Studies on genetic variability and character association in fennel (*Foeniculum vulgare* Mill.)

ABSTRACT

Aim: To study the genetic variability and character association in fennel.

Study Design: Randomised Complete Block Design (RCBD)

Place and Duration of study: Horticultural Research Farm, Department of Horticulture, Naini Agricultural Institute, SHUATS, Prayagraj. Between November 2021 to April 2022.

Methodology: 10 genotypes of fennel were sown in three replications in RCB design. In each replication data were observed on five plants and averaged for all twelve characters under study.

Results: Analysis of variance showed the presence of significant variation among different genotypes for all characters studied. Number of primary branches per plant and seed yield per hectare exhibited moderate estimates of GCV and PCV and also High estimates of Heritability (Broad-sense). Positive and significant correlation was observed for number of umbels per plant, number of umbellets per umbel, number of seeds per umbel, seed yield per hectare and seed index with seed yield per plant at both phenotypic and genotypic level. Path Coefficient analysis revealed that days to maturity, number of primary branches per plant, number of seeds per umbel, seed index and harvest index had direct positive effect on seed yield per plant at genotypic level. While days to 50% flowering, days to maturity, number of umbels per plant, number of umbellets per umbel, number of seeds per umbel, seed yield per hectare and seed index had direct positive effect on seed yield per plant at phenotypic level.

Conclusion: Selection in these traits will lead to higher efficiency in breeding programme for improving yield. Thus these traits may be ranked as most important attributing traits for seed yield per plant in fennel.

Keywords: Fennel, GCV, PCV, Heritability, Genetic Advance, Path coefficient analysis.

1. INTRODUCTION

Fennel is a flowering plant species in the carrot family. It is a hardy, perennial herb with yellow flowers and feathery leaves. It is indigenous to the shores of the Mediterranean but has become widely naturalized in many parts of the world, especially on dry soils near the sea-coast and on riverbanks. Botanically, fennel known as ***Foeniculum vulgare*** **Mill.** belongs to family *Apiaceae.* It is a cross pollinated diploid crop species with chromosome number, 2n=2X=22 (**Karpechenko, 1925**) [1] and native of Europe (**De Candolle, 1967**) [2]. It is an annual, biennial, or perennial herbaceous plant, depending on the variety, which grows in good soils from sunny mild climatic regions and is a well-known aromatic plant species. The leaves and seeds of fennel are used in many culinary traditions**.**

India ranks first in fennel production producing 60% of world's fennel production followed by China and Bulgaria (**FAOSTAT, 2019)** [3]. The area under Fennel production in India accounts to 82.72 thousand ha with production of 137.29 million tonnes in year 2020-21. (*Source: **NHB,*** **Ministry of Agriculture & Farmers Welfare, Government of India, 2020-21**) [4]. Gujarat ranks first in area and production of fennel in year 2020-21 followed by Rajasthan and Madhya Pradesh. The production of fennel in Uttar Pradesh is 0.64 million tonnes for year 2020-21. A raw fennel bulb (235 g) consists of 212 g of water, 2.91 g of protein, 0.47 g of fat, and 17.2 g of carbohydrate (including 7.28 g of dietary fibre and 9.24 g of sugars), providing a total of 72.8 Calories (kcal) of energy. The 235g bulb provides 115 mg of calcium, 1.72 mg of iron, 40 mg of magnesium, 188 mg of phosphorus, 973 mg of potassium, 122 mg of sodium, trace amounts of zinc, copper, and selenium, 28.2 mg of vitamin C, as well as choline, several B vitamins, folate, beta-carotene, lutein, zeaxanthin, vitamin E, and vitamin K. (**FDC, USDA, 2021)** [5].

