



ISSN (E): 2277-7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2022; 11(5): 2035-2039
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www.thepharmajournal.com

Received: 03-03-2022

Accepted: 08-04-2022

Bharath Kumar TK

M.Sc. Student, Department of Genetics and Plant Breeding, College of Sericulture, Chintamani, University of Agricultural Sciences, Bangalore, Karnataka, India

Venkataramana P

Professor and Dean, College of Sericulture, Chintamani, University of Agricultural Sciences, Bangalore, Karnataka, India

Ramanappa TM

Special Officer Seeds, GKVK Bangalore, Karnataka, India

Priyadarshini SK

Assistant Professor, Department of Genetics and Plant Breeding, College of Sericulture, Chintamani, University of Agricultural Sciences, Bangalore, Karnataka, India

Mohan Kumar NV

Assistant Professor, Department of Genetics and Plant Breeding, College of Sericulture, Chintamani, University of Agricultural Sciences, Bangalore, Karnataka, India

Corresponding Author:

Venkataramana P

Professor and Dean, College of Sericulture, Chintamani, University of Agricultural Sciences, Bangalore, Karnataka, India

Breeding potential of connected crosses involving tmv-2 as a common parent in groundnut (*Arachis hypogaea* L.)

Bharath Kumar TK, Venkataramana P, Ramanappa TM, Priyadarshini SK and Mohan Kumar NV

Abstract

TMV-2 is widely adaptable high yielding groundnut which is highly accepted for its climate resilience and pod and kernel characters. With an objective of developing high yielding, widely adaptable cultivars similar to TMV-2 type pods and kernels, three crosses were effected involving TMV-2 as female parent. Breeding potential of three crosses (TMV-2 × ICGV-91114, TMV-2 × TG-69 and TMV-2 × ICGV-00350) in F₅ generations were evaluated for ten quantitative traits. In the segregating generation as expected lot of variability was noticed for yield attributing traits like pods plant⁻¹, pod yield plant⁻¹, kernel yield plant⁻¹, branches plant⁻¹ among the segregating population of all the three crosses which was justified by the statistical significant mean sum of squares values and higher estimates of GCV and PCV. There was closeness among estimates of GCV and PCV which indicated less influence of environment on all the traits which was amply reflected by high broad sense heritability along with high expected GAM, suggesting involvement of additive gene action in controlling these traits. The comparative observation and estimates among the three crosses pointed that TMV-2 × ICGV-00350 is predicted to have better breeding potential.

Keywords: Breeding potential, Segregating generation, GAM, GCV and PCV

Introduction

Groundnut (*Arachis hypogaea* L.) is an important oilseed crop in the world as well as in India, in terms of both acreage and production. Groundnut stands fourth in global production of oil seeds after soybean, rapeseed, and sunflower with a total area of 26.71 million hectares, a total production of 46.45 million metric tones and an average productivity of 1686.8 kg/ha worldwide (Anon., 2019a)^[1]. India is the second largest producer of groundnut, after China. Over 60% of world groundnut production is used to produce oil for both edible and industrial use, while 40% is utilized for table purposes and as seed for the following season's sowing. Current productivity level of groundnut in Karnataka (0.73 t ha⁻¹) is less than half of the national average (1.8 t ha⁻¹) (Anon., 2019a)^[1]. TMV-2, the variety developed and released in 1940 (80 years back) is still ruling despite other varieties better than TMV-2 with pod yield. But this TMV-2 is still preferred by traders and oil mills for oil extraction due to its even-sized pods and kernels with high-quality oil. There is an immense demand for a variety with higher yield potential than TMV-2 but with similar pod and kernel type in order to close the gap between Karnataka's present groundnut productivity and the national average. It is well known fact that natural and/or generated genetic variability is a prerequisite for any crop improvement program which involves selection. The effectiveness of selection of superior plant/ genotype depends on the nature and magnitude of genetic variability present in the genetic material and the degree of heritability. Thus here we crossed lines which are best among available genotypes and forwarded till F₅ generation to give chance to that desirable meiotic recombination to get fixed in the populations of crosses TMV-2 × ICGV-91114, TMV-2 × TG-69 and TMV-2 × ICGV-00350 which were evaluated with an objective to study their breeding potential so that best parental combination is put forward for further selection and breeding.

