

Correlation and path analysis studies in maintainer and restorer lines of sunflower (*Helianthus annuus* L.)

Sree vathsa sagar U.S.¹, *Vikas Kulkarni², Hemalatha³, Diwan J.R.⁴, Rajanna B.⁵, Umesh M.R.⁶.

¹ M. Sc. (Agri), Department of Genetics and Plant Breeding, College of Agriculture, Raichur

² Scientist (Breeding) and Head, AICRP on Sunflower, MARS, Raichur

³ M. Sc. (Agri), Department of Genetics and Plant Breeding, College of Agriculture, Raichur

⁴ Associate professor, Department of Genetics and Plant Breeding, UAS, Raichur

⁵ Scientist (Breeding), AICRP on Groundnut, MARS, Raichur

⁶ Scientist, AICRP on Sunflower, MARS, Raichur

ABSTRACT

Sunflower is the annual plant cultivated mainly as oil seed crop, it contains 40 to 50 % oil. Oil majorly has oleic acid and linolic acid as fatty acids, making this a high quality oil. The correlation and path analysis studies among the sixty five sunflower genotypes was done which includes 55 restorer lines, 5 maintainer lines and 5 checks for sixteen yield attributing traits. The correlation results revealed that the traits like number of seeds per head, number of leaves per plant, seed filling per cent, head diameter and plant height exhibited significant positive correlation with seed yield at phenotypic and genotypic level. In path analysis the traits like by test weight, seed filling per cent, number of leaves per plant, NDVI, SPAD, head diameter, days to 50% flowering, total chlorophyll, chlorophyll a, plant height and days to maturity exhibited positive direct effects on seed yield per plant. While oil content, volume weight and chlorophyll b exhibited negative direct effects on seed yield per plant, at phenotypic level and genotypic level. Traits like number of seeds per head, test weight, seed filling per cent, seed yield per plant, number of leaves per plant and head diameter can be used for selection for sunflower improvement.

Key words : Sunflower, restorer lines, maintainer lines, correlation and path analysis.

INTRODUCTION

Sunflower (*Helianthus annuus* L.) is the world's fourth largest oil-seed crop and its seeds are used as source of quality oil its dried stalk as fuel. Yield is the very important trait in sunflower hybrids for achieving high yield, highly potential and diverse inbreeds need to be crossed that would result in best hybrid. Selection of maintainer and restorer lines is the crucial and initial step in hybrid breeding programme, mere direct selection of better genotypes based on the yield is not effective, as yield is the polygenic trait that is governed by many genes and other component traits. Thus both direct and indirect selection for yield requires correlation study which, reveal the association of yield with other attributing traits, However path analysis divides the correlation into direct and indirect effects by studying the effects of component

traits on the yield from which individual traits contribution for yield could be understood more precisely. Thus in present investigation newly derived sunflower restorer and maintainer lines were subjected for correlation study to understand association between the yield and its attributing traits and path analysis for understanding the direct and indirect effects on yield.

MATERIAL AND METHODS

Fifty five restorer lines and five maintainer lines along with five checks were evaluated at Main Agricultural Research Station, Raichur. The experiment was laid out in Augmented block design with four blocks with a spacing of 60 cm between rows and 30 cm between plants. Each genotype was grown in two rows of 4 mt length. Crop was raised by following recommended package of practice. Random five plants were selected from each genotype for recording observations for sixteen traits *viz.* SPAD (Soil Plant Analysis Development), NDVI(Normalized Difference Vegetation Index), chlorophyll a (mg/g), chlorophyll b (mg/g), total chlorophyll (mg/g), days to 50 % flowering, number of leaves per plant, days to maturity, plant height (cm), head diameter (cm), seed yield per plant (g), test weight (g), number of seeds per head, seed filling per cent (%), oil content (%) and volume weight (g/100 ml).

Genotypic and phenotypic correlation co-efficients were calculated using the method given by Johnson *et al.* (1955). The significance of correlation co-efficient was tested by comparing the genotypic and phenotypic correlation co-efficients with F table value at (n-2) degree of freedom at 5 per cent and 1 per cent levels of significance. The direct and indirect effects of the yield components on the yield was estimated by Path co-efficient analysis as suggested by Wright (1921) and elaborated by Dewey and Lu (1959).

