*Original Research Article*

Studies on Variability, Heritability, Genetic Advance and Character Association for Yield and Yield Attributing Traits in Sunflower (*Helianthus annuus* L.) Inbreds

.

ABSTRACT

|  |
| --- |
| The genetic variability, heritability, genetic advance and association studies were carried out in thirty two sunflower inbreds collected from Oilseeds Reseach Station, Latur (Maharashtra) and were evaluated using a randomized block design for yield and its contributing traits. Results showed that highly significant mean sum of squares for all the traits indicating presence of sufficient variability in inbreds. Wide range of variation was noticed in plant height followed by seed yield/plant and seed filling per cent. High phenotypic and genotypic coefficient of variation were recorded for seed yield/plant, 100 seed weight, husk content and head diameter. High heritability coupled with high genetic advance as per cent of mean was exhibited for seed yield/plant followed by 100 seed weight, volume weight, head diameter and oil content indicated direct selection could be effective. The seed yield/plant showed positive and highly significant association with head diameter, seed filling per cent, 100 seed weight and plant height both at genotypic and phenotypic levels. However, husk content exhibited significant and negative correlation at both levels. Hence, selecting plants with tall stature, larger heads, higher 100 seed weight, higher seed filling per cent and lower husk content said trait effective in sunflower breeding. |

*Keywords: Genetic variability, Heritability, Character Association, Inbreds, Sunflower (Helianthus annuus L.), Genetic advance as per cent of mean (GAM).*

1. INTRODUCTION

Sunflower has emerged as a promising oilseed crop with notable economic value in India, having been commercially introduced in 1972. It competes globally with key oilseed crops like Soybean, Groundnut, Rapeseed, and Mustard. As of 2024–25, sunflower cultivation covers in India, area 1.74 Lakh Hectares with a yield of 1129 kg/ha and production 1.96 Lakh Tones. In Maharashtra, area 0.14 Lakh Hectares are under cultivation with yield 494 kg/ha and production 0.07 lakh Tones (Anonymous, 2024). Andhra Pradesh, Harayana, Karnataka, Maharashtra, Telangana collectively contribute around 75% of India’s total production.

The cultivated sunflower (*Helianthus annuus* L.), belonging to the family Compositae (Asteraceae), has a fundamental chromosome count of 2n = 34. The genus *Helianthus* consists of diploid, tetraploid, and hexaploid types. Its name originates from Greek "*helios*" meaning sun and "*anthos*" meaning flower and it is locally known in India as “Surajmukhi” and in Marathi "Suryaphul." Introduced in North America in the late 19th century (Putt, 1997), sunflower entered India as a foreign crop in 1969. Its popularity surged significantly in the late 20th century after the release of the first hybrid, BSH-1 (Seetharam, 1984). The oil enjoys high consumer preference due to elevated levels of mono and polyunsaturated fats, making it suitable for heart health. Moreover, the oil is a rich reservoir of vitamin E, especially α-tocopherol (Fernandez-Martínez *et al.*, 2009).

Genetic variability indicated the presence of differences within breeding groups. Variability play privotal role in utilization of heterosis.The first step in development of hybrids is identification of inbreds for the valid traits and these inbrdes can be utilized in development of new CMS lines or as restorers based on their maintainer / restorer behaviour with the corresponding promising CMS lines. Hence, the present study is concentrated to evaluate different inbreds for yield and its contributing traits, genetic variability studies and the association of different traits with seed yield. The identified variation in populations had been divided into inheritable and non-inheritable components, which were assessed using genetic measures such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, and genetic advance. These metrics helped breeders to devise efficient selection procedures.