Material and Methods

Material: The material for the present investigation consisted of F₅ populations of three connected crosses viz., TMV-2 × ICGV-91114, TMV-2 × TG-69 and TMV-2 × ICGV-00350 where, TMV-2 was the common female parent, which is comparatively low yielding but has desirable pod and kernel type.

The F₄ generation plants of these crosses were forwarded to F₅ generation and were evaluated on plant-to-row progeny basis in Randomized complete block design with two replications along with six checks viz., GKVK-5, KCG-6, TMV-2, ICGV-91114, GKVK-27 and K-6 during *rabi* 2020 with an inter row spacing of 30 cm and 10 cm intra row at an experimental field units of National Seed Project, UAS, GKVK, Bengaluru. The crop was raised by following all the agronomic practices as per the package of practices recommended for Eastern Dry Zone of Karnataka (Anon., 2019b) [2].

Data collection and computation: In F₅ generation data was recorded on 15 randomly selected plants from each of the progeny/ genotype and checks. The mean data of 15 plants was subjected to statistical analysis using WINDOSTAT 8.5 version. The genotypic and phenotypic co-efficient of variations was computed as suggested by Robinson *et al.*, (1949) [6]. Heritability and genetic advance were worked out as per the method outlined by Johnson *et al.*, (1955) [3]. The Analysis of variance was performed following Randomized complete block Design as suggested by Panse and Sukhatme, (1961) [5].

Criteria to assess breeding potential of crosses

The quantitative trait mean values, phenotypic coefficient of variation, absolute and standardized range (SR) and heritability and GAM were used as predictors to compare the three crosses and predict the breeding potential of crosses.

Results and Discussion

Segregation of genes creates variability which was evident among progenies as Significant mean sum of squares noticed for all the traits suggesting the existence of significant variability in all the three crosses except for branches plant⁻¹ in the cross TMV-2 × ICGV-0035 (Table 1). To substantiate it further and to predict breeding potential of all the three crosses in F₅ generation. Comparison of quantitative trait mean values of all traits was carried out. The highest value of mean for plant height, branches plant⁻¹, pods plant⁻¹, pod yield plant⁻¹, shelling *per cent*, SMK *per cent* and kernel yield

plant⁻¹ was observed in the cross TMV-2 × ICGV-00350. Whereas the same cross exhibited lowest mean value for days to fifty *per cent* flowering, test weight and oil content. The segregating progenies of the cross TMV-2 × TG- 69 recorded lowest value of mean among the crosses for plant height, branches plant⁻¹ and SMK *per cent* and highest mean value for days to fifty *per cent* flowering and oil content. The F₅ progenies of the cross TMV-2 × ICGV-91114 showed highest value of mean for test weight and lowest value of mean for the quantitative trait for pods plant⁻¹, pod yield plant⁻¹, shelling *per cent*, SMK *per cent* and kernel yield plant⁻¹ (Table 2). The results indicated that, the mean performance of F₅ generation population of three crosses were comparable for all the traits. However, mean performance of cross TMV 2 × ICGV-00350 was higher for most of the yield traits indicating that, this cross combination is better than the other two crosses. Krishnappa *et al.* (2009) [4] in finger millet, Suresh *et al.* (2017) [8] in dolichos bean and Shweta (2018) [9] in cowpea, Uma *et al.* (2018) [10] in groundnut have also identified promising crosses among a number of crosses utilizing quantitative trait mean values, which are expected to recover superior pure-lines in advanced generations.