RESULT AND DISCUSSION

There is need to develop the good sunflower hybrids for diverse climatic conditions and requirements, thus for that elite breeding lines are necessary. The analysis of variance revealed that there was significant difference between mean sum of squares for all the traits studied except SPAD, NDVI, and days to maturity (Table 1) indicating that there is enough variability exists in present genotypes. Selection of the lines would be effective if it is done according to the traits that are correlated to the yield. The phenotypic and genotypic correlations for yield and yield related traits are represented in Table 2 and 3 respectively. The correlation coefficients data revealed that genotypic correlations were higher than phenotypic correlations indicating that traits were less influenced by environment. Seed yield per plant exhibited the highly significant positive correlation with number of seeds per head (0.581) and number of leaves (0.400), as number of seeds increases yield per plant would obviously increase, while significant positive correlation with plant height (0.373), NDVI (0.350), seed filling per cent (0.313) and plant height (0.250) at phenotypic level. Whereas at genotypic level NDVI (0.777), number of leaves (0.619) and number of seeds per head (0.581) exhibited high significant positive correlation with seed yield per plant, while significant positive correlation with head diameter (0.337), seed filling per cent (0.289) and SPAD (0.297). These findings indicates that the direct selection of these traits *viz.* seed filling per cent, head diameter, number of seeds per

head and number of leaves are effective. Thus signifying that priority should be given for these traits in crop improvement of sunflower for yield. These findings were in agreement with Göksoy *et al.* (2007), Neelima *et al.* (2012), Tyagi *et al.* (2013), Bu (2014), Kulkarni *et al.* (2015), Lake and sandras (2016), Andrade *et al.* (2016), Pepó and Novak (2016) and Riyaz *et al.* (2019). Number of seeds per head, number of leaves, seed filling per cent and NDVI exhibited the significant positive correlation with seed yield per plant at both genotypic and phenotypic level. While oil content exhibited negative non-significant correlation with seed yield per plant (- 0.043) which is very low and this is in contrasting with earlier results by Sowmya *et al.* (2010) where significant negative correlation was obtained, this will reveal that negative correlation of yield with oil has reduced to non-significant negative. Indicating the new population or gene pool development needs to be attempted where both seed yield and oil content can be improved simultaneously.

The path analysis results revealed that direct effects was found from the number of seeds per head which was highest and followed by test weight, seed filling per cent, number of leaves per plant, NDVI, SPAD, head diameter, days to 50% flowering, total chlorophyll, chlorophyll a, plant height and days to maturity. While oil content, volume weight and chlorophyll b exhibited negative direct effects on seed yield per plant, at phenotypic level represented in Table 4 and Fig 1, these similar results were also obtained by Abrar *et al.* (2010), Darvishzadeh *et al.* (2011), Jocković *et al.* (2015) Riyaz *et al.* (2019) and Kulkarni *et al.* (2022). Where as at genotypic level number of seeds per head followed by chlorophyll a, days to 50% flowering, days to maturity, SPAD, head diameter, plant height and number of leaves exhibited positive direct effects on seed yield per plant. While volume weight followed by oil content, NDVI, seed filling %, total chlorophyll and chlorophyll b recorded negative direct effects on seed yield per plant represented in Table 5 and Fig 2. Similar findings were also reported by Teklewold *et al.* (2000), Vidhyavathi *et al.* (2005), Abrar *et al.* (2010), Darvishzadeh *et al.* (2011), Jocković *et al.* (2015) kulkarni *et al.* (2015) Baraiya *et al.* (2018) and Kulkarni *et al.* (2022). These results indicates that number of seeds per head, head diameter, number of leaves per plant, plant height and days to maturity can be considered for more effective selection in crop improvement programme having yield as objective. The residual effect will measure the role of other independent variables on the dependent variable which were not included in study. Residual effect in present study were 0.456 and 0.362 at phenotypic level and genotypic level, respectively indicating major portion of direct and indirect effects were captured by observations studied in present experiment depicted in Fig 3 and 4 respectively.

