



ISSN (E): 2277-7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2023; 12(8): 1940-1944
© 2023 TPI
www.thepharmajournal.com
Received: 06-06-2023
Accepted: 13-07-2023

Gopi V
Department of Genetics and
Plant Breeding, TNAU,
Coimbatore, Tamil Nadu, India

Kalaimagal T
Department of Oilseeds, TNAU,
Coimbatore, Tamil Nadu, India

Sasikala R
Department of Oilseeds, TNAU,
Coimbatore, Tamil Nadu, India

Harish S
Department of Oilseeds, TNAU,
Coimbatore, Tamil Nadu, India

Senthivelu M
Department of Oilseeds, TNAU,
Coimbatore, Tamil Nadu, India

Corresponding Author:
Kalaimagal T
Department of Oilseeds, TNAU,
Coimbatore, Tamil Nadu, India

Study on genetic parameters, correlation and path analysis in elite sunflower (*Helianthus annuus* L.) inbreds

Gopi V, Kalaimagal T, Sasikala R, Harish S and Senthivelu M

Abstract

The experimental research was performed with twenty peculiar and elite inbred lines in sunflower following Randomized block statistical design with three replications in the Department of oilseeds, Tamil Nadu Agricultural University (TNAU). Eight quantitative traits were considered to study genetic variability parameters, correlation and path association analysis. Owing to the analysis of variance (ANOVA), it revealed higher significant difference among all the traits at 1% probability level. High PCV and GCV values were found for volume weight (g), seed yield per plant (g) and head diameter (cm) which indicates that the sufficient amount of variability is present in the 20 inbreds and these traits can be suitably employed in the breeding programme. Traits such as days to 50% flowering, 100-seed weight (g) were having high heritability and high genetic advance hence selection will be effective for these traits. The polygenic traits Seed yield per plant (g) was found to be significant and in positively correlation with hundred seed weight and negatively correlated with days to 50% flowering (DF) and days to maturity (DM). The path analysis showed that significant positive direct effect of days to maturity, volume weight (g) and oil content (%) and hundred seed weight on seed yield per plant (SYPP). On the other hand, days to 50% flowering and head diameter (cm) had negative direct effect on seed yield per plant (SYPP). Residual effects of 0.55 reveals that the traits had contributed 45.5% to the variability and other unaccounted traits must be included to fully acknowledge the other independent and contributing traits to the seed yield per plant(g). Therefore the selection efficiency can be attained for the traits such as days to 50% flowering, 100-seed weight(g) and oil content(%) with high heritable differences and high genetic advance and simultaneously their association also favours for the selection of these traits and to genetically improve the sunflower inbreds with increased seed yield and in turn the oil yield.

Keywords: Sunflower, inbreds, variability, heritability, correlation, selection

Introduction

Sunflower is a widely consumed edible oil crop and industrially valuable crop with a high content of healthy poly unsaturated fatty acid (PUFA), making it popular in cooking and food processing industries. Its importance has gone to the extent of growing Organic sunflower in Romania. Although sunflower has its origin from the North America, the progression of genetic improvement has taken place after its introduction in the Russian federation after late 1800 by selection process. Because of their very short growth season (annual), they are cultivated all over the world especially in the tropics and subtropical regions in the world. In India, sunflower occupied an area of 0.22 m. ha with a productivity of 0.23 million tons and yield of 1023 kg per hectare (Agricultural statistics at a glance, 2021) [1]. As Safavi *et al.* (2015) [18] emphasized, the advancement of the breeding process is dependent on the features of both genotypic and non-genotypic variation in morphological attributes. Genetic parameters such as mean, standard deviation, coefficient of variance and heritability help to quantify the variability of traits and the extent to which they are inherited. In fact, the selection process operates well quite on the high heritable differences. Traits with high heritability are more likely to respond to selection, meaning that the frequency of the desired trait in the population can be increased over time. Through the estimation of genetic parameters, the quantum of variability which is paramount for crop breeding and the selection efficiency for traits can be accomplished. Understanding the relationship of other related traits with seed yield and oil content in sunflower is critical in any successful breeding strategy because the magnitude and direction of association of the traits with the seed yield determines the effectiveness of selection (Rani *et al.*, 2017) [17].