2. material and methods

The present experiment was carried out during *Kharif* 2024 at Oilseeds Research Station, Latur, Maharashtra. Geographically Latur is situated at an elevation of 633.85 m above mean sea level, 760 26” North latitude and 760 47” East longitude. The experimental material utilized for the present study, comprised 30 inbreds, along with 2 check varieties (Phule Bhaskar, DRSF-108) was obtained from Oilseeds Research Station, Latur and were evaluated using a randomized block design with two replications. A complete fertilizer dose of 60:30:30 NPK kg/ha (TNAU, 2013) had been used, with half the nitrogen (as urea) given at sowing and the rest one month later. Agronomic measures had been performed timely to promote proper plant growth and ensure the experiment's success. In each entry, five plants were tagged at random per replication. Observations were recorded for ten yield and its attributes in these tagged plants Plant height at maturity (cm), Head diameter (cm), 100 seed weight(g), Volume weight (g/100ml), Seed filling (%),Husk content (%),Oil content (%),Seed yield per plant (g) except for days to 50 per cent flowering and days to maturity that were recorded on plot basis.

The overall mean values of different characters were subjected to statistical analysis. The analysis of variance for Randomized Block Design (RBD) was carried out to test the significance of differences between treatments for all metric characters (Panse and Sukhatme, 1985). The coefficient of variation being a standardized form of variance is useful for comparing the extent of variance between different characters with different scales Singh and Choudhary (1977). According to Burton and Devane (1953), genotypic and phenotypic coefficients of variation were estimated based on the estimates of genotypic and phenotypic variances. Heritability in broad sense (h2bs) was calculated as the ratio of genotypic variance to the phenotypic variance and expressed as percentage (Falconer, 1981). Genetic advance as per cent of mean for each character was worked out as suggested by Johnson *et al.* (1955). Both genotypic correlation coefficient and phenotypic correlation coefficient were estimated from the variance and covariance components as given by Al-jibouri *et al.*, (1958).

3. results and discussion

3.1 Analysis of Variance and Mean Performance

Wide range of variability was noticed in all the traits in the genotypes studied. The mean, maximum and minimum values and coefficient of variation (CV) of these characters have been tabulated accordingly. The analysis of variance (ANOVA) of 32 sunflower inbreds with respect to 10 quantitative traits (Table 1). The mean squares due to genotypes for all the above characters were highly significant which indicated genetic variability among the experimental materials. Wide range of variation was observed for plant height (100-175.60) followed by seed yield per plant (16.45-46.41), seed filling per centage (63.85-89.122), volume weight (22.51-47.98) and oil content (21.4-40.09). These results are in agreement with Neelima *et al.*, (2016) and Varalaskhmi *et al.*, (2019).

**3.2 Genotypic and Phenotypic coefficient of Variation**

The results of genetic parameters studied were presented in Table 2, Fig 1 & 2. Phenotypic coefficient of variation (PCV) reflects the combined influence of genetic makeup and environmental factors, while genotypic coefficient of variation (GCV) indicates the inheritable component alone. In this study, GCV values ranged from 3.416 to 21.97 and PCV from 3.655 to 24.96. The slightly lower GCV values compared to PCV for observed traits suggest limited environmental effects, highlighting that most of the trait variation was genetically driven. The trait seed yield per plant recorded high GCV (21.97) and PCV (24.96) values. The 100 seed weight showed moderate GCV (19.57) along with high PCV (21.51). Moderate GCV and PCV values were noted for husk content (16.77, 19.02) followed by volume weight (14.29, 17.53), head diameter (12.78, 15.09) and oil content (10.86, 11.88). Traits like seed filling percentage (5.20, 7.98) followed by days to 50% flowering (5.73, 5.92), and days to maturity (3.41, 3.65) exhibited low GCV and PCV values and results similar findings were noted by Sujatha *et al.* (2002), Khan *et al.* (2007), Kumar *et al.* (2014), Lakshman *et al.* (2021) and Anuradha *et al.* (2023).

**3.3 Heritability and Genetic Advance as per cent of mean**

In this study, heritability estimates were high for days to 50% flowering (93.65%), days to maturity (87.31%), head diameter (71.69%), 100 seed weight (82.74%), volume weight (66.43%), husk content (77.74%), oil content (83.48%) and seed yield/plant (77.47%) indicating that these traits were less influenced by the environment and selection based on phenotypic observations would be effective. Low heritability was noticed for plant height (56.41%) and seed filling per cent (42.56%).

