & 0 & \cdots & 0 \\ 0 & \sigma^2_{e_2} & \cdots & \cdot \\ \cdot & \cdot & \cdots & \cdot \\ \cdot & \cdot & \cdots & \cdot \\ \cdot & \cdot & \cdots & \cdot \\ 0 & \cdot & \cdots & \sigma^2_{e_s} \end{bmatrix} \otimes I_{rg},$$

Where,

$I_r$ and $I_{rg}$ = Identity matrices of orders r and rg, respectively,

$\Sigma_r$ and $\Sigma_e$ = Replicate and residual variance matrices, respectively.

$\otimes$ = Kronecker (or direct) product operator.

The unstructured variance-covariances are transformed to heterogeneity of within environment genetic variance (CSH model), in which case $\Sigma_{gi}$ or $\Sigma_{ge}$ has structure:

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

## RESULTS AND DISCUSSION

### Analysis of variance

Analysis of variance (ANOVA) (Table 3) was performed to determine the significance of genotypes, environments and their interaction effect on the performance of the given

**Table 1:** List of the advanced breeding lines (ABL) of groundnut used for evaluation in Multi-Environment Trial (MET).

| 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 |

groundnut genotypes for the test traits: pod yield (kg/ha), pods per plant, shelling percentage, seeds per pod, sound mature kernels, 100 seed weight (g) and oil % under different crop durations *i.e*., spring and *kharif*. The combined analysis of variance showed the significant GEI, depicting the influence of environment on the test genotypes in terms of their response to agronomically important traits.

**Mean yield performance of genotypes**

The mean yield of the genotypes is presented in Table 4. The mean yield of genotypes ranged from 4509 kg/ha (CGL-23) to 1784 kg/ha-(CGL-63) and 3474 kg/ha (CGL-22) to 1255 kg/ha (CGL-63) during *kharif* season. The five top ranked lines for pod yield wereCGL-23 (4509 kg/ha) CGL-11 (4491 kg/ha), J-87 (4423 kg/ha), CGL-22 (4291 kg/ha) and CGL-50 (4193 kg/ha) during spring season. CGL-22 (3474 kg/ha) followed by CGL-23 (3336 kg/ha), J-87 (3199 kg/ha), Mallika (3141 kg/ha) and CGL-11 (3138 kg/ha), was highest yielding during *kharif* season. Genotypes M-13, Gangapuri, CGL-46 and CGL-63 had consistently low yield performance during both the seasons. All the genotypes had overall 36.87% higher productivity in the spring sown crop than, *kharif.* This variability in the yield reflects the overall influence of environmental conditions during growing seasons such as temperature, relative humidity and disease pressure. Thus, selection of genotypes based on their phenotypic performance alone may hinder varietal selection and recommendation, as it is not known whether the genotype or the environment is responsible for the interaction causing a change in the genotypic ranking.

**Stability analysis**

For estimating the adaptability of genotypes, the pooled data was partitioned into fixed effects of sites across seasons and BLUP genotypic values (G*gge*). The BLUP genotypic values are further partitioned into genetic value (G*g*) and their interaction with the environment (G*ge*) to assess the adaptability of genotypes across seasons (Table 5). The ranking of top ten genotypes based on their pooled G*g* values is CGL-22 followed by CGL-04, CGL-36,

**Table 2a:** Weather parameters during spring (2019) for: Temperature (°C), relative humidity (RH%) and rainfall (mm).

| Month | Temperature (°C) | | | Relative humidity (RH%) | | | Rainfall |
|---|---|---|---|---|---|---|---|
| | Maximum | Minimum | Mean | M | E | Mean | (mm) |
| March | 25 | 12 | 19 | 89 | 46 | 67 | 7 |
| April | 35 | 20 | 27 | 71 | 30 | 50 | 42 |
| May | 38 | 22 | 30 | 52 | 22 | 37 | 10 |
| June | 40 | 27 | 34 | 55 | 30 | 42 | 30 |
| Average | 35 | 20 | 27 | 67 | 32 | 49 | 89 |

(Source: Department of Climate Change and Agricultural Meteorology, Punjab Agricultural University, Ludhiana).