High magnitude of phenotypic coefficient of variation for most of the yield traits like plant height, pods plant⁻¹, pod yield plant⁻¹, SMK *per cent* and kernel yield plant⁻¹ was recorded in the cross TMV-2 × ICGV-00350. Whereas TMV-2 × TG-69 cross showed maximum phenotypic coefficient of variation for the days to fifty *per cent* flowering, branches plant⁻¹. Traits like shelling *per cent*, test weight and oil content showed highest phenotypic coefficient of variation in progenies of cross TMV-2 × ICGV-91114 (Table 3). Such high phenotypic coefficient of variation suggests that there is scope for selection in the future generations of these crosses which in an indicative of better breeding potential. The similar results for breeding potential of crosses were also predicted based on phenotypic coefficient of variation by Krishnappa *et al.* (2009) [4] in finger millet and Suresh *et al.* (2017) [8] in dolichos bean, Uma *et al.* (2018) [10] in groundnut and Shweta (2018) [9] in cowpea.

Table 1: ANOVA for pod yield and its attributing traits in F₅ generation of three crosses C1, C2 and C3

| Source of variation | df | Crosses | Plant height (cm) | Branches plant ⁻¹ | Days to 50% flowering | Pods plant ⁻¹ | Pod yield plant ⁻¹ (g) | Kernel yield plant ⁻¹ (g) | Shelling (%) | SMK (%) | Test weight (g) | Oil content (%) |
|---------------------|----|---------|-------------------|------------------------------|-----------------------|--------------------------|-----------------------------------|--------------------------------------|--------------|----------|-----------------|-----------------|
| Replications | 1 | C1 | 2.59 | 0.46 | 3.28 | 12.41 | 0.01 | 0.2 | 33.45 | 43.27 | 56.06 | 0.28 |
| | 1 | C2 | 8.9 | 0.46 | 1.28 | 0.74 | 0.85 | 0.531 | 17.08 | 8.1 | 5.06 | 0.07 |
| | 1 | C3 | 1.11 | 1.66 | 2.01 | 7.66 | 4.24 | 1.42 | 5.25 | 42.21 | 12.53 | 0.39 |
| Genotypes | 38 | C1 | 8.60** | 1.42* | 11.42** | 77.16** | 50.91** | 28.51** | 48.24** | 98.13** | 97.51** | 6.84** |
| | 38 | C2 | 26.41** | 1.68* | 14.66** | 50.54** | 35.26** | 19.61** | 58.94** | 99.43** | 71.73** | 6.86** |
| | 29 | C3 | 33.18* | 1.16 | 12.37** | 183.68** | 148.54** | 92.82** | 47.02** | 104.38** | 63.90** | 4.44** |
| Error | 38 | C1 | 3.3 | 0.81 | 4.15 | 3.07 | 1.07 | 0.87 | 15.43 | 11.12 | 21.79 | 0.34 |
| | 38 | C2 | 3.34 | 0.9 | 2.54 | 3.54 | 1.03 | 0.91 | 4.8 | 6.01 | 3.16 | 0.22 |
| | 29 | C3 | 3.41 | 0.8 | 2.49 | 2.1 | 1.1 | 0.59 | 9.51 | 10.65 | 3.59 | 0.52 |

Note: C1: TMV-2 × ICGV-91114; C2: TMV-2 × TG-69 and C3: TMV-2 × ICGV-00350

Table 2: Estimates of mean, range and standardized range for morphometric traits, pod yield and yield traits in F₅ population derived from three crosses in groundnut

| Traits | Crosses | Mean | Min. | Max. | Absolute range | Standardized range |
|------------------------------|----------------|-------|-------|-------|----------------|--------------------|
| Plant height (cm) | C ₁ | 32.11 | 25.31 | 36.99 | 11.68 | 0.36 |
| | C ₂ | 31.36 | 21.5 | 41.35 | 19.85 | 0.63 |
| | C ₃ | 32.31 | 24.35 | 41.03 | 16.68 | 0.52 |
| Branches plant ⁻¹ | C ₁ | 6.38 | 4.00 | 8.00 | 4.00 | 0.36 |
| | C ₂ | 6.1 | 4.00 | 8.00 | 4.00 | 0.66 |
| | C ₃ | 6.43 | 5.00 | 7.00 | 2.00 | 0.31 |