Yield is a complex character and depends upon number of component characters which are quantitatively inherited. As such before launching any breeding programme, a thorough knowledge of the nature and magnitude of genetic variability and extent of association between yield and other components is essential. Evaluation of genotypes to assess the existing variability is considered as preliminary step in any crop improvement programme. Information on the magnitude of variation in the available genetic material and the part played by the environment on the expression of plant characters are prime importance for the appraisal of the magnitude of possible improvement. Variability for different traits in the source population is a prerequisite for crop improvement since all attempts of breeding and selection would be futile

unless major portion of variability is heritable. Further, estimate of genetic advance and heritability would give the best picture of the extent of improvement expected from selection and reliability of selection based on phenotype. Path coefficient is defined as the ratio of the standard deviation of the effect due to a given cause to the total standard deviation of the effect. The path analysis is simply standardized partial regression coefficient analysis which may be useful in choosing the characters that have direct and indirect effect on yield. The correlation coefficient provides information about the degree of association between two characters. However, it is now known that almost all characters are polygenic and almost all genes are pleiotropic in action such that each gene, apart from its direct contribution to a particular character contributes to several other characters also. Therefore, correlation coefficient alone would not provide a clear picture about the contribution of a particular character. For example, the estimates of correlation coefficient between two characters may be positive but the direct effect of the characters to the correlation coefficient may be negative. In this case, indirect effects are the cause of correlation coefficient and have masked the direct effect of the character. In such instances, indirect effect should be taken into consideration in formulating a selection strategy. Path analysis was initially suggested by **Wright (1921)** [6] and he gave the concept and methodology of path analysis but was applied for the first time in plant breeding by **Dewey and Lu (1959)** [7].

2. MATERIAL AND METHODS

The experimental material for present investigation comprised of 10 genotypes of fennel (*Foeniculum vulgare* Mill.) were obtained from the different sources (Table 2.1) and sown at Horticultural Research Farm, Department of Horticulture, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj. The experiment was conducted in Randomized Block Design comprising 10 (9 genotypes +1 check) genotypes with three replications between month of November 2021-April 2022. The unit plot size was 1 m^2. The plants were planted with a spacing of 30 cm between the rows and 15 cm between the plants. There were ten plants in each plot. The observations were recorded on randomly selected five plants on characters comprising days to Germination (DM), days to 50% flowering (DF50), days to maturity (DM), plant height (cm) (PH), number of primary branches per plant (NPB), number of umbels per plant (NUPP), number of umbellets per umbel (NUPU),

number of seeds per umbel (NSPU), seed yield per plant (g/plant) (SYPP), seed yield per hectare (q/ha) (SYPH), seed Index (g) (SI) [1000 seed weight], harvest index (%).

Analysis of Variance was calculated at both 1% and 5% level of significance using the ANOVA skeleton suggested by **Fisher and Yates, 1963** [8]**;** Coefficient of variation including Genotypic coefficient of Variation and Phenotypic Coefficient of Variation was calculated using the formula suggested by **Burton, 1952** [9]**;** Heritability (broad sense) was calculated using the formula suggested by **Allard, 1960** [10]**;** Genetic advance was calculated using the formula suggested by **Johnson *et al.*, 1955** [11]**,** Correlation coefficient Analysis was calculated using formula given by **Al-Jibouri *et al.*, 1958** [12], while Path Coefficient Analysis was calculated using formula given by **Dewey and Lu, 1959** [13] all at 5% level of significance.

Table 2.1 List of genotypes and their sources

Varieties	**Source**
Ajmer fennel - 1	NRCSS, Ajmer
Ajmer fennel - 2	NRCSS, Ajmer
Sugandha – 111	Ratan Seed Company, Ajmer
Gujarat fennel – 1	Ratan Seed Company, Ajmer
Surbhi	Pruthvi Hybrid Seeds pvt. Ltd. Ahmedabad
Sonata	Nissan Seeds pvt. Ltd Ahmedabad
Suhana	Uma Seeds Corporation, Gandhinagar
Avani - dona	Avani Seeds pvt. Ltd Gujarat
Hara sona	Ved Seed, Ajmer
Kalyan	Bharat Krishi Kendra, Ajmer