**Table 2b:** Weather parameters during *kharif* (2019) for: Temperature (°C), relative humidity (RH%) and rainfall (mm).

| Month | Temperature (°C) | | | Relative humidity (RH%) | | | Rainfall |
|---|---|---|---|---|---|---|---|
| | Maximum | Minimum | Mean | M | E | Mean | (mm) |
| July | 34 | 27 | 30 | 29 | 29 | 29 | 218 |
| August | 40 | 27 | 34 | 55 | 30 | 42 | 30 |
| September | 33 | 26 | 29 | 86 | 68 | 77 | 265 |
| October | 31 | 18 | 24 | 90 | 46 | 68 | 0 |
| Average | 34.5 | 24.5 | 29.25 | 65 | 43.25 | 54 | 513 |

(Source: Department of Climate Change and Agricultural Meteorology, Punjab Agricultural University, Ludhiana).

**Table 3:** Combined analysis of variance across six environments for the test characters of the groundnut test genotypes.

| Characteristics | | Pods per plant | Pod yield (kg/ha) | Shelling % | Seeds per pod | Sound mature kernels | 100 seed weight (g) | Oil % |
|---|---|---|---|---|---|---|---|---|
| Source | df | Mean sum of squares | | | | | | |
| Replication | 12 | 4.05 | 0.04 | 11.71 | 0.01 | 16.96 | 36.79 | 2.38 |
| Genotypes | 39 | 351.25** | 8.25** | 206.81** | 0.61** | 1324.88** | 1059.50** | 24.29** |
| Environment | 5 | 171.48** | 26.75** | 346.43** | 0.01** | 523.12** | 1131.29** | 151.07** |
| Genotype × Environment | 195 | 11.32** | 0.16** | 74.26** | 0.02** | 41.18** | 141.49** | 6.10** |
| Error | 468 | 2.42 | 0.11 | 5.11 | 0.002 | 8.12 | 14.50 | 1.01 |

** significant at 0.01% level of probability.

CGL-23, J-87, TG-37A, CGL-53, M-548, CGL-14 and Mallika, but this ranking differs from the ranking with respect to G*gge* values (Table 5). Genotype CGL-23 has the highest G*gge* value followed by CGL-22 and CGL-11. Although CGL-22 ranks 2 with respect to G*gge* but ranks 1 with respect to G*g* value with low G*ge* value, thus performance of the line is not much affected by the environment, implying the genotype is the main contributing factor for the yield performance. Further, CGL-23 having the highest G*gge* value (rank 1) but has low G*g* value (rank 4) with quite high G*ge*, implying environment has a significant contribution for the yield performance of the genotype. Similarly,

**Table 4:** Mean pod yield (kg/ha) of 40 advanced breeding lines of groundnut along with the checks at three locations across seasons: Spring and *kharif* three locations.

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

(Values in the bold depict the ranking of the genotypes with respect to their mean yield during spring and *kharif* season).

genotype CGL-11 has high G*ge* value with low G*g* value but overall, third highest G*gge* value. Thus, these genotypes are adapted to particular season or environmental conditions. Certain genotypes such as CGL-01, CGL-02, CGL-03, CGL-08, CGL-20, CGL-27, CGL-35, CGL-37, CGL-46 CGL-48, CGL-50, CGL-58, CGL-61, CGL-62 had negative G*g* values, hence, these genotypes will contribute poorly for their overall yield even if environmental conditions contribute positively for the yield. J-87 (G*g*=524 kg/ha, G*ge*=1064 and G*gge*=1588) which was used as a

**Table 5:** Pooled genetic values (G*g*), genetic value-by-environment interaction (G*ge*) and BLUP genotypic values (G*gge*) for the advance breeding lines of groundnut.