| | | | | | | |
|--------------------------------------|----------------|-------|-------|-------|-------|------|
| Days to 50% flowering | C ₁ | 41.56 | 37.00 | 47.00 | 10.00 | 0.24 |
| | C ₂ | 42.89 | 37.00 | 49.00 | 12.00 | 0.28 |
| | C ₃ | 41.25 | 34.00 | 48.00 | 14.00 | 0.34 |
| Pods plant ⁻¹ | C ₁ | 23.06 | 10.50 | 40.06 | 29.56 | 1.28 |
| | C ₂ | 23.13 | 14.60 | 36.58 | 21.98 | 0.95 |
| | C ₃ | 26.21 | 11.60 | 53.60 | 42.00 | 1.61 |
| Pod yield plant ⁻¹ (g) | C ₁ | 17.87 | 7.23 | 30.18 | 22.95 | 1.28 |
| | C ₂ | 18.32 | 10.30 | 29.68 | 19.38 | 1.06 |
| | C ₃ | 19.62 | 5.73 | 43.51 | 37.78 | 1.93 |
| Kernel yield plant ⁻¹ (g) | C ₁ | 12.72 | 4.90 | 22.08 | 17.78 | 1.35 |
| | C ₂ | 13.17 | 6.50 | 22.44 | 15.94 | 1.21 |
| | C ₃ | 15.18 | 5.00 | 35.65 | 30.65 | 2.02 |
| Shelling (%) | C ₁ | 71.5 | 58.95 | 83.64 | 24.69 | 0.35 |
| | C ₂ | 73.98 | 61.61 | 81.31 | 27.70 | 0.37 |
| | C ₃ | 77.56 | 65.99 | 87.22 | 21.23 | 0.27 |
| SMK (%) | C ₁ | 74.64 | 62.50 | 93.60 | 31.10 | 0.42 |
| | C ₂ | 74.63 | 64.60 | 92.60 | 28.00 | 0.38 |
| | C ₃ | 76.92 | 57.40 | 92.50 | 35.10 | 0.46 |
| Test weight (g) | C ₁ | 38.28 | 20.05 | 56.10 | 36.05 | 0.94 |
| | C ₂ | 38.18 | 23.20 | 55.30 | 32.10 | 0.84 |
| | C ₃ | 35.67 | 23.60 | 52.00 | 28.40 | 0.80 |
| Oil content (%) | C ₁ | 48.89 | 45.98 | 53.81 | 7.83 | 0.16 |
| | C ₂ | 49.09 | 46.58 | 53.42 | 6.84 | 0.14 |
| | C ₃ | 48.44 | 45.30 | 52.07 | 6.77 | 0.14 |

Note: C1: TMV-2 × ICGV-91114; C2: TMV-2 × TG-69 and C3: TMV-2 × ICGV-00350

The comparison of absolute and standardized range

The absolute and standardized ranges for all the traits in F₅ generation of three crosses were computed and indicated in Table 3. In F₅ generation the absolute and standardized range as well as upper limit for the days to fifty *per cent* flowering, pods plant⁻¹, pod yield plant⁻¹, SMK *per cent* and kernel yield plant⁻¹ was higher in the cross TMV-2 × ICGV-00350, while plant height, branches plant⁻¹ and shelling *per cent* higher standardized range was reported in TMV-2 × TG-69 population while the absolute range and highest value for the branches plant⁻¹ was reported in both TMV-2 × ICGV-91114 and TMV-2 × TG-69 population.