3. RESULTS AND DISCUSSION

The analysis of variance for all characters of fennel genotypes revealed presence of good extant of significant differences among the genotypes for all traits. Table 3.1 depicts the ANOVA for all 12 characters studied. Thereafter, the data for all 12 characters that showed sufficient amount of significant differences were subjected to further statistical analysis. These results obtained were in agreement with the studies conducted by **Alam *et al.* (2003)** [14], **Lal (2007)** [15], **Kumawat *et al.* (2010)** [16], **Jaydev *et al.* (2020**) [17].

3.1 Genetic variability

Both Moderate GCV and PCV (Table 3.2 & Figure 3.1) were recorded for number of primary branches per plant and seed yield per hectare which suggests that improvement in these characters might be gained to a reasonable extent. Both low GCV and PCV (Table 3.2 & Figure 3.1) were recorded for days to 50% flowering, days to maturity, Plant length. Number of umbellets per umbel, number of seeds per umbel, seed yield per plant and seed index. While days to germination, number of umbels per plant and harvest index had low GCV but moderate PCV (Table 3.2 & Figure 3.1). Similar results for high GCV and PCV were concluded earlier by was earlier reported by **Alam *et al.* (2003)** [14]**, Lal (2007)** [15]**, Kumawat *et al.* (2010)** [16]**, Mohan *et al.* (2017)** [18]**, Jaydev *et al.* (2020)** [17] in fennel, **Dhunde *et al* (2021)** [25] in mungbean. This also suggests that improvement in these characters might be gained to a reasonable extent therefore, selection for these characters would be effective because response to selection is directly proportional to the variability present in the experimental material. In present study, High heritability (broad sense) estimates (60% and above) (Table 3.2 & Figure 3.1) had been observed for days to 50% flowering, number of primary branches per plant, number of umbels per plant, number of seeds per umbel, seed yield per plant (g/plant), seed yield per hectare (q/ha), and harvest index (%). Therefore, these characters are predominantly governed by additive gene action and could be improved through individual plant selection owing to their high heritability values. Similar inferences were reported earlier by **Rohit *et al.* (2018)** [19]**, Patel *et al.* (2018)** [20] **and Rajput *et al.* (2022)** [21] in fennel. Moderate GCV along with high heritability was observed for Number of primary branches per plant and seed yield per hectare. This indicated that these traits were comparatively under less influence of environment henceforth, desirable for selection in breeding programme. High estimates of heritability coupled with moderate genetic advance as % of mean (Table 3.2 & Figure 3.1) was

recorded for number of primary branches per plant, number of umbels per plant, seed yield per plant (g/plant), seed yield per plant (g/plant), seed yield per hectare (q/ha), and harvest index (%). While moderate estimates of heritability coupled with moderate genetic advance as % of mean (Table 3.2 & Figure 3.1) was observed for days to germination and Plant height (cm). These traits are governed by additive gene action and thus can be improved through direct selection. This indicates closeness of respective σ^2p and σ^2g value thereby low environmental effect on expression of these characters. Such values may be attributed to the additive gene effects and direct selection for these traits would be fruitful. Thus, phenotypic selection might be effective for these characters. Similar inferences were drawn by reported earlier by **Alam *et al.* (2003)** [14]**, Sastry *et al.* (2009)** [22]**, Sengupta *et al.* (2014)** [23] in fennel**, Hemavanthy *et al.* (2015)** [24] in mungbean, **Rohit *et al.* (2018)** [19]**, Patel *et al.* (2018)** [20] **and Rajput *et al.* (2022)** [21] in fennel.

Table 3.1 Analysis of variance (ANOVA) for 12 characters studied in fennel.