| Genotype | G*g* | | G*ge* | G*gge* | |
|---|---|---|---|---|---|
| CGL-01 | -327 | 25 | 1001 | 675 | 17 |
| CGL-02 | -357 | 26 | 797 | 440 | 22 |
| CGL-03 | -235 | 22 | 599 | 364 | 24 |
| CGL-04 | 778 | 2 | 438 | 1216 | 5 |
| CGL-07 | 225 | 12 | 454 | 679 | 16 |
| CGL-08 | -214 | 21 | 678 | 464 | 21 |
| CGL-11 | 247 | 11 | 1359 | 1606 | 3 |
| CGL-13 | 5 | 15 | 462 | 467 | 20 |
| CGL-14 | 439 | 7 | 538 | 977 | 10 |
| CGL-20 | -670 | 35 | 1138 | 468 | 19 |
| CGL-22 | 1108 | 1 | 542 | 1650 | 2 |
| CGL-23 | 718 | 4 | 989 | 1707 | 1 |
| CGL-27 | -664 | 33 | 761 | 97 | 27 |
| CGL-29 | -459 | 29 | 309 | -149 | 32 |
| CGL-33 | 126 | 14 | 209 | 335 | 25 |
| CGL-35 | -65 | 18 | 1000 | 935 | 13 |
| CGL-36 | 733 | 3 | -354 | 379 | 23 |
| CGL-37 | -28 | 16 | 996 | 968 | 11 |
| CGL-39 | -391 | 27 | 364 | -27 | 29 |
| CGL-40 | -50 | 17 | -190 | -241 | 34 |
| CGL-46 | -612 | 32 | 4 | -608 | 40 |
| CGL-48 | -946 | 40 | 687 | -260 | 35 |
| CGL-49 | 150 | 13 | 977 | 1128 | 7 |
| CGL-50 | -118 | 19 | 1290 | 1172 | 6 |
| CGL-53 | 374 | 8 | 115 | 489 | 18 |
| CGL-58 | -680 | 37 | 419 | -261 | 36 |
| CGL-61 | -666 | 34 | 892 | 226 | 26 |
| CGL-62 | -747 | 38 | 698 | -48 | 30 |
| CGL-63 | -439 | 28 | -158 | -597 | 39 |
| M-13 | -585 | 30 | 255 | -330 | 37 |
| M -522 | -676 | 36 | 442 | -234 | 33 |
| GJG(HPS-1) | -806 | 39 | 745 | -61 | 31 |
| J-87 | 524 | 5 | 1064 | 1588 | 4 |
| Raj-Mig 3 | -196 | 20 | 195 | -1 | 28 |
| Mallika | 262 | 10 | 642 | 904 | 14 |
| SG-99 | -288 | 24 | 1414 | 1126 | 8 |
| TG-37A | 446 | 6 | 622 | 1068 | 9 |
| M-548 | 371 | 9 | 582 | 953 | 12 |
| TAG-24 | -263 | 23 | 950 | 686 | 15 |
| Gangapuri | -599 | 31 | 101 | -499 | 38 |
| Mean | -114 | | 601 | 486 | |
| Overall fixed environmental effects | | | 2219 | | |

The values in the bold depict the ranking of the genotype for their genetic value and BLUP genotypic values.

check had overall rank 4 for G*gge* value and rank 5 for G*g* value. The line had quite high G*ge* value indicating the significant contribution of the environmental effects for the yield, thus is adapted to particular season.

Table 6 represents the genetic values (G*g*), genotype-environment interaction (G*ge*) values and BLUP (G*gge*) genotypic values of lines across the seasons. During spring, genotype CGL-11, followed by CGL-23, CGL-04, CGL-22 and CGL-50 had the highest G*gge* value. During *kharif,* CGL-04, followed by CGL-23, CGL-11, CGL-22 and TG-37A had the highest G*gge*. On partitioning of G*gge* value, CGL-04 had the highest G*g* value (rank 1) during both season

**Table 6:** Genetic values (G*g*), genetic value-by-environment interaction (G*ge*) and BLUP genotypic values (G*gge*) for advanced breeding lines of groundnut.