High heritability coupled with genetic advance were observed for traits such as head diameter, 100 seed weight, volume weight, husk content, oil content, and seed yield per plant, suggesting additive gene action for the said selection is effective. Traits like days to 50% flowering and days to maturity showed high heritability with moderate genetic advance, indicating mixed gene effects and limited selection efficiency. Plant height and seed filling percentage showed moderate heritability and genetic advance, pointing to non-additive gene action and low selection effectiveness. These results are in line with Madhavi Latha *et al.* (2017), Varalakshmi *et al.* (2019), Anuradha *et al.* (2023) and Varshitha *et al.* (2023).

**3.4 Character Association**

The correlation coefficient is a statistical measure that indicates the degree and direction of the relationship between traits (Singh, 2012). Since yield is a complex trait governed by multiple genes, it is closely linked to several yield-contributing components. The expression of yield is influenced by the interaction among these components, making it essential to consider their interrelationships in genetic improvement programs. Correlations often arise due to pleiotropic gene effects or genetic linkage between traits. Relying solely on yield for selecting superior genotypes can be misleading, as it may not reflect the true potential of a genotype. Therefore, a comprehensive understanding of how yield components relate to each other is crucial. This helps breeders identify desirable traits more effectively and simplifies the selection process, ultimately contributing to more accurate and successful yield enhancement in crop improvement efforts.

The genotypic and phenotypic correlations among yield and its attributes of 32 sunflower genotypes were presented in Table 3. In this study, seed yield per plant showed a strong and positive relationship with several traits. It had a highly positive and significant correlation at both genotypic and phenotypic levels with plant height (G = 0.542, P = 0.3976), head diameter (G = 0.918, P = 0.6672), 100 seed weight (G = 0.6511, P = 0.4809), and seed filling percentage (G = 0.7917, P = 0.4661). These results suggest that improving these traits could help increase seed yield. There was a positive but non-significant connection with days to 50% flowering (G = 0.0555, P = 0.0771), days to maturity (G = 0.1531, P = 0.1077), and oil content (G = 0.1016, P = 0.0359), indicating limited influence on yield. A negative and significant association was found with hull content (G = -0.6705, P = -0.5548), suggesting it may reduce yield. Volume weight showed a positive and significant correlation at the genotypic level (G = 0.3515), though it was not significant at the phenotypic level (P = 0.2025), pointing to a possible genetic effect. Similar research findings were recorded by Tyagi *et al.* (2013), Pandya *et al.* (2015), Baraiya *et al.* (2018), Gangavati & Kulkarni (2021) and Hilli *et al.* (2021).

The trait plant height showed a positive and significant association with 100 seed weight (G = 0.5166, P = 0.3384), oil content (G = 0.3597, P = 0.3424), and seed yield/plant (G = 0.542, P = 0.3976) at both genetic and observed levels. It had a positive but non-significant connection with volume weight and seed filling percentage and a negative significant relationship with husk content (G = -0.3624) at the genetic level. A positive and significant correlation with head diameter was observed only at the phenotypic level. Head diameter had a significant positive correlation with 100 seed weight (G = 0.5967, P = 0.4437) and seed yield/plant (G = 0.918, P = 0.6672) at both levels. It showed a negative significant relation with husk content (G = -0.4703, P = -0.2936). Volume weight and seed filling percentage had a positive but non-significant association, while oil content showed a negative and non-significant correlation (G = -0.0534, P = -0.021). Yasin and Singh (2010), Baraiya *et al.* (2018) and Lakshman et al, (2021) found similar result for plant height, head diameter and 100 seed weight.