Characters	**Mean sum of Squares**		
	Replication (df=2)	**Treatment/ Genotypes (df=9)**	**Error (df=18)**
Days to Germination	1.60	3.48**	0.78
Days to 50% Flowering	0.70	19.57**	2.23
Days to Maturity	11.23	21.41**	5.23
Plant Height (cm)	7.88	492.30**	97.79
No of Primary Branches per Plant	1.40	51.28**	4.46
Number of Umbels per Plant	0.79	19.40**	2.09
Number of Umbelletes per Umbel	1.76	2.27*	0.88
Number of seeds per umbel	91.82	296.15**	46.03
Seed yield per plant (g/plant)	0.04	8.70**	0.30
Seed yield per hectare (q/ha)	0.51	3.59**	0.15
Seed Index (g) {1000 seed weight}	0.08	0.23*	0.06
Harvest Index (%)	6.80	28.02**	3.40
***, ** Significant at 5% and 1% respectively**			

Table 3.2 Range, variability and genetic parameters of 12 characters studied in fennel genotypes.

Sl No	Characters	Range	GCV (%)	PCV (%)	h2 (Heritability Broad Sense) (%)	GA (5% LOS)	GA as % Mean
1	Days to Germination	9.67-13.00	8.54	11.69	53.40	1.42	12.86
2	Days to 50% Flowering	99.00-108.33	2.33	2.76	71.52	4.18	4.06
3	Days to Maturity	157.64-164.00	1.44	2.03	50.33	3.40	2.12
4	Plant Height (cm)	143.07-184.24	6.96	9.20	57.34	17.88	10.87
5	Number of Primary Branches	29.20-42.62	10.28	11.66	77.77	7.17	18.69
6	Number of Umbels Per Plant	22.29-29.75	9.12	10.65	73.33	4.23	16.09
7	Number of Umbellets Per Umbel	44.17-47.02	1.49	2.55	34.42	0.82	1.81
8	Number of Seeds Per Umbel	278.47-304.12	3.13	3.90	64.42	15.09	5.18
9	Seed Yield Per Plant (g/plant)	25.12-29.96	6.09	6.41	90.27	3.27	11.92
10	Seed Yield Per Hectare (q/ha)	7.48-10.57	12.46	13.29	87.95	2.06	24.08
11	Seed Index (g)	4.84-5.84	4.44	6.68	44.07	0.31	6.07
12	Harvest Index (%)	25.00-36.38	9.58	11.39	70.69	4.96	16.59