Table 1. Analysis of variance for yield and yield attributing traits of sunflower genotypes

	Df	SPAD	NDVI	Chl a	Chl b	T Chl	DFF	NOL	DM	PH	HD	SFP	TW	NSPH	OC	VW
Block (ignoring Treatments)	3	15.7	0.08**	0.2	0.01	0.4**	45.2 **	12.2	19.8	1412.3 **	10.4 *	75.7**	2.2 **	0.5 **	7489 **	1398 **
Treatment (eliminating Blocks)	64	12.7	0.02	0.4 *	0.12*	0.5 **	23.5 **	19.2*	27.2	380.6 **	11.1 **	17.1 *	11.2 **	2.7 **	21550 **	1632 **
Checks	4	19.6	0.02	3.4 **	0.12**	3.9 **	29.3 **	70.8 **	104.1	1573.4 **	77.2 **	58.4 **	43.8 **	11.8 **	15163 **	54 **
Checks+Var vs. Var.	60	12.2	0.01	0.2	0.01	0.2 **	23.1 **	15.8*	22.1	301.1 **	6.7 *	14.3 *	9.0 **	2.1 **	21976 **	1738 **
Block (eliminating Check+Var.)	3	13.2	0.02	0.07	0.01	0.07	6.5	6.1	19.4	53.6	2.0	5.3	0.3	0.04	391	0.08
Entries (ignoring Blocks)	64	12.8	0.01	0.4 *	0.02	0.5 **	25.3 **	19.5* *	27.3	444.3 **	11.5 **	20.4 **	11.3 **	2.8 **	21883 **	1698 **
Varieties	59	12.2	0.01	0.2	0.01	0.3 **	16.1 **	10.9	15.0	368.7 **	5.8*	17.6 *	6.4 **	1.5 **	21148 **	1833 **
Checks vs. Varieties	1	17.8	0.02	0.9 *	0.02	0.2	555.1 **	324.3 **	440.3**	386.3 *	85.6 **	30.1 *	167.7 **	42.0 **	92120 **	296 **
ERROR	12	6.2	0.01	0.1	0.09	0.05	2.03	5.5	40.1	68.6	2.1	5.5	0.3	0.01	268.0	0.01

Table 2. Phenotypic correlation coefficient for yield and yield attributing traits in sunflower

	SPAD	NDVI	Chl a	Chl b	Chl a+b	DFF	NOLP	DM	PH	HD	SFP	SYPP	TW	NSPH	OC	VW
SPAD	1.000	0.184	-0.059	-0.005	-0.034	-0.078	0.169	-0.005	0.171	0.140	0.181	0.141	-0.045	-0.216	0.277*	0.173
NDVI		1.000	0.024	-0.051	0.012	0.279*	0.074	0.154	0.502**	0.253*	0.117	0.102	0.151	-0.051	0.275*	0.350*
Chl a			1.000	0.520**	0.815**	-0.071	-0.103	0.024	-0.074	0.037	-0.021	0.106	0.036	0.007	-0.057	0.075
Chl b				1.000	0.576**	0.089	-0.034	0.065	-0.115	-0.035	-0.008	0.009	-0.016	-0.109	-0.103	-0.100
Chla+b					1.000	0.034	-0.121	0.044	0.003	0.119	0.058	0.098	0.098	-0.016	0.010	0.142
DFF						1.0000	-0.107	0.480**	0.295*	0.131	-0.194	0.263*	0.176	-0.108	0.271*	0.031
NOLP							1.000	-0.086	0.212	0.098	0.006	-0.184	0.451**	0.120	0.125	0.400**
DM								1.000	0.265*	-0.060	-0.170	-0.239	0.138	-0.172	0.248*	-0.0206
PH									1.000	0.367*	0.207	0.071	0.181	0.032	0.027	0.373*
HD										1.000	0.316*	0.362*	-0.187	-0.049	-0.211	0.250*
SFP											1.000	0.169	0.020	0.080	0.109	0.313*
SYPP												1.000	0.577**	-0.039	0.027	0.168
TW													1.000	-0.011	0.169	0.581**
NSPH														1.000	0.215	-0.041
OC															1.000	0.174
VW																1.000

Table 3. Genotypic correlation coefficient for yield and yield attributing traits in sunflower