| Genotype | Spring | | | | | *Kharif* | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | G*g* | | G*ge* | G*gge* | | G*g* | | G*ge* | G*gge* | |
| CGL-01 | 248 | 13 | 738 | 986 | 11 | -57 | 14 | -279 | -336 | 26 |
| CGL-02 | -811 | 38 | 837 | 26 | 28 | -1092 | 39 | 646 | -446 | 27 |
| CGL-03 | -277 | 26 | 546 | 269 | 22 | -339 | 22 | 214 | -125 | 20 |
| CGL-04 | 1439 | 1 | 155 | 1594 | 4 | 2129 | 1 | -621 | 1508 | 1 |
| CGL-07 | 273 | 11 | 410 | 683 | 17 | 145 | 8 | 91 | 236 | 13 |
| CGL-08 | -265 | 25 | 692 | 426 | 19 | -678 | 29 | 438 | -240 | 22 |
| CGL-11 | 543 | 6 | 1393 | 1936 | 1 | 107 | 9 | 835 | 942 | 3 |
| CGL-13 | -92 | 22 | 456 | 363 | 21 | -481 | 25 | 339 | -141 | 21 |
| CGL-14 | 591 | 5 | 495 | 1087 | 9 | 371 | 4 | 128 | 499 | 7 |
| CGL-20 | -440 | 29 | 1157 | 716 | 15 | -839 | 34 | 580 | -259 | 24 |
| CGL-22 | 868 | 3 | 685 | 1552 | 5 | -225 | 18 | 816 | 590 | 5 |
| CGL-23 | 900 | 2 | 962 | 1862 | 2 | 750 | 2 | 470 | 1220 | 2 |
| CGL-27 | -720 | 37 | 468 | -252 | 35 | -818 | 33 | 321 | -497 | 30 |
| CGL-29 | -353 | 27 | 385 | 32 | 27 | -616 | 27 | 41 | -574 | 31 |
| CGL-33 | 103 | 17 | 85 | 188 | 25 | 32 | 11 | 38 | 70 | 17 |
| CGL-35 | 97 | 18 | 605 | 702 | 16 | -18 | 13 | 385 | 366 | 10 |
| CGL-36 | 162 | 14 | -42 | 120 | 26 | 22 | 12 | -49 | -27 | 18 |
| CGL-37 | -176 | 23 | 1015 | 839 | 13 | -543 | 26 | 635 | 92 | 16 |
| CGL-39 | 133 | 15 | 119 | 252 | 23 | -92 | 16 | -164 | -256 | 23 |
| CGL-40 | -71 | 21 | -104 | -175 | 32 | -270 | 19 | -193 | -463 | 28 |
| CGL-46 | -571 | 31 | -29 | -600 | 40 | -625 | 28 | -147 | -772 | 37 |
| CGL-48 | -813 | 39 | 619 | -194 | 33 | -1069 | 38 | 261 | -808 | 39 |
| CGL-49 | 353 | 8 | 930 | 1282 | 8 | 78 | 10 | 410 | 488 | 9 |
| CGL-50 | 267 | 12 | 1278 | 1545 | 6 | -71 | 15 | 290 | 218 | 15 |
| CGL-53 | 326 | 10 | 82 | 408 | 20 | 331 | 5 | -61 | 270 | 12 |
| CGL-58 | -626 | 33 | 397 | -228 | 34 | -802 | 32 | 91 | -711 | 35 |
| CGL-61 | -598 | 32 | 840 | 242 | 24 | -879 | 35 | 411 | -468 | 29 |
| CGL-62 | -667 | 35 | 648 | -19 | 30 | -902 | 36 | 278 | -625 | 32 |
| CGL-63 | -424 | 28 | -162 | -587 | 39 | -473 | 24 | -225 | -698 | 34 |
| M-13 | -655 | 34 | 224 | -431 | 36 | -771 | 31 | 40 | -731 | 36 |
| M-522 | -917 | 40 | 473 | -444 | 37 | -1275 | 40 | 392 | -882 | 40 |
| GJG(HPS-1) | -686 | 36 | 708 | 22 | 29 | -927 | 37 | 281 | -647 | 33 |
| J-87 | 778 | 4 | 1014 | 1792 | 3 | 409 | 3 | 443 | 852 | 4 |
| Raj-Mig 3 | -252 | 24 | 151 | -102 | 31 | -305 | 20 | 8 | -297 | 25 |
| Mallika | 43 | 19 | 466 | 510 | 18 | -113 | 17 | 333 | 220 | 14 |
| SG-99 | 117 | 16 | 1342 | 1459 | 7 | -314 | 21 | 625 | 311 | 11 |
| TG-37A | 484 | 7 | 585 | 1069 | 10 | 264 | 6 | 254 | 518 | 6 |
| M-548 | 331 | 9 | 537 | 868 | 12 | 256 | 7 | 240 | 495 | 8 |
| TAG-24 | -67 | 20 | 905 | 838 | 14 | -461 | 23 | 391 | -70 | 19 |
| Gangapuri | -566 | 30 | 79 | -487 | 38 | -698 | 30 | -85 | -783 | 38 |
| Mean | -114 | | 601 | 486 | | -50 | | 554 | 504 | |
| Fixed effects | | | 2626 | | | | | 2333 | | |