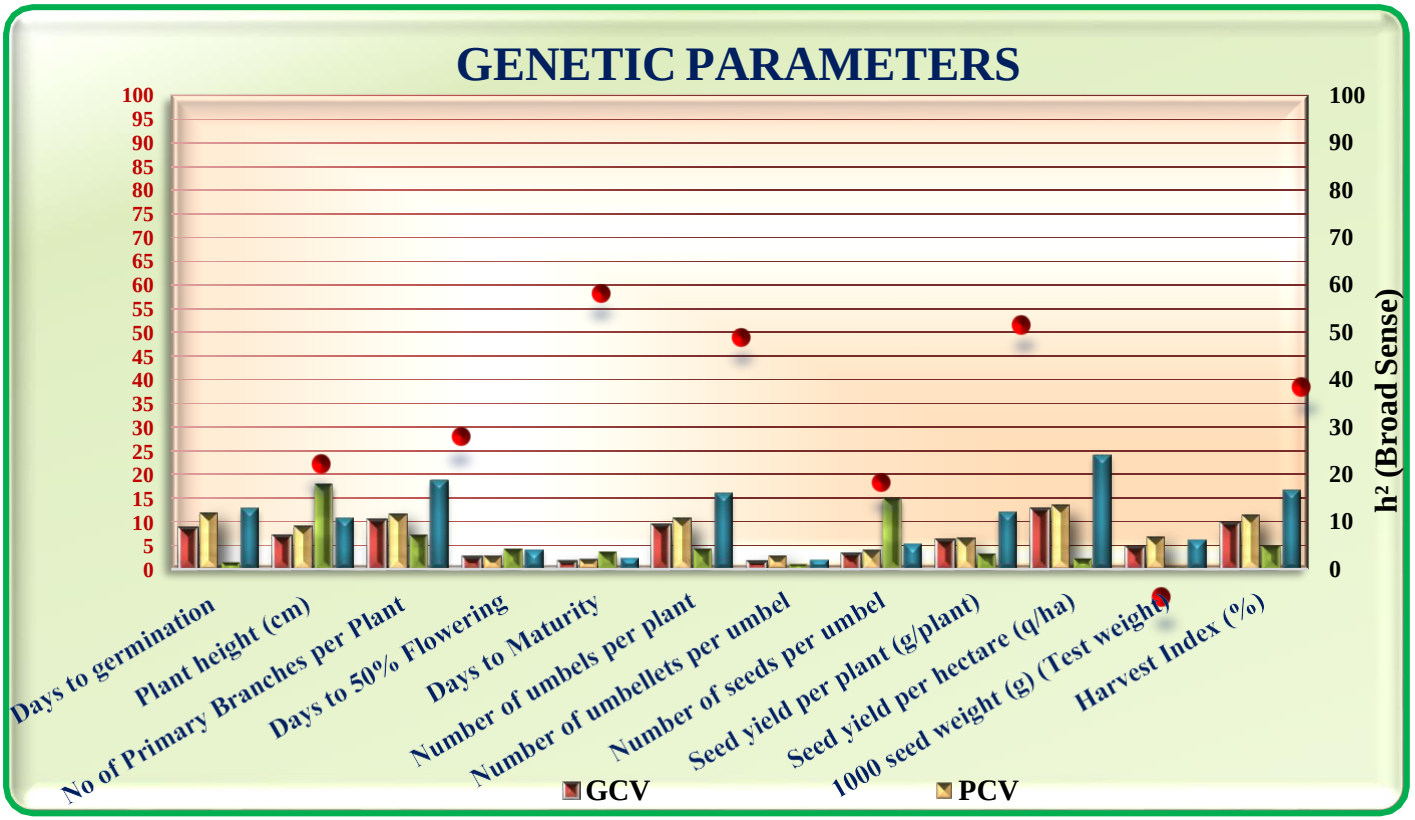

Figure 3.1 Histogram representing the relationship among the GCV, PCV, Heritability, Genetic Advance and Genetic Advance as percent of mean in Fennel.

3.2 Correlation coefficient analysis

Positive and significant correlation (Table 3.3) was observed for number of umbels per plant, number of umbellets per umbel, number of seeds per umbel, seed yield per hectare and seed index with seed yield per plant at both phenotypic and genotypic level. Therefore, these characters emerged as most important attributing associates of seed yield per plant in fennel. Thus, selection practiced for the improvement in one character will automatically result in the improvement of the other character even if direct selection for improvement has not been made for the yield character.

Table 3.3 Estimates of phenotypic (above diagonal) and Genotypic (Below diagonal) correlation coefficients among 12 different quantitative characters in Fennel genotypes.