	SPAD	NDVI	Chl a	Chl b	Chl a+b	DFP	NOLP	DM	PH	HD	SFP	SYPP	TW	NSPH	OC	VW
SPAD	1.000	0.222	-0.743**	-0.678**	-0.344*	-0.154	0.451**	-0.205	0.430**	0.399**	0.168	0.218	-0.090	-0.329*	0.398*	0.297*
NDVI		1.000	-0.720**	-0.546**	-0.640**	0.697**	0.741**	-0.687**	0.732**	0.844**	0.587**	0.134	0.435**	-0.127	0.543**	0.777**
Chl a			1.000	0.779**	0.833**	-0.038	0.187	0.406**	-0.308*	0.372*	-0.159	0.092	0.076	0.007	-0.276*	-0.010
Chl b				1.000	0.681**	0.073	-0.278*	-0.137	-0.190	-0.275*	-0.676**	-0.077	-0.075	-0.216	-0.360*	-0.140
Chla+b					1.000	0.017	-0.024	0.069	-0.101	0.242	-0.034	0.093	0.128	-0.018	-0.024	0.178
DFP						1.000	-0.219	0.951**	0.338*	0.063	-0.264*	-0.287*	0.191	-0.118	-0.293*	0.039
NOLP							1.000	-0.223	0.353*	-0.102	-0.104	-0.283*	0.673**	0.182	0.192	0.619**
DM								1.000	-0.130	-0.733**	0.273*	0.238	-0.117	0.177	0.294*	0.051
PH									1.000	0.769**	0.452**	0.082	0.246*	0.037	0.031	0.506**
HD										1.000	0.456**	0.478**	-0.249*	-0.065	-0.273*	0.337*
SFP											1.000	0.186	-0.018	0.101	0.100	0.289*
SYPP												1.000	-0.583**	-0.040	0.016	0.160
TW													1.000	-0.012	0.169	0.581**
NSPH														1.000	0.216	-0.043
OC															1.000	0.162
VW																1.000

	SPAD	NDVI	Chl a	Chl b	Chl a+b	DFF	NOLP	DM	PH	HD	SFP	SYPP	TW	NSPH	OC	VW
SPAD	0.070	0.013	-0.004	-0.004	-0.002	-0.005	0.012	-0.004	0.012	0.009	0.012	0.010	-0.003	-0.015	0.019	0.173
NDVI	0.014	0.078	0.001	-0.004	0.001	0.021	0.005	0.012	0.039	0.019	0.009	0.008	0.011	-0.004	0.021	0.350*
Chl a	-0.001	0.005	0.020	0.010	0.016	-0.001	-0.002	0.005	-0.001	0.008	-0.004	0.002	0.007	0.001	-0.001	0.075
Chl b	0.000	0.006	-0.064	-0.124	-0.071	-0.011	0.004	-0.008	0.014	0.004	0.001	-0.001	0.002	0.013	0.012	-0.100
Chla+b	-0.001	0.005	0.033	0.023	0.041	0.001	-0.005	0.001	0.002	0.004	0.002	0.004	0.004	-0.007	0.004	0.141
DFF	-0.004	0.015	-0.004	0.004	0.001	0.055	-0.005	0.026	0.016	0.007	-0.010	-0.014	0.009	-0.006	-0.014	0.031
NOLP	0.017	0.008	-0.010	-0.003	-0.012	-0.011	0.103	-0.009	0.022	0.010	0.006	-0.019	0.046	0.012	0.013	0.400**
DM	0.000	0.005	0.001	0.002	0.001	0.001	-0.003	0.003	0.008	-0.002	-0.005	-0.008	0.004	-0.005	-0.008	-0.020
PH	0.001	0.003	-0.004	-0.007	0.000	0.001	0.001	0.001	0.006	0.002	0.001	0.004	0.001	0.002	0.002	0.373*
HD	0.009	0.016	0.002	-0.002	0.007	0.008	0.006	-0.004	0.023	0.065	0.020	0.023	-0.012	-0.003	-0.013	0.250*
SFP	0.027	0.018	-0.003	-0.001	0.009	-0.030	0.009	-0.026	0.031	0.048	0.154	0.026	0.003	0.012	0.016	0.313*
TW	0.091	0.066	0.069	0.006	0.063	-0.170	-0.119	-0.155	0.046	0.234	0.109	0.648	-0.374	-0.025	0.017	0.167
NSPH	-0.040	0.136	0.032	-0.014	0.087	0.158	0.405	0.124	0.162	-0.168	0.018	-0.518	0.898	-0.010	0.151	0.581**
OC	0.008	0.002	0.000	0.004	0.001	0.004	-0.004	0.006	-0.001	0.000	-0.003	0.001	0.000	-0.003	-0.008	-0.041
VW	-0.013	-0.013	0.002	0.005	-0.005	0.013	-0.006	0.011	-0.001	0.010	-0.005	-0.001	-0.008	-0.010	-0.048	0.174
SYPP	0.173	0.350*	0.075	-0.100	0.141	0.031	0.400**	-0.020	0.373*	0.250*	0.313*	0.167	0.581**	-0.041	0.174	1.000