The path coefficient analysis is an important association studies that splits the correlation coefficient value into the measures of direct and indirect effects of independent characters on the dependent variable trait. Further the path analysis helps in knowing the contribution of other crucial traits contributing to the dependent characters through their residual effects and relationships among various traits, including yield components, seed yield, seed length, oil and hull content, as well as other agronomic traits, aids in the indirect selection for yield (Nadkarni *et al.*, 2017) [14]. In this way an experimental attempt was conducted to evaluate the genetic variability parameters, correlation with their path analysis in the twenty-elite sunflower inbreds which would be used to estimate the variability and the traits to be selected for achieving higher seed yield and simultaneously the oil content.

Materials and Methods

The experiment was conducted in the research farm of Department of Oilseeds, TNAU, Coimbatore located at 11°N latitude, 77°E longitude and 426 m above Mean Sea level. A sum of 20 sunflower inbreds were taken into consideration for the study. Inbreds was sown in randomized block statistical design (RBD) with 3 replications during *rabi*, 2023. The spacing followed for sowing was 60 × 45 cm in a row of 5 m ridge. All the agronomical practices such as thinning, gap filling, weeding was practiced and followed to ensure and maintain the optimum plant population. To prevent cross pollination from honeybees and to ensure selfing, the sunflower head was covered with white cloth bag at the time of flowering probably after 45 days. Quantitative traits such as head diameter(HD), plant height(PH),100-seed weight (HSW), days to 50 percent flowering (DF), days to maturity(DM), oil content (OC), volume weight(VW), seed yield per plant(SYPP) were evaluated. DF was observed on the basis of the number of days taken for 50% of the plants to initiate the flowering. DM was judged on the basis of physiological maturity that the back of the head turns from green colour to yellow and the seed moisture is about 35%. The seed oil content (%) was calculated by using a Near-infrared (NIR) spectroscopy instrument through which the accuracy of the value is well established. For traits namely, PH, HD and SYPP were recorded on five random plants per entry per replication and the derived mean data were used for analysis. The data of all the quantitative traits recorded in all the three replications were used to study the genetic variability parameters, correlation and path analysis. The genetic variability attributes were analyzed in the TNAU STAT package program -Statistical package (Manivannan, 2014) [11]. Genotypic correlations and path analysis were analyzed using the R based shiny package PB-Perfect (Allan, 2023) [2].

Results and Discussion

Estimation of analysis of variance (ANOVA) showed significant differences exists for all the traits observed under the study (Table 1) at 1% level of probability. This means that there is a 99% chance that the observed differences are not due to chance which itself signifies that further studies can be carried out. The estimates of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2) and Genetic advance as percentage of mean (GAM) which were used to measure the genetic variability

and potential for improvement of a trait. were given in Table 2. The coefficient of variation (cv) which is a statistical measure of dispersion expressed its higher value for SYPP (18.59%) and lower value for HD (3.67%). Other statistics, in addition to CV, should be analyzed for inferences regarding experimental quality, such as genetic variation and selective correctness, which are critical for appropriate interpretation of genotypic value from phenotypic assessments (RESENDE, 2002). By comparing the values of PCV with GCV, higher values were recorded in PCV than GCV for all the eight characters thus confirming the expression (Phenotypic variance = Genotypic variance + Environmental variance). High values of PCV and GCV were obtained for volume weight, seed yield per plant, head diameter which indicates significant role of these traits in the breeding programme. Similar kinds of results were also given by Singh *et al.*, 2017 [17]. Heritability helps to figure out the proportion of variance from the total variance. The heritable portion of the traits is very important for the effective selection of the inbreds since they suggest the possibility of their inheritance. High heritability (h^2) with greater than 80% was reported in OC, DF and HSW. High heritability in these three traits were also given earlier by Supriya *et al.*, 2016 [20]. The lowest heritability (h^2) was recorded in SYPP since environmental influence is much pronounced on the yield aspects which is governed by polygenic action. Lowest heritability (h^2) has been earlier reported in seed yield by Dafaallah *et al.*, (2015) [4]. The parameter genetic advance which preferably used to measure the genetic gain reflects the genetic increment that can be achieved in the successive generations. It was higher in DF, VW, HSW, SYPP and OC. Baraiya *et al.*, (2018) [3] came across with the same kind of high GMA in the study of forty-eight sunflower genotypes under irrigated conditions. It is desirable to select the traits with higher amount of heritability (h^2) together with genetic advance rather than concentrating particularly on heritability (Johnson *et al.*, 1955) [10]. Hence heritability coupled with GAM are the most suitable selection criteria for the improvement of the traits. In that note DF, HSW, and OC were having high heritability and high genetic advance. The heritability in these traits is mostly due to the additive nature of gene effects. Careful selection needs to be employed in order to genetically improve these traits in the breeding programme.