Characters	DG	DF50	DM	PH (cm)	NPB	NUPP	NUPU	NSPU	SYPH (q/ha)	SI (g)	HI (%)	SYPP(g)
DG	**1.000**	-0.068	-0.270	-0.471*	-0.222	0.282	0.282	-0.154	0.379*	0.260	-0.037	0.152
DF50	-0.328	**1.000**	0.023	0.411*	0.070	0.224	-0.132	-0.002	-0.100	0.368*	0.256	0.131
DM	-0.472*	0.276	**1.000**	0.2499	-0.030	-0.033	-0.295	-0.103	-0.252	-0.177	0.218	-0.152
PH (cm)	-0.528*	0.785**	0.252	**1.000**	0.449*	0.071	-0.146	0.249	-0.311	0.131	0.034	-0.201
NPB	-0.387*	0.240	-0.197	0.638**	**1.000**	0.542*	0.079	0.640**	0.081	0.205	0.036	-0.045
NUPP	0.336	0.300	-0.277	0.185	0.655**	**1.000**	0.288	0.564*	0.531*	0.435*	0.127	0.519*
NUPU	0.384*	0.015	-0.966**	-0.353	0.021	0481*	**1.000**	0.305	0.522*	0.159	-0.087	0.558*
NSPU	0.038	0.084	-0.023	0.406*	0.715**	0.881*	0.520*	**1.000**	0.296	0.246	-0.281	0.372*
SYPH (q/ha)	0.569*	-0.167	-0.356	-0.439*	0.142	0.657*	0.924**	0.416*	**1.000**	0.429*	0.183	0.773**
SI (g)	0.185	0.519*	-0.570	0.227	0.413*	0.663**	0.888**	0.722**	0.722**	**1.000**	0.101	0.445*
HI (%)	0.107	0.431*	0.133	-0.263	-0.050	0.082	-0.202	-0.573**	0.304	0.149	**1.000**	0.063
SYPP (g)	0.311	0.126	-0.205	-0.244	-0.010	0.607**	0.824**	0.484*	0.836**	0.709**	0.067	**1.000**

Abbreviations used**:- DG:** Days to Germination**; DF50:** Days to 50% Flowering**; DM:** Days to Maturity**; PH:** Plant Height (cm)**; NPB:** Number of Primary Branches per plant**; NUPP:** Number of Umbels Per Plant**; NUPU:** Number of Umbellets Per Umbel**; NSPU:** Number of Seeds Per Umbel**; SYPP:** Seed Yield Per Plant (g/plant)**; SYPH:** Seed Yield Per Hectare (q/ha)**; SI:** Seed Index (g) [1000 seed weight]**; HI:** Harvest Index (%).

3.3 Path coefficient analysis

Path Coefficient analysis (Table 3.4 and 3.5 & Figure 3.2 and 3.3) revealed that days to maturity, number of primary branches per plant, number of seeds per umbel, seed index and harvest index had direct positive effect on seed yield per plant at genotypic level. While days to 50% flowering, days to maturity, number of umbels per plant, number of umbellets per umbel, number of seeds per umbel, seed yield per hectare and seed index had direct positive effect on seed yield per plant at phenotypic level. Selection in these traits would lead to higher efficiency in breeding programme for improving yield. Thus these traits may be ranked as most important attributing traits for seed yield per plant in fennel. The similar results were reported earlier by **Alam *et al.* (2003)** [14]**, Sastry *et al.* (2009)** [22]**, Kumawat *et al.* (2010)** [16]**, Sengupta *et al.* (2014)** [23] in fennel**, Hemavanthy *et al.* (2015)** [24] in mungbean, **Mohan *et al.* (2017)** [18]**, Rohit *et al.* (2018)** [19] **and Jaydev *et al.* (2020)** [17] in fennel, **Dhunde *et al.* (2021)** [25] in mungbean.

Table 3.4. Estimates of phenotypic path matrix for seed yield per plant in fennel genotypes.