Table 4. Phenotypic path coefficient showing direct and indirect effects of different quantitative traits on seed yield

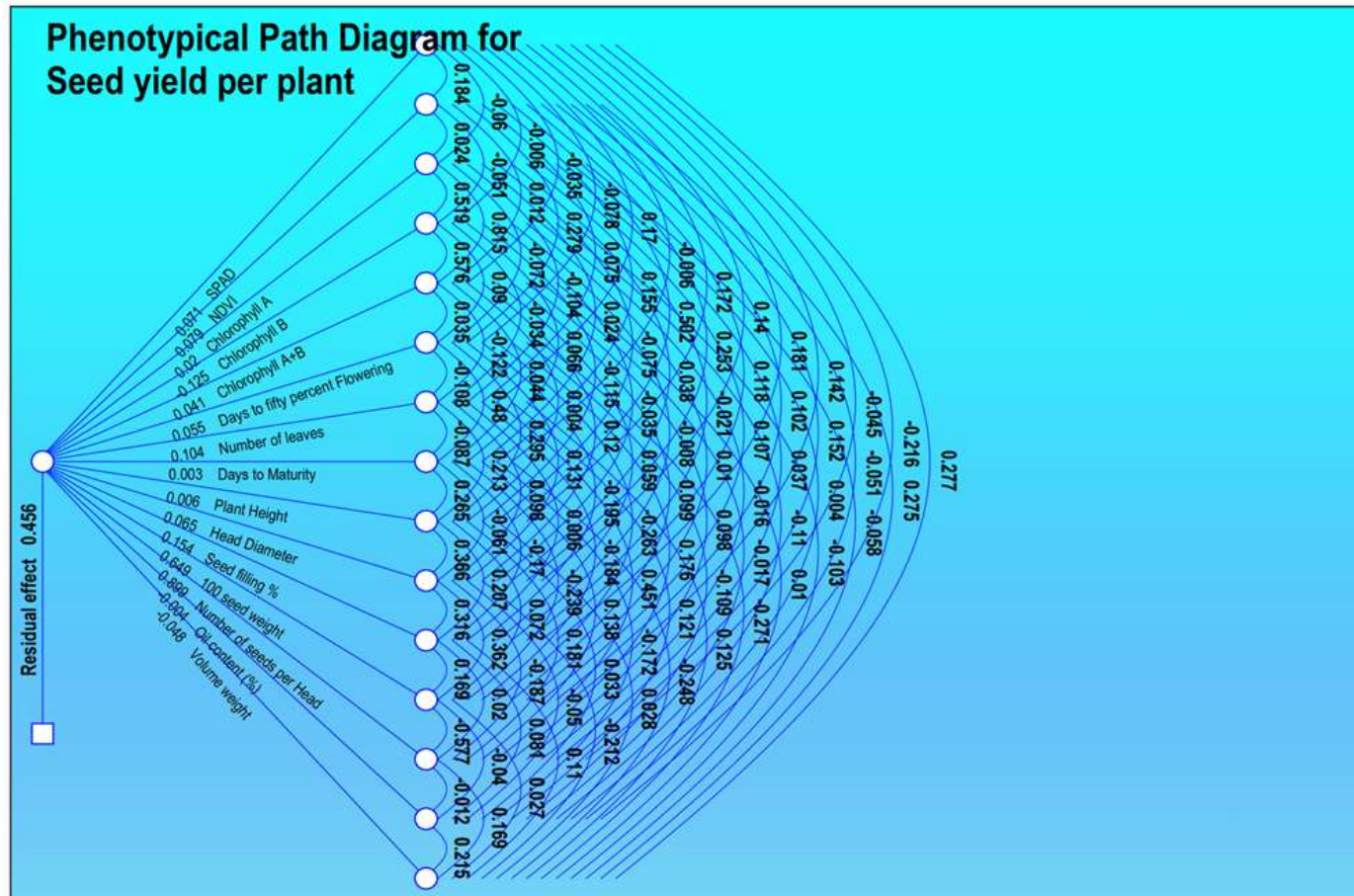


Fig. 1. Phenotypic path diagram for seed yield per plant in sunflower

	SPAD	NDVI	Chl a	Chl b	Chl a+b	DFP	NOLP	DM	PH	HD	SFP	TW	NSPH	OC	VW	SYPP
SPAD	0.249	0.055	-0.185	-0.169	-0.085	-0.038	0.112	-0.051	0.107	0.099	0.042	0.054	-0.022	-0.082	0.099	0.297*
NDVI	-0.010	-0.046	0.106	0.103	0.029	-0.032	-0.081	0.031	-0.065	-0.038	-0.027	-0.006	-0.020	0.005	-0.025	0.777**
Chl a	-0.404	-1.261	0.543	0.423	0.662	-0.020	0.101	0.221	-0.167	0.202	-0.086	0.050	0.041	0.004	-0.149	-0.010
Chl b	0.330	1.095	-0.380	-0.487	-0.332	-0.035	0.135	0.067	0.092	0.134	0.329	0.037	0.036	0.105	0.175	-0.140
Chla+b	0.107	0.199	-0.380	-0.212	-0.312	-0.005	0.007	-0.021	0.031	-0.075	0.010	-0.029	-0.040	0.005	0.007	0.178
DFP	-0.054	0.246	-0.013	0.025	0.006	0.353	-0.077	-0.336	0.119	0.022	-0.093	-0.101	0.067	-0.041	-0.103	0.039
NOLP	0.015	0.060	0.006	-0.009	-0.008	-0.007	0.033	-0.007	0.011	-0.003	-0.003	-0.009	0.022	0.006	0.006	0.619**
DM	-0.064	-0.213	0.126	-0.042	0.021	-0.295	-0.069	0.310	-0.040	-0.227	0.084	0.074	-0.036	0.055	0.091	0.051
PH	0.055	0.184	-0.039	-0.024	-0.013	0.043	0.045	-0.016	0.129	0.099	0.058	0.010	0.031	0.004	0.004	0.506**