The trait 100 seed weight was positively and significantly associated with seed filling percentage (G = 0.5147, P = 0.2579) and seed yield per plant (G = 0.6511, P = 0.4809), and had a non-significant positive link with volume weight (G = 0.1456, P = 0.0986) and oil content (G = 0.2023, P = 0.1672). A negative and non-significant relation was seen with husk content (G = -0.1782, P = -0.1074). Seed filling percentage showed a strong positive and significant correlation with seed yield per plant (G = 0.7917, P = 0.4661) at both levels. It had a positive but non-significant association with oil content (G = 0.128, P = 0.0397) and a negative significant link with husk content (G = -0.5465, P = -0.2968). Husk content had a significant negative correlation with oil content (G = -0.4105, P = -0.3318) and seed yield per plant (G = -0.6705, P = -0.5548) at both genotypic and phenotypic levels. These results were in accordance for husk content with Rani *et al.* (2016) and Singh *et al.* (2018). for seed filling per cent were observed by Neelima *et al.* (2016) and Rani *et al.* (2017).

Finding revealed that Selecting sunflower plants with taller stature, bigger head size, greater 100 seed weight, and better seed filling percentage was proven useful to boost seed yield per plant. Tall plants had more leaves, leading to increased photosynthesis and dry matter buildup, while larger heads carried more seeds. Higher seed filling meant more fully developed seeds, directly improving yield. Traits like plant height, head diameter, 100 seed weight, and seed filling percentage were key traits for boosting productivity. Additionally, late flowering and late-maturing plants showed weak but positive correlations with yield, suggesting they may be beneficial. Lower husk content, which had a strong negative link with seed yield, emerged as an important trait to select for improving overall sunflower performance.

4. Conclusion

In conclusion, the present study has shown wider range of variability, high PCV and GCV, high heritability and high GAM for seed yield indicating variability in the material. Also narrow gap between values of GCV and PCV indicate that low influence of environment on expression of traits and direct selection could be effective. This direct selection for seed yield in sunflower can be achieved if selection is practiced for head diameter, plant height, 100 seed weight and seed filling per cent.

References

**Anonymous (2024). Agricultural Statistics at a Glance 2024-25, *Directorate of Economics and Statistics, Department of Agriculture & Farmers Welfare (DA&FW), Govt. of India.***

**Putt, E. D., (1997). The chapter of “Early History of Sunflower *”. Willey Online Library, Sunflower Technology and Production (Agronomy Monographs),* volume-35.**

**Seetharam, A. (1984). BSH-1 Sunflower hybrid for stable and high yields. *Current Research*, 13: 49-50.**

**Fernandez-Martınez, J. M., Perez-Vich, B. and Velasco, L. (2009). Sunflower. *In J. Vollmann*, I. Rajcan (eds.), Oil Crops. Springer New York, pp. 155-232.**

**Tamil Nadu Agricultural University (2013*). Nutrient Management for Sunflower Production.***

**Panse, V. G. and Sukhatme, P. V. (1985). Statistical Methods for Agricultural Workers. ICAR, New Delhi, pp. 359.**

**Singh, R.K. & Choudhary, B.D. (1977). Biometrical methods in quantitative genetic analysis. *Kalyani Publishers*, New Delhi, pp. 178-185.**

**Burton, G.W. & De-Vane, E.H. (1953). Estimating heritability in tall fescue (*Festuca arundinancea*) from replicated clonal materials. *Agronomy Journal*, 45: 478-481.**

**Falconer, D.S. (1981). Introduction to Quantitative Genetics, 2nd edition. Oliver and Boyd, *Edinburg, London*, UK, pp. 316.**

**Johnson, H. W., Robinson, H. F. and Comstock, R. E., (1955). Estimates of genetic and environment variability in soybeans. *Agronomy Journal*, 47: 314-318.**

**Al-jibouri, H.A., Miller, P.A. & Robinson, H.F. (1958). Genotypic and environmental variances in an upland cotton cross of inter-specific origin. *Agronomy Journal*, 50: 663-667.**

**Neelima, S., Ashok, K., Venkataramanamma, K., & Padmalatha, Y. (2016). Genetic variability and genetic diversity in sunflower. *Electronic Journal of Plant Breeding*, 7(3), 703-707.**