Table 1: Analysis of variance for various traits in sunflower

Characters	Genotype
Degree of freedom	19
	Mean sum of square
Days to 50 Flowering	291.3122**
Days to maturity	71.4877**
Plant height(cm)	628.8147**
Head diameter(cm)	15.2879**
Volume weight(g/100ml)	87.2109**
100 seed weight (g)	3.7112**
seed yield per plant(g)	28.4681**
Oil content (%)	45.0784**

**significance at 1% probability level

If there are no particular variables altering the strength of selection, it won't matter much in which environment (Phenotypic correlation) the selection is conducted if the genetic correlation between the two traits is high, and they may be considered to be nearly identical (Falconer *et al.*,

1981) [8]. In fact, the phenotype is a good indicator of the genotype when the genetic correlations are stronger than the environmental and phenotypic correlations. In our analysis by acknowledging Falconer comments the genotypic correlation coefficient was higher than phenotypic correlation for all the characters and the results of the genotypic correlation were given in the Table 3. Seed yield and oil content are the two important characters to be looked upon in sunflower and their performance are correlated with their associated characters. In the genotypic analysis, HSW has shown significant and positively correlation with OC. DF expressed its highly significance and positively correlated value with DM which indicates that the late flowering will slightly extend the days of the physiological maturity. The HD has shown high significantly positive correlated value with PH. The positively correlated value of VW with PH and HD was also noted. Both DF and DM are in negative correlation with SYPP. Their negative correlation indicated that early days of flowering and early stage of attaining maturity will leads to increased SYPP. Tyagi *et al.* (2010) [21] reported the negative correlation of the trait days for 50% flowering with seed yield. The dependent trait SYPP was significant and in positive association with HSW. The point is that the increase in HSW will results in the increased SYPP. Hence while making selection to improve the yield priority must be emphasized on these associated characters.

Path analysis finds a way to simplify and clarify the the exact contribution of each component to the overall yield. The genotypic path analysis was given in the Table.4 with seed yield per plant (SYPP) being the dependent character. Among the component traits DM, HSW, VW and OC had significant positive direct effect with SYPP or positive and significant

direct contribution to the SYPP. The positive direct effect of HSW on seed yield has been previously reported by Gjorgjieva *et al.* (2015) [5], Hladni *et al.* (2010) [9] and Gonzales *et al.* (2000) [6]. Only negligible direct effect of the trait PH on SYPP has been recorded. This shows that the trait plant height need not necessarily had a significant direct effect on the seed yield. DM and HD had significant negative direct effect on SYPP. The greatest positive indirect effect was seen in DF via DM and PH via DF on seed yield. These kinds of indirect effects were previously reported by Zia *et al.* (2013) [22] and Maria *et al.* (2018) [12]. The residual effects of 0.55 were accounted Since the independent characters contribute nearly 45.5% to the seed yield. Therefore, it is suggested to get into the knowledge of other characters which have not been studied here to fully account and acknowledge the variation contributing to the dependent trait. Contradictory results on residual effects with less than value of 0.5 were obtained by MOGALI & Virupakshappa (1994) [13]. The path analysis can be further well understood by the genotypic path diagram (Fig.1). The visualization of the array of various lines for the traits and their interrelationship with the component yield helps to decipher the complex nature of path association compared to the path table. The level of intensity of the colour of the arrow represents the degree of effects on dependent character. The SYPP was enlisted in the centre of the diagram as green dark circle. All the traits with direct positive effect are pointed to the single yield per plant with the arrow denoted in the green colour. Plant height has only negligible effect and it was denoted with light green arrow. DM and DM have negative direct effect on SYPP and it was denoted with red arrow.