The values in the bold depict the ranking of the genotype for their genetic value and BLUP genotypic values.

but, low and positive G*ge* during spring and negative G*ge* during *kharif.* This positive G*ge* is responsible for the high yield of CGL-04 during the spring season than *kharif.* Similarly, although genotype CGL-23 has rank 2 during both the seasons, but there is a significant difference on the G*gge* values: 1862 kg/ha and 1220 kg/ha during spring and *kharif,* respectively. The genotype has high G*g* and G*ge* value during the spring than *kharif,* thus, environment is a major contributing factor for the high yield of the genotype during spring. Similarly, other top-ranking genotypes with respect to their yield performance CGL-22, CGL-50, SG-99, CGL-49 and CGL-14 were found to be more adapted to spring season. Thus, spring is more favourable growing season as depicted from overall higher fixed effects (2626 kg/ha) than *kharif* (2333 kg/ha). These, results are in agreement with the released check variety J-87 which has been released for the spring season by Punjab Agricultural University, Ludhiana, Punjab in 2020 for commercial cultivation. J-87 had similar rank during both seasons, but with large difference in the G*gge* value 1792 kg/ha and 852 kg/ha during spring and *kharif,* respectively. This variety had high G*g*=778 kg/ha and G*ge*=1014 kg/ha value during spring season, but low G*g*=409 kg/ha and G*ge*=443 kg/ha during *kharif*. Similarly, another variety TG-37A having higher yield performance with higher G*ge* coupled with high G*g* values during spring has been released for commercial cultivation in 2019.

In plant breeding, Multi-Environment Trials (MET) are important as it allows the evaluation of genotype(s) under different environmental condition, which enables to assess and compare their response, overall stability and adaptation. Thus, best genotype(s) can be selected for a specific environment and across environments for further testing, but it is not easy because of the presence of Genotype by Environment Interaction (GEI). For sustainable agricultural system the adaptability of genotype(s) is of paramount importance for marginal farmers, as low GEI gives assurance for more guaranteed yield in the targeted environment. In the absence of GEI, means across environments can be used as indicator, however, in the presence of GEI, the use of means across environments ignores the fact that genotypes differ in their relative performance over environments (Voltas *et al*., 2002). In such situation, if genotype and environment means are used to predict the yield potential of the recommended cultivar(s), it will cause a failure of formal breeding to serve small resource-poor farmers in marginal fragile environments (Ceccarelli *et al*., 2006).