**Varalakshmi, K., Neelima, S., Reddy, R. N., & Sreenivasulu, K. N. (2019). Genetic variability studies for yield and its component traits in newly developed sunflower (Helianthus annuus L.) hybrids. *Electronic Journal of Plant Breeding*, 11(01), 301-305.**

**Sujatha, H. L., Chikkadevaiah, & Nandini. (2002). Genetic variability study in sunflower inbreds. *HELIA*, 25(37), 93-100.**

**Khan, H., Muhammad, S., Shah, R. and Iqbal, N. (2007). Genetic analysis of yield and some yield components in sunflower. *Sarhad Journal of Agriculture*, 23(4).**

**Kumar, P., Dhillon, S. K and Sao, A. (2014). Genetic analysis of sunflower genotypes under water stress environments. *International Journal of Farm Sciences*, 4(4): 26-35.**

**Lakshman, S. S., Chakraborty, N. R., Debnath, S., & Kant, A. (2021). Genetic variability, character association and divergence studies in sunflower (*Helianthus annuus* L.) for improvement in oil yield. *African Journal of Biological Sciences*, 3(1), 129-145**.

**Anuradha, B., Manivannan, N., Sasikala, R., Harish, S., & Senthivelu, M. (2023). Genetic variability and association studies in BC3F1 population of sunflower (*Helianthus annuus* L.). *Electronic Journal of Plant Breeding*, 14(3), 923–927.**

**Madhavi Latha K, Durgaprasad AV S, Neelima S and Uma Maheswari P (2017). Genetic variability studies for yield and its attributes in sunflower. *Bull. Env. Pharmacol. Life Sci.,* 6(2), 117-120.**

**Varshitha, V., Prabhavathi, K., Meena, H. P. and Yadav, p. (2023). Study of genetic variability for yield and quality parameters in newly developed sunflower (*Helianthus annuus* L.) Interspecific derivatives over two seasons. *International Journal of Environment and Climate Change*, 13(10), 3226-3234.**

**Singh, P. (2012). Objective Quantitative Genetics (1st ed.). *Bio-Green Books*. ISBN 978-9327217957.**

**Tyagi, V., Dhillon, S. K., Bajaj, R. K., & Kaur, J. (2013). Divergence and association studies in sunflower (*Helianthus annuus* L.). *Helia*, 36(58), 77-94.**

**Pandya, M. M., Patel, P. B., & Narwade, A. V. (2015). A study on correlation and path analysis for seed yield and yield components in Sun flower (*Helianthus annuus* L.). *Electronic Journal of Plant Breeding*, 7(1), 177-183.**

**Baraiya, V. K., Jagtap, P. K., Sangani, J. L., & Malviya, A. V. (2018). "Genetic Correlation and Path Analysis of Seed Yield and Associated Traits in Irrigated Sunflower (*Helianthus annuus* L.). *Journal of Pharmacognosy and Phytochemistry*, 7(5): 2730-2732.**

**Gangavati, L., & Kulkarni, V. V. (2021). Correlation and path analysis in advanced inbred lines of sunflower. *International Journal of Current Microbiology and Applied Sciences*, 10(1), 1381-1389.**

**Hilli, H. J., Immadi, S. & Amandeep (2021). Variability and correlation studies in sunflower lines (*Helianthus annuus* L.). *Journal of Pharmacognosy and Phytochemistry*, 10(3), 221-223.**

**Yasin, A. B., & Singh, S. (2010). Correlation and path coefficient analyses in sunflower. *Journal of Plant Breeding and Crop Science*, 2(5), 129-133.**

**Rani, R., Sheoran, R. K., & Chander, S. (2016). Association analysis for yield and component traits in sunflower (*Helianthus annuus* L): Association analysis for yield and component traits in sunflower. *Journal of Oilseeds Research*, 33(3).**

**Singh, V. K., Sheoran, R. K., & Chander, S. (2018). Correlation analysis for seed yield and its component traits in sunflower. *Journal of Pharmacognosy and Phytochemistry*, 7(3), 2299–2301.**