Table 2: Estimation of genetic parameters for eight quantitative traits in sunflower

Parameters	Days to 50% flowering	Days to maturity	Plant height (cm)	Head diameter (cm)	Volume weight (g/100ml)	100-seed weight (g)	Seed yield per plant (g)	Oil content (%)
Mean	57.08	88.87	134.41	13.22	33.31	3.40	14.97	29.87
PCV (%)	13.03	6.26	12.99	20.69	17.80	34.87	25.58	13.56
GCV (%)	11.95	5.07	9.47	14.94	15.32	31.60	17.56	12.67
h ² (%)	84.16	65.47	53.19	52.16	74.00	82.14	47.13	87.31
GAM (%)	22.59	8.44	14.23	22.23	27.14	59.00	24.84	24.39

Table 3: Genotypic Correlation table for eight quantitative traits in sunflower

	DF	DM	PH	HD	HSW	VW	SYPP	OC
DF	1.00	0.91 **	0.21	-0.40	-0.22	-0.19	-0.47*	-0.15
DM	0.91**	1.00	0.23	-0.30	-0.24	-0.32	-0.48*	-0.31
PH	0.21	0.23	1.00	0.59 **	0.32	0.54*	0.13	0.30
HD	-0.40	-0.30	0.59 **	1.00	0.38	0.48*	0.26	0.43
HSW	-0.22	-0.24	0.32	0.38	1.00	0.04	0.39 *	0.47*
VW	-0.19	-0.32	0.54*	0.48*	0.04	1.00	0.24	0.24
SYPP	-0.47*	-0.48*	0.13	0.26	0.39	0.24	1.00	0.43
OC	-0.15	-0.31	0.30	0.43	0.47*	0.24	0.43	1.00

DF- days to 50% flowering

DM- Days to maturity

PH- Plant height

HD- Head diameter

HSW- 100-seed weight

VW- Volume weight

SYPP- Single yield per plant

OC- Oil content

**significance at 1% probability level, * significance at 1% probability level

Table 4: Genotypic path analysis for eight quantitative traits in sunflower

	DF	DM	PH	HD	HSW	VW	OC	Correlations with SYPP
DF	-1.041	0.525	0.028	0.177	-0.046	-0.049	-0.067	-0.472
DM	-0.956	0.571	0.031	0.132	-0.050	-0.082	-0.133	-0.486
PH	-0.216	0.132	0.136	-0.266	0.068	0.140	0.132	0.125
HD	0.411	-0.168	0.081	-0.449	0.080	0.124	0.186	0.265

HSW	0.225	-0.135	0.043	-0.168	0.212	0.009	0.207	0.394
VW	0.198	-0.181	0.074	-0.217	0.008	0.257	0.102	0.240
OC	0.160	-0.175	0.041	-0.192	0.101	0.061	0.433	0.428
Residual effect: 0.55								

DF- days to 50% flowering **DM**- Days to maturity **PH**- Plant height **HD**- Head diameter
HSD- 100-seed weight **VW**- Volume weight **SYPP**- Single yield per plant **OC**- Oil content
Bold values - direct effect on SYPP