The absolute and standardized range was observed highest in TMV-2 × ICGV-91114 cross for test weight and oil content (Table 2). The higher magnitude of absolute range and standardized range for most of the yield attributing traits in F₅ generation was found in TMV-2 × ICGV-00350 cross suggested the presence of desirable extreme phenotypes in this cross. The higher estimates of standardized range and absolute range in F₅ generation of TMV-2 × ICGV-00350 cross followed by TMV-2 × TG-69, suggested better breeding potential in these crosses. Krishnappa *et al.* (2009) [4], Suresh *et al.* (2017) [8], Shweta (2018) [9] and Uma *et al.* (2018) [10] groundnut also predicted the breeding potential of crosses based on absolute and standardized range in finger millet, dolichos bean, cowpea and groundnut respectively.

Comparison of broad sense heritability and expected genetic advance as *per cent* mean (GAM) in three crosses

High magnitude of broad sense heritability accompanied with

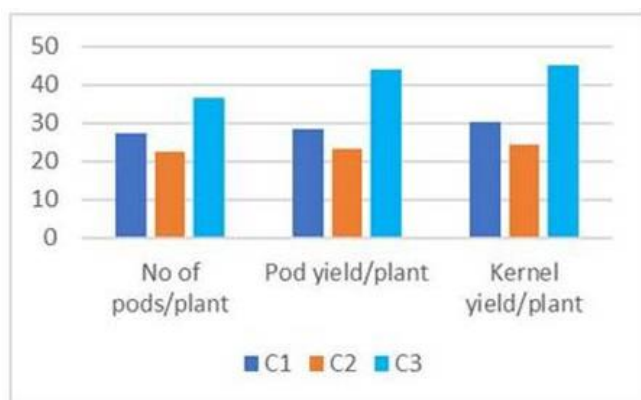
high expected GAM was recorded for pods plant⁻¹ (97.73% and 74.02%), pod yield plant⁻¹ (98.52% and 89.46%), test weight (95.38% and 31.38%) and kernel yield plant⁻¹ (98.71% and 91.52%) in F₅ population of cross TMV-2 × ICGV-00350. Moderate heritability and GAM was exhibited by branches plant⁻¹ in TMV-2 × TG-69 while Moderate heritability and low GAM in TMV-2 × ICGV-91114 and both low in TMV-2 × ICGV-00350 Days to fifty *per cent* flowering, SMK *per cent* and shelling *per cent* showed high heritability in F₅ population of cross TMV-2 × TG-69. Low GAM was exhibited by days to fifty *per cent* flowering and shelling *per cent*. Oil content showed high heritability in all the crosses. Plant height showed high magnitude of broad sense heritability accompanied with high expected GAM in population of cross TMV-2 × ICGV-00350, high heritability and moderate GAM in population of cross TMV-2 × TG-69 and moderate heritability and low GAM in population of cross TMV-2 × ICGV-91114 (Table 3). Altogether, all the yield traits in both generations of all the three crosses showed high broad sense heritability accompanied with high genetic advance as *per cent* of mean. Hence it can be inferred as the phenotypic performance of these crosses in both the generations was basically due to higher contribution of its genotype and is less influenced by environment and genotype and environment interaction effects. In other words, the phenotype of the individuals is predominantly due to the genotypic constitution of the individual itself. Hence selection would be effective in this population as the variability is predominantly governed by the genetic constitution of the genotypes.

Table 3: Genetic variability parameters for morphometric traits, pod yield and yield traits in F₅ populations derived from three crosses in groundnut