**Rani, R., Sheoran, R. K., & Sharma, B. (2017). Studies on variability, heritability and genetic advance for quantitative traits in sunflower (*Helianthus annuus* L.) genotypes. *Research in Environmental and Life Sciences*, 10(6), 491-493.**

**Table 1: Analysis of variance (ANOVA) for seed yield and yield component characters studied in Sunflower (mean sum of squares).**

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Sr. No.** | **Source of variation** | **d.f.** | **Days to 50% flowering** | **Days to maturity** | **Plant height (cm)** | **Head diameter (cm)** | **100 Seed weight (g)** | **Volume weight (g)** | **Seed filling (%)** | **Husk content (%)** | **Oil content (%)** | **Seed Yield / plant (g)** |
| **1** | **Replication** | 1 | 0.5625 | 0.5625 | 30.71 | 0.8337 | 0.01377 | 10.311 | 43.775 | 1.099 | 0.0025 | 19.947 |
| **2** | **Treatment** | 31 | **23.07 \*\*** | **19.25\*\*** | **373.91\*\*** | **7.327\*\*** | **2.489\*\*** | **62.38\*\*** | **56.38\*\*** | **35.28\*\*** | **27.07\*\*** | **97.19\*\*** |
| **3** | **Error** | 31 | 0.756 | 1.3044 | 104.21 | 1.2082 | 0.23514 | 12.582 | 22.72 | 4.419 | 2.4365 | 12.34 |

\* Indicates significance at 5% level \*\* Indicates significance at 1% level

**Table 2: Genetic parameters for yield and yield contributing characters of sunflower over *Kharif* season.**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Sr. No.** | **Parameters** | **Range** | **Mean** | **Genotypic variance (δ2g)** | **Phenotypic variance (δ2p)** | **GCV (%)** | **PCV (%)** | **Heritability (h2bs)** | **Genetic Advance as *per cent* of Mean (%) (GAM)** |
| **1** | **Days to 50% flowering** | 49 - 64 | 58.2812 | 11.1532 | 11.9092 | 5.7302 | 5.9212 | 93.65 | 11.4234 |
| **2** | **Days to maturity** | 81 - 94 | 87.6875 | 8.9728 | 10.2772 | 3.4161 | 3.6559 | 87.31 | 6.5754 |
| **3** | **Plant height (cm)** | 100 - 175.6 | 148.99 | 134.8595 | 239.0585 | 7.7939 | 10.3773 | 56.41 | 12.0586 |
| **4** | **Head diameter(cm)** | 9.62 - 18.20 | 13.68 | 3.0594 | 4.2676 | 12.7841 | 15.0988 | 71.69 | 22.298 |
| **5** | **100 Seed weight (g)** | 3.17 - 8.239 | 5.4244 | 1.1269 | 1.362 | 19.57 | 21.5147 | 82.74 | 36.6694 |
| **6** | **Volume weight(g)** | 22.51 - 47.98 | 34.9152 | 24.899 | 37.4808 | 14.2915 | 17.5344 | 66.43 | 23.9956 |
| **7** | **Seed filling %** | 63.8495 - 89.122 | 78.7835 | 16.8315 | 39.552 | 5.2075 | 7.9827 | 42.56 | 6.9979 |
| **8** | **Husk content (%)** | 14.24 - 33.087 | 23.4233 | 15.433 | 19.8516 | 16.7717 | 19.0217 | 77.74 | 30.4628 |
| **9** | **Oil content (%)** | 21.4 - 40.09 | 32.3047 | 12.3164 | 14.7529 | 10.8637 | 11.8898 | 83.48 | 20.4478 |
| **10** | **Seed Yield / plant (g)** | 16.45 - 46.41 | 29.6439 | 42.4224 | 54.7622 | 21.9716 | 24.9635 | 77.47 | 39.8369 |

GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation

Fig.1. Genotypic and phenotypic coefficient of variation for ten characters in sunflower

**Fig.2. Heritability and Genetic advance as per cent of mean for ten characters in sunflower**

**Table 3: Estimates of genotypic (G) and phenotypic (P) correlation coefficient for different in sunflower**

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Characters** |  | **Days to 50% flowering** | **Days to maturity** | **Plant height (cm)** | **Head diameter (cm)** | **100 Seed weight (g)** | **Volume weight (g)** | **Seed filling (%)** | **Husk content (%)** | **Oil content (%)** | **Seed Yield / plant (g)** |
| **Days to 50% flowering** | rg | **1 \*\*** | 0.8595 \*\* | 0.7293 \*\* | 0.0405 | -0.0216 | 0.0588 | -0.0345 | -0.3695 \* | 0.3086 | 0.0555 |
| rp | **1 \*\*** | 0.7817 \*\* | 0.4951 \*\* | -0.0025 | -0.0038 | 0.0455 | -0.0227 | -0.3261 \*\* | 0.2586 \* | 0.0771 |
| **Days to maturity** | rg |  | **1 \*\*** | 0.7355 \*\* | 0.1424 | 0.107 | 0.152 | -0.0355 | -0.2856 | 0.3279 | 0.1531 |
| rp |  | **1 \*\*** | 0.5575 \*\* | 0.0874 | 0.146 | 0.1417 | -0.0026 | -0.2813 \* | 0.2968 \* | 0.1077 |
| **Plant height (cm)** | rg |  |  | **1 \*\*** | 0.207 | 0.5166 \*\* | 0.2314 | 0.3424 | -0.3624 \* | 0.3597 \* | 0.542 \*\* |
| rp |  |  | **1 \*\*** | 0.3372 \*\* | 0.3384 \*\* | 0.187 | 0.1759 | -0.2088 | 0.3424 \*\* | 0.3976 \*\* |
| **Head diameter (cm)** | rg |  |  |  | **1 \*\*** | 0.5967 \*\* | 0.3138 | 0.2393 | -0.4703 \*\* | -0.0534 | 0.918 \*\* |
| rp |  |  |  | **1 \*\*** | 0.4437 \*\* | 0.1775 | 0.1329 | -0.2936 \* | -0.021 | 0.6672 \*\* |
| **100 Seed weight (g)** | rg |  |  |  |  | **1 \*\*** | 0.1456 | 0.5147 \*\* | -0.1782 | 0.2023 | 0.6511 \*\* |
| rp |  |  |  |  | **1 \*\*** | 0.0986 | 0.2579 \* | -0.1074 | 0.1672 | 0.4809 \*\* |
| **Volume weight (g)** | rg |  |  |  |  |  | **1 \*\*** | 0.0521 | -0.1484 | 0.0561 | 0.3515 \* |
| rp |  |  |  |  |  | **1 \*\*** | 0.1371 | -0.124 | 0.049 | 0.2025 |
| **Seed filling (%)** | rg |  |  |  |  |  |  | **1 \*\*** | -0.5465 \*\* | 0.128 | 0.7917 \*\* |
| rp |  |  |  |  |  |  | **1 \*\*** | -0.2968 \* | 0.0397 | 0.4661 \*\* |
| **Husk content (%)** | rg |  |  |  |  |  |  |  | **1 \*\*** | -0.4105 \* | -0.6705 \*\* |
| rp |  |  |  |  |  |  |  | **1 \*\*** | -0.3318 \*\* | -0.5548 \*\* |
| **Oil content (%)** | rg |  |  |  |  |  |  |  |  | **1 \*\*** | 0.1016 |
| rp |  |  |  |  |  |  |  |  | **1 \*\*** | 0.0359 |
| **Seed Yield / plant (g)** | rg |  |  |  |  |  |  |  |  |  | **1 \*\*** |
| rp |  |  |  |  |  |  |  |  |  | **1 \*\*** |

\* and \*\* Significant at 5 and 1 per cent level respectively.