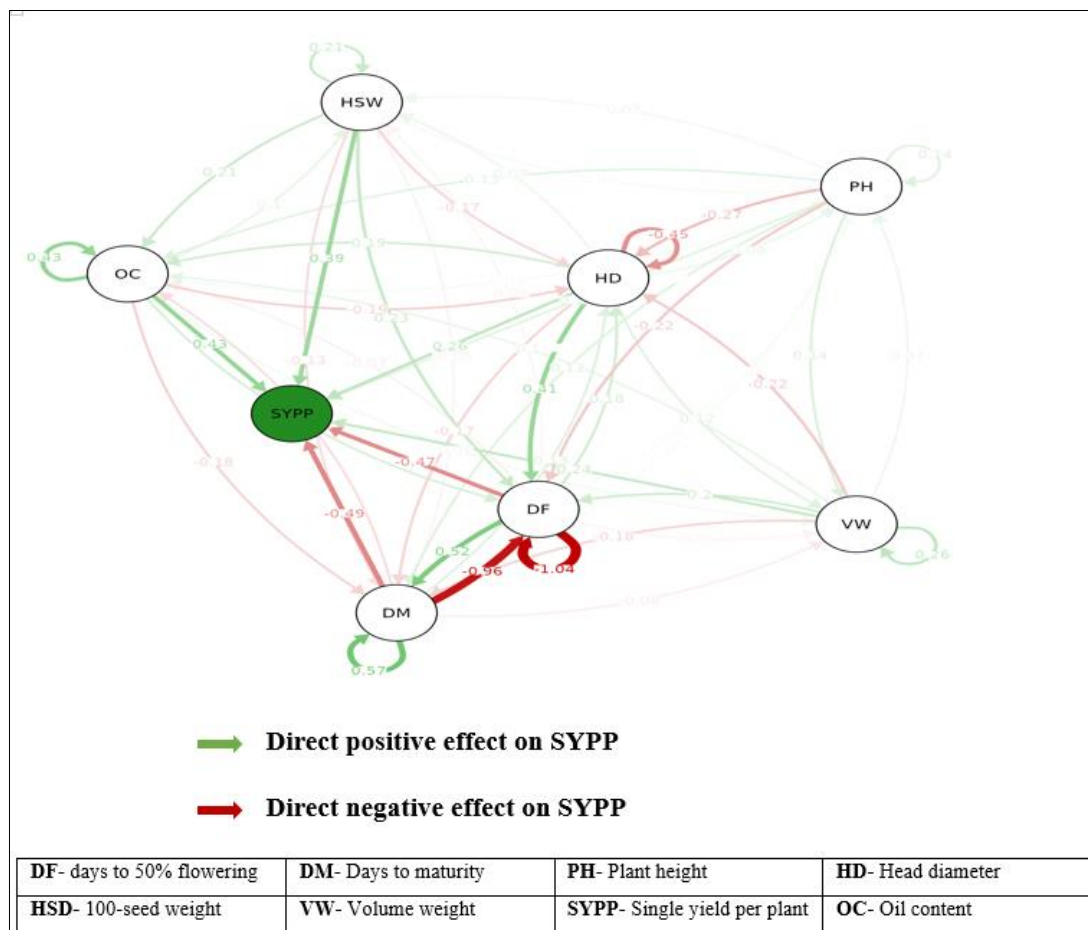


Fig 1: Genotypic path diagram for eight quantitative traits in sunflower inbreds

Conclusion

It can be concluded that the traits such as VW (g), HSW (g) and OC (%) which possess high heritability (h^2), high GMA and their positive association with increase in SYPP through association studies paves an immense scope to improve these traits through selection and in turn the oil yield. The inbreds with the selected traits possessing high variability responds well to the selection which can be utilized in the hybridization programme to release new cultivars or hybrids in sunflower with increased seed yield and oil content. Moreover, the future research priorities can be ascertained with these studies for the genetic improvement of sunflower inbreds.

Acknowledgement

The authors share our gratitude to the Director R. Ravikesavan, CPBG, TNAU for the permission and constant support to carry out the research. It is our immense pleasure to thank all the Agricultural officers, research scholars, farm and non-farm labour who has given their best and possible efforts to all the technical supports in the Department of Oilseeds, TNAU.

Conflict of Interest: None

References

1. Agricultural statistics at a glance, Directorate of Economics and Statistics, Department of Agriculture and Cooperation, New Delhi; c2021. [https://eands.dacnet.nic.in/PDF/Agricultural%20Statistics%20at%20a%20Glance%20-%202021%20\(English%20version\).pdf](https://eands.dacnet.nic.in/PDF/Agricultural%20Statistics%20at%20a%20Glance%20-%202021%20(English%20version).pdf)
2. Allan V. PB-Perfect - Statistical package; c2023. Retrieved from <https://allanbiotools.shinyapps.io/pbperfect/>
3. Baraiya VK, Patel PJHR. Genetic variability, heritability and genetic advance for seed yield in sunflower (*Helianthus annuus* L.). Indian J Crop Sci. 2018;6(5):2141-2143.
4. Dafaallah HMM. Genetic Variability and Stability Analysis of Five Sunflower (*Helianthus annuus* L.) Hybrids for Seed Yield, Gezira State, Sudan (Doctoral dissertation, University of Gezira; c2015).
5. Gjorgjieva B, Karov I, Mitrev S, Ruzdik N, Kostadinovska E, Kovacevik B. Correlation and Path Analysis in Sunflower (*Helianthus annuus* L.). Helia. 2015;38(63):201-210. <https://doi.org/10.1515/helia-2015-0008>