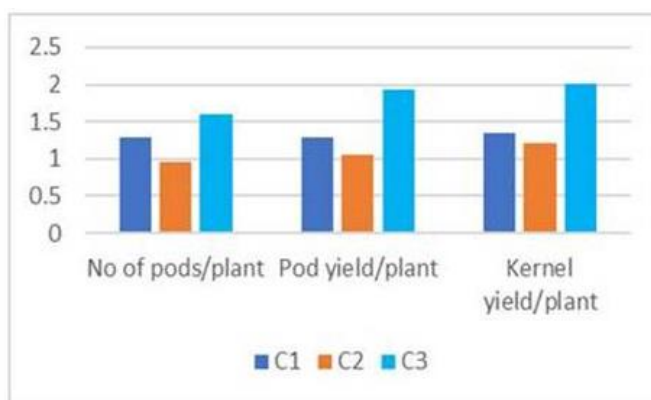
| Traits | Crosses | GCV % | PCV % | h ² (BS) % | GAM % |
|------------------------------|---------|-------|-------|-----------------------|-------|
| Plant height (cm) | C1 | 5.07 | 7.6 | 44.54 | 6.97 |
| | C2 | 10.82 | 12.29 | 77.51 | 19.63 |
| | C3 | 11.93 | 13.23 | 81.33 | 22.18 |
| Branches plant ⁻¹ | C1 | 9.37 | 16.01 | 34.24 | 9.06 |
| | C2 | 11.29 | 18.67 | 30.02 | 11.55 |

| | | | | | |
|--------------------------------------|----|-------|-------|-------|--------|
| Days to 50% flowering | C3 | 6.58 | 15.41 | 18.22 | 5.78 |
| | C1 | 4.59 | 6.71 | 46.71 | 6.46 |
| | C2 | 5.73 | 6.83 | 70.41 | 9.91 |
| Pods plant ⁻¹ | C3 | 5.38 | 6.61 | 66.38 | 9.03 |
| | C1 | 26.4 | 27.47 | 92.33 | 52.25 |
| | C2 | 20.95 | 22.47 | 86.9 | 40.23 |
| Pod yield plant ⁻¹ (g) | C3 | 36.35 | 36.75 | 97.73 | 74.02 |
| | C1 | 27.94 | 28.53 | 95.85 | 56.34 |
| | C2 | 22.57 | 23.24 | 94.28 | 45.15 |
| Kernel yield plant ⁻¹ (g) | C3 | 43.75 | 44.07 | 98.52 | 89.46 |
| | C1 | 29.32 | 30.13 | 94.06 | 58.4 |
| | C2 | 23.21 | 24.31 | 91.12 | 45.64 |
| Shelling (%) | C3 | 44.71 | 45.00 | 98.71 | 91.52 |
| | C1 | 5.66 | 7.89 | 51.51 | 8.37 |
| | C2 | 7.03 | 7.63 | 84.91 | 13.34 |
| SMK (%) | C3 | 5.56 | 6.83 | 63.33 | 9.34 |
| | C1 | 8.83 | 9.9 | 79.63 | 16.24 |
| | C2 | 9.15 | 9.72 | 88.59 | 17.75 |
| Test weight (gm) | C3 | 9.22 | 10.07 | 83.95 | 17.41 |
| | C1 | 16.07 | 20.17 | 63.46 | 26.37 |
| | C2 | 15.33 | 16.02 | 91.54 | 30.231 |
| Oil content % | C3 | 15.59 | 15.97 | 95.38 | 31.38 |
| | C1 | 3.68 | 3.87 | 90.53 | 7.23 |
| | C2 | 3.71 | 3.83 | 93.62 | 7.39 |
| | C3 | 2.89 | 3.25 | 78.98 | 5.29 |

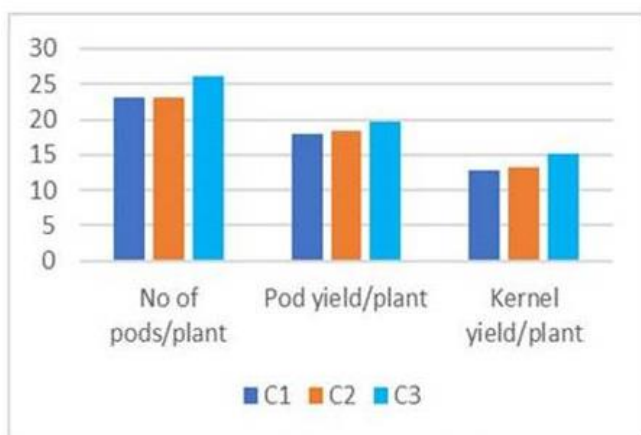
Note: C1: TMV-2 × ICGV-91114; C2: TMV-2 × TG-69 and C3: TMV-2 × ICGV-00350