In Punjab, groundnut is mainly grown during the *kharif* season in an area of 1.3 thousand hectares (2018-19) but the prevailing cropping pattern of paddy-wheat is diverting some acreage to potato, green pea and other vegetable crops in spring season as these climatic conditions are favourable for high groundnut productivity, therefore characterization of germplasm for spring and *kharif* season is crucial to get maximum pod yield potential of groundnut as a third crop in paddy-green pea/another vegetable-spring groundnut pattern. The significant differential response of genotypes across the seasons, as implied by crossover interaction, recommended the evaluation of advance breeding lines in the target environment for variety testing for release of stable and adapted varieties to particular ecologies. The selection of candidature genotype(s) solely on the basis of phenotypic value will be misleading. Hence, the selection should be emphasised on genotypic values and its interaction with the environment. The conventional phenotypic values in the present study are sum of the fixed effects and BLUP genotypic values. BLUP serve as a great tool to select best individuals as it maximizes the correlation of true genotypic values and the predicted genotypic values (Searle *et al*., 1992). The partitioning of BLUP genotypic values specifies the contribution of genotypic value (*Gg*) and environmental effects (G*ge*) to the yield potential of the genotype. The change in the ranking of genotypes with respect to G*g* and G*gge* values indicates the differential response of genotype(s) across the seasons. These observations based on the ranking of genetic values are in agreement with the findings of Smith and Cullis (2018) and Crossa *et al*. (2006) as they have suggested that the random modelling gives more precise estimate of the genetic values. All the genotypes were found to have high BLUP genotypic values, which on partitioning showed the significant contribution of environment to the overall performance of the genotype, coupled with high genetic values. All the genotypes were found to have high genetic values along with moderate to high G*ge* value during the spring season, than during the *kharif* season in which they had low G*ge* value. Thus, the genotypes were found to be specifically adapted to spring season. Hu (2015) compared two statistical methods for analysing rape cultivar multilocation trials: separate ANOVA and BLUP. He found that BLUP provided more accurate and efficient predictions of location-specific genotype effects compared to separate ANOVA. The Pearson correlation of genotype prediction between locations was higher for BLUP and the average variance of differences between genotype estimates was lower for BLUP. These results suggest that BLUP is a more effective method for analyzing rape cultivar in multilocation trials which corresponds to the result of current study.

## CONCLUSION

The results of the study indicated that the high G*g* values of genotypes is alone not a capable factor for the commercialization as, G*ge* is the deciding factor for the adaptability to the targeted region. Hence, the selection should be emphasized on the high G*g* value coupled with low G*ge* value for wide adaptability or high G*g* with high G*ge* for specific season to harvest maximum yield potential of the genotype. This will ensure the optimum productivity for small scale farmers.

### Conflict of interest

All authors declare that they have no conflicts of interest.

## REFERENCES


Basu, M.S. and Ghosh, P.K. (1995). The Status of Technologies Used to Achieve High Groundnut Yields in India. In Achieving High Groundnut Yields. Patancheru, India: ICRISAT, pp 300.

Ceccarelli, S., Grando, S., Booth, R.H. (2006). International breeding programmes and resourcepoor farmers: Crop improvement in difficult environments. The International Center for Agricultural Research in the Dry Areas (ICARDA), Aleppo, Syria.

Cornelius, P.L., Crossa, J. (1999). Prediction assessment of shrinkage estimators of multiplicative models for multi-environment cultivar trials. Crop Science. 39: 998-1009. https://doi.org/10.2135/cropsci1999.0011183X003900040007x.

Cornelius, P.L., Crossa, J., Seyedsadr, M.S. (1996). Statistical Tests and Estimators of Multiplicative Models for Genotype-by-Environment Data. In: Genotype-by-Environment Interaction. [Kang, M.S., Gauch, H.G.J.R. (eds)], CRC Press, Boca Raton, pp 199-234.

Cornelius, P.L., Crossa, J., Seyedsadr, M.S., Liu, G. and Viele, K. (2001). Contributions to multiplicative model analysis of genotype-environment data. Statistical Consulting Section, American Statistical Association, Joint Statistical Meetings. 2001 Proceedings, American Statistical Association, Aug. 7, 2001 [CDROM]. Atlanta, GA.