6. Gonzales J, Mancuso N, Oliva C. Factores geneticos, ambientales y correlaciones entre rendimiento y calidad de girasol. In Proc. 15th Intl. Sunflower Conf., Toulouse, France; c2000. p. 12-15.
7. Hussain T, Tariq MA, Ahmad I, Saghir M, Batool M, Safdar M, *et al.* Characters association analysis in Safflower (*Carthamus tinctorius* L.). Journal of Biology, Agriculture and Healthcare. 2014;4(6):63-65.
8. Falconer DS. Introduction to quantitative genetics. Pearson Education India; c1996.
9. Hladni N, Jocić S, Miklič V, Mijić A, Saftić-Panković D, Škorić D. Effect of morphological and physiological traits on seed yield and oil content in sunflower. Helia. 2010;33(53):101-116.
10. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans 1. Agronomy journal. 1955;47(7):314-318.
11. Manivannan N. Tnaustat-Statistical package; c2014. Retrieved from <https://sites.google.com/site/tnaustat>
12. Maria G, Farooq AK, Sajida H, Rizwana Q, Fida H, Hafiz SBM, *et al.* Genetic Variability Studies for Economically Important Traits in Sunflower (*Helianthus annuus* L.). Curr Inves Agri Curr Res; c2014-2018, 2(2). CIACR. MS. ID, 135.
13. Mogali SC, Virupakshappa K. Inter character Association and Path Coefficient Analysis in Sunflower (*Helianthus annuus* L.). Indian Journal of Genetics and Plant Breeding. 1994;54(04):366-370.
14. Nadkarni SR, Goud IS, Sheshaiah KC, Dalawai N, Hosamani M. Genetics of seed colour in sunflower (*Helianthus annuus* L.). Int. J Pure Appl. Biosci. 2017;5:1207-1214.
15. Pandya MM, Patel PB, Narwade AV. A study on correlation and path analysis for seed yield and yield components in Sunflower [*Helianthus annuus* (L.)]. Electronic Journal of Plant Breeding. 2016;7(1):177-183.
16. Resende MD. Biometric and statistical genetics in breeding perennials. Brasília, DF: Embrapa Informação Tecnológica; c2002.
17. Rani MAMTA, Sheoran OP, Sheoran RK, Chander SUBHASH. Genetic variability, character association and path analysis for agronomic traits in sunflower (*Helianthus annuus* L.). Annals of Agri-Bio Research. 2017;22(1):31-35.
18. Safavi SM, Safavi AS, Safavi SA. Assessment of genetic diversity in sunflower (*Helianthus annuus* L.) genotypes using agro-morphological traits. J. Bio. & Env. Sci. 2015;6(1):152-159.
19. Singh VK, Sheoran RK, Chander S, Sharma B. Genetic variability, evaluation and characterization of sunflower (*Helianthus annuus* L.) germplasm. Bangladesh Journal of Botany. 2019;48(2):253-263.
20. Supriya SM, Kulkarni VV, Lokesh R, Govindappa MR. Genetic variability studies for yield and yield components in sunflower (*Helianthus annuus* L.). Electronic Journal of Plant Breeding. 2016;7(3):737-741.
21. Tyagi SD, Tyagi JP. Correlation and path coefficient analysis of the components of yield in sunflower cultivars (*Helianthus annuus* L.). Indian Journal of Plant Genetic Resources. 2010;23(03):321-323.
22. Zia-Ullah Z, Sadaqat HA, Tahir MHN, Sadia B. Path coefficient analysis of various traits in sunflower (*Helianthus annuus* L.). Journal of Global Innovations in