HD	0.059	0.126	0.055	-0.041	0.036	0.009	-0.015	-0.109	0.115	0.149	0.068	0.071	-0.037	-0.009	-0.040	0.337*
SFP	-0.029	-0.101	0.027	0.116	0.006	0.045	0.017	-0.047	-0.077	-0.078	-0.172	-0.032	0.003	-0.017	-0.017	0.289*
TW	0.117	0.071	0.049	-0.041	0.050	-0.153	-0.151	0.128	0.044	0.256	0.100	0.536	-0.313	-0.021	0.008	0.160
NSPH	-0.077	0.370	0.064	-0.064	0.109	0.162	0.573	-0.100	0.209	-0.212	-0.015	-0.496	0.851	-0.010	0.144	0.581**
OC	0.013	0.005	-0.003	0.008	0.008	0.004	-0.007	-0.007	-0.001	0.002	-0.004	0.001	0.005	-0.041	-0.008	-0.043
VW	-0.01	-0.016	0.008	0.010	0.007	0.008	-0.005	-0.008	-0.009	0.008	-0.003	-0.005	-0.005	-0.006	-0.030	0.162
SYPP	0.29*	0.777**	-0.010	-0.404**	0.178	0.039	0.619**	0.0517	0.506**	0.337*	0.289*	0.160	0.581**	-0.043	0.162	1.000

Table 5. Genotypic path coefficient showing direct and indirect effects of different quantitative traits on seed yield

SP : SPAD; **NV**: NDVI; **Chl a**: Chlorophyll a (mg/g); **Chl b**: Chlorophyll b (mg/g); **Chl a+b** : Total chlorophyll (mg/g); **DFP**: Days to 50% Flowering; **NOL**: Number of leaves; **DM**: Days to Maturity; **SFP**: Seed filling (%); **SYPP**: Seed yield per plant(g); **TW**: Test weight (g); **PH**: Plant height (cm); **NSPH**: Number of seeds per Head; **HD**: Head Diameter (cm); **OC**: Oil content (%); **VW**: Volume weight (g/ml).