Crossa, J., Burgueño, J., Cornelius, P.L. and McLaren, G. (2006). Modelling genotype x environment interaction using additive genetic covariances of relatives for predicting breeding values of wheat genotypes. Crop Science. 46: 1722-1733. https://doi.org/10.2135/cropsci2005.11-0427.

Crossa, J., van Eeuwijk, F., Vargas, M. and Cornelius, P.L. (2001). Linear, bilinear and linear-bilinear models for analyzing genotype 3 environment interaction. Statistical Consulting Section, American Statistical Association, Joint Statistical Meetings, Proceedings, American Statistical Association, CDROM.

FAOSTAT, (2018). Area, production and average yield of groundnut worldwide.

Federer, W.T. (1997). Recovery of interblock, intergradient and intervariety information in incomplete block and lattice rectangle designed experiments. Biometrics. 54(2): 471-781.

Finlay, K.W., Wilkinson, G.N. (1963). The analysis of adaptation in a plant breeding program. Australian Journal of Agricultural Research. 14: 742-754. https://doi.org/10.1071/AR9630742.

Hardwick, R.C. and Wood, J.T. (1972). Regression methods for studying genotype-environment interactions. Heredity. 28: 209-222. doi: 10.1038/hdy.1972.26.

Henderson, C.R. (1975). Best linear unbiased prediction under a selection model. Biometrics. 31: 423-447 https://doi.org/10.2307/2529430.

Hu, X. (2015). A comprehensive comparison between ANOVA and BLUP to valuate location-specific genotype effects for rape cultivar trials with random locations. Field Crops Res. 179: 144-49.

Malosetti, M., Ribaut, J.M., van Eeuwijk, F.A. (2013). The statistical analysis of multi-environment data: Modeling genotype-by-environment interaction and its genetic basis. Frontiers in Physiology. 4: 44. https://doi.org/10.3389/fphys.2013.00044.

Mekontchou, T., Ngueguim, M., Fobasso, M. (2006). Stability analysis for yield and yield components of selected peanut breeding lines (*Arachis hypogaea* L.) in the North province of Cameroon. Tropicultura. 24(2): 90-94.

Piepho, H.P., Mohring, J., Melchinger, A.E. and Buchse, A. (2008) BLUP for phenotypic selection in plant breeding and variety testing. Euphytica. 161: 209-228. doi:10.1007/s10681-007-9449-8.

Searle, S.R., Casella, G., McCulloch, C.E. (1992). Variance Components. John Wiley and Sons, New York.

Sindagi, S.S. and Reddy, B.S.G. (1972). Effect of Sowing Date and Rainfall Distribution on the Yield of Groundnut Crop. In: Proceedings of Drought Seminar, University of Agricultural sciences, Bangalore, India.

Smith, A.B. and Cullis, B.R. (2018). Plant breeding selection tools built on factor analytic mixed models for multi-environment trial data. Euphytica. 214: 143. doi: 10.1007/s10681-018-2220-5.

Smith, A.B., Cullis, B.R. and Thompson, R. (2005) The analysis of crop cultivar breeding and evaluation trials: An overview of current mixed model approaches. Journal of Agricultural Science. 143: 449-462. doi: https://doi.org/10.1017/S0021859605005587.

Vijaya, K.P. (2007). Agrometeorology and groundnut production. Chapter 13 B.

Voltas, J., Van, E.F., Igartua, E., García del Moral L.F., Molina-Cano, J.L. and Romagosa, I. (2002). Genotype by Environment Interaction and Adaptation in Barley Breeding: Basic Concepts and Methods of Analysis. In: Barley Science: Recent Advances from Molecular Biology to Agronomy of Yield and Quality. [Slafer, G.A., Molina-Cano, J.L., Savin, R., Araus, J.L. and Romagosa, I. (ed)], The Harworth Press Inc., New York. pp. 205-224.

Wolfinger, R.D., Tobias, R. (1998). Joint estimation of location, dispersion and random effects in robust design. Technometrics. 40(1): 62-71.