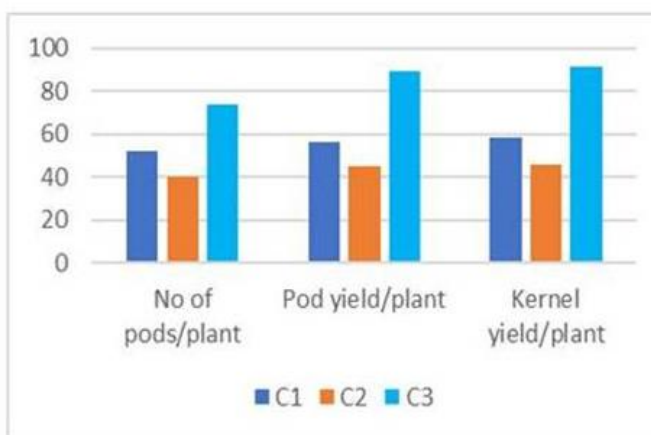
Comparison of PCV



Comparison of SR



Comparison of mean yield



Comparison of GAM

Fig 1: Comparison of Breeding potential predictors for yield and its attributing traits of three crosses of F₅ generation in groundnut (C1: TMV-2 × ICGV-91114; C2: TMV-2 × TG-69 and C3: TMV-2 × ICGV-00350)

Conclusion

Thus by comparing these predictors such as, quantitative trait

means, absolute and standardized range, phenotypic coefficient of variation in terms of their magnitude, it can be

suggested that cross TMV-2 × ICGV00350 is predicted to have better breeding potential in terms of recovery of desirable high yielding genotypes in future generations followed by TMV-2 × ICGV-91114 from among the three crosses studied. High broad sense heritability, coupled with moderate to high genetic advance as *per cent* of mean for these crosses, supports the above statement (Fig.1).

References

1. Anonymous, Indiastat, 2019a.
2. Anonymous, Package of practice book, Univ. Agric. Sci. Bengaluru, 2019b, P. 157-162.
3. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soyabean. *Agron. J.* 1955;47(7):314-318.
4. Krishnappa M, Ramesh S, Chandraprakash J, Jayaramgowda Bharathi, Dayal DD. Breeding potential of selected crosses for genetic improvement of finger millet. *J SAT Agric. Res.* 2009, 7.
5. Panse VG, Sukhatme PV. Statistical methods for agricultural workers, ICAR Publication, New Delhi, 1961, 145.
6. Robinson HF, Comstock RE, Harvey P. Estimation of heritability and degree of dominance in corn. *Agron. J* 1949;41:353-359.
7. Swati M, Radadia BB, Manish V, Ashok KV. A review of chemical characteristics (acid value and iodine value) of peanut oil. *J Weekly Sci. Res.* 2014;1(30):1-4.
8. Suresh, Shivakumar MS, Chandrakant, Ramesh S, Keerthi CM. Breeding potential of crosses in Dolichos bean (*Lablab purpureus* L. sweet var lignosus). *Environ. Ecol.* 2017;35(1):33-38.
9. Shweta HR. Genetics of, and breeding potential of four crosses for quantitative traits in cowpea (*Vigna unguiculata* L. Walp) M.Sc. (Ag.) Thesis, Univ. Agric. Sci., Bangalore, India, 2018.
10. Uma RB, Venkataravana P, Priyadarshini SK. Genetic variability studies in F₂ and F₃ population of three crosses of groundnut (*Arachis hypogaea* L.). *J Pharmacogn. Phytochem.* 2018;7(5):3139-3143.