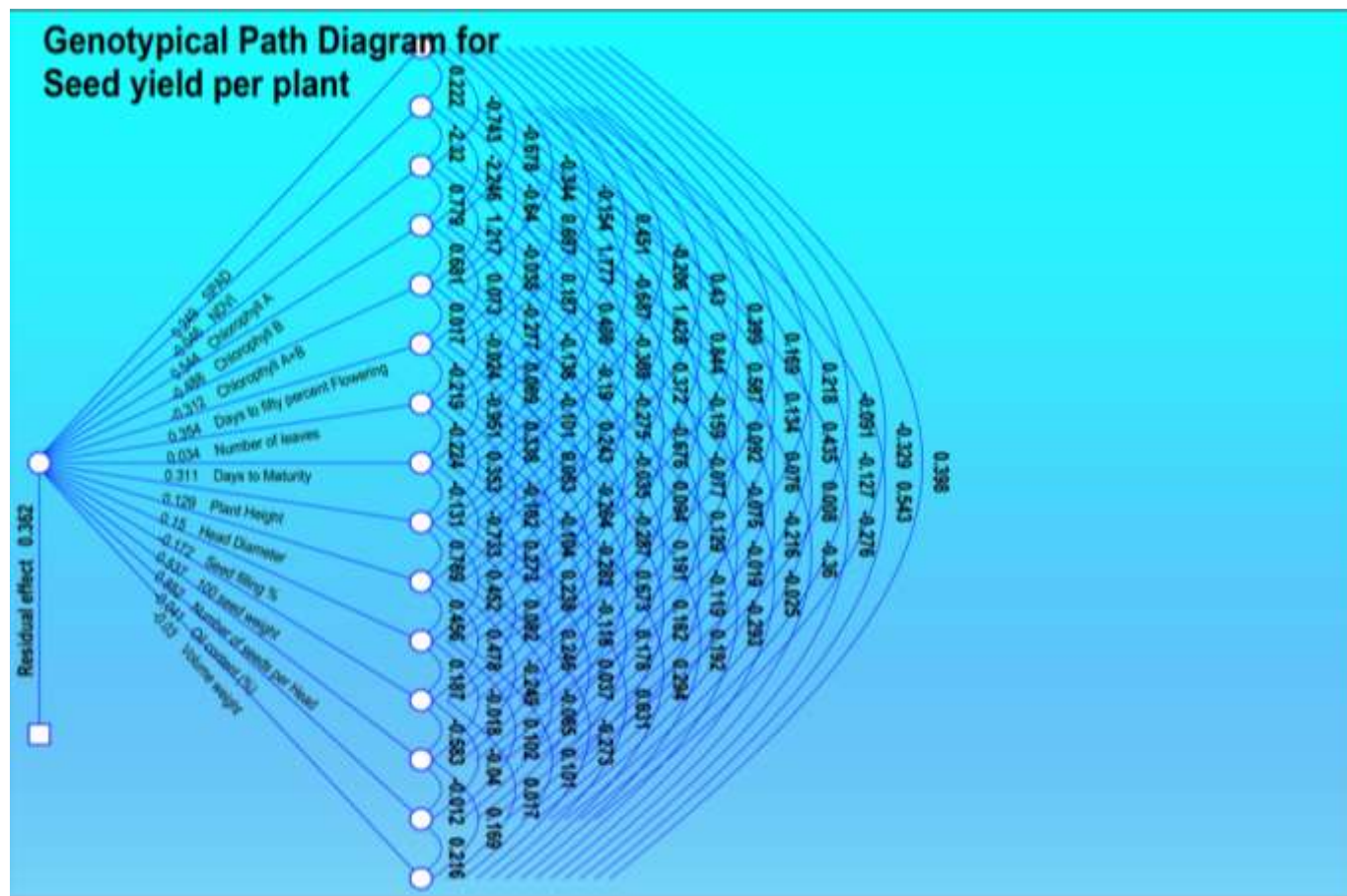


Fig. 2. Genotypic path diagram for seed yield per plant in sunflower

Conclusion

Sunflower crop improvement relies on the quality and potential of the breeding lines used in the programme, thus for development of the elite lines, selection between the lines from the population should be based on the few important traits. Choice of traits for selection must be made on basis of traits that are correlated with seed yield per plant. In present investigation the results revealed that traits like number of seeds per head, test weight, head diameter, number of leaves and NDVI exhibited the significant positive correlation with seed yield per plant. Whereas path analysis revealed direct effects of SPAD, NDVI, number of seeds per head, number of leaves, plant height, head diameter and seed filling per cent on seed yield per plant. While in path analysis studies traits exhibited direct and indirect effects on seed yield per plant, thus selection based on correlation and path analysis of identified traits are important and must be prioritised while selecting elite breeding lines for crop improvement in sunflower.

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