Characters	DG	DF50	DM	PH (cm)	NPB	NUPP	NUPU	NSPU	SYPH (q/ha)	SI (g)	HI (%)
DG	**-0.296**	0.020	0.080	0.139	0.066	-0.083	-0.025	0.045	-0.112	-0.077	0.011
DF50	-0.010	**0.148**	0.003	0.060	0.010	0.033	-0.019	0.000	-0.014	0.054	0.038
DM	-0.006	0.001	**0.025**	0.006	-0.001	-0.001	-0.007	-0.002	-0.006	-0.004	0.005
PH (cm)	0.043	-0.037	-0.023	**-0.092**	-0.041	-0.006	0.013	-0.023	0.028	-0.012	-0.017
NPB	0.108	-0.034	0.015	-0.218	**-0.488**	-0.264	-0.038	-0.312	-0.040	-0.100	-0.017
NUPP	0.094	0.0748	-0.011	0.023	0.180	**0.333**	0.096	0.182	0.177	0.145	0.042
NUPU	0.014	-0.021	-0.048	-0.023	0.013	0.046	**0.162**	0.049	0.085	0.025	-0.014
NSPU	-0.034	0.000	-0.023	0.056	0.145	0.123	0.069	**0.226**	0.067	0.055	-0.063
SYPH (q/ha)	0.205	-0.054	-0.136	-0.168	0.044	0.287	0.282	0.160	**0.541**	0.232	0.099
SI (g)	0.033	0.048	-0.023	0.017	0.026	0.056	0.020	0.032	0.056	**0.130**	0.013
HI (%)	0.001	-0.012	-0.010	-0.001	-0.001	-0.006	0.004	0.013	-0.008	-0.004	**-0.0474**
SYPP (g)	0.152	0.131	-0.152	-0.201	-0.045	0.51*	0.558*	0.372*	0.773**	0.445*	0.063

Abbreviations used**:- DG:** Days to Germination**; DF50:** Days to 50% Flowering**; DM:** Days to Maturity**; PH:** Plant Height (cm)**; NPB:** Number of Primary Branches per plant**; NUPP:** Number of Umbels Per Plant**; NUPU:** Number of Umbellets Per Umbel**; NSPU:** Number of Seeds Per Umbel**; SYPP:** Seed Yield Per Plant (g/plant)**; SYPH:** Seed Yield Per Hectare (q/ha)**; SI:** Seed Index (g) [1000 seed weight]**; HI:** Harvest Index (%).

Table 3.5. Estimates of genotypic path matrix for seed yield per plant in fennel genotypes.

Characters	DG	DF50	DM	PH (cm)	NPB	NUPP	NUPU	NSPU	SYPH (q/ha)	SI (g)	HI (%)
DG	**0.7442**	-0.244	-0.351	-0.393	-0.287	0.250	0.285	0.028	0.423	0.137	0.079
DF50	0.135	**-0.413**	-0.114	-0.324	-0.099	-0.124	-0.006	-0.035	0.069	-0.214	-0.177
DM	-0.288	0.169	**0.611**	0.154	-0.120	-0.169	-0.590	-0.014	-0.217	-0.348	0.081
PH (cm)	0.899	-1.337	-0.430	**-1.702**	-1.086	-0.315	0.601	-0.691	0.747	-0.387	0.448
NPB	-0.106	0.066	-0.054	0.176	**0.276**	0.180	0.006	0.197	0.039	0.114	-0.014
NUPP	-0.428	-0.383	0.354	-0.236	-0.835	**-1.275**	-0.613	-1.123	-0.837	-0.845	-0.105
NUPU	-0.082	-0.003	0.208	0.076	-0.004	-0.103	**-0.215**	-0.111	-0.221	-0.277	0.043
NSPU	0.084	0.185	-0.052	0.892	1.570	1.934	1.141	**2.196**	0.913	1.526	-1.258
SYPH (q/ha)	-1.203	0.354	0.753	0.928	-0.300	-1.388	-2.170	-0.879	**-2.115**	-1.526	-0.064
SI (g)	0.422	1.183	-1.299	0.519	0.942	1.512	2.941	1.647	1.646	**2.281**	-0.341
HI (%)	0.136	0.548	0.169	-0.335	-0.064	0.105	-0.257	-0.729	0.387	0.190	**1.273**
SYPP (g)	0.311	0.126	-0.205	-0.244	-0.010	0.607**	1.121	0.484*	0.836**	0.709**	0.067

Abbreviations used**:- DG:** Days to Germination**; DF50:** Days to 50% Flowering**; DM:** Days to Maturity**; PH:** Plant Height (cm)**; NPB:** Number of Primary Branches per plant**; NUPP:** Number of Umbels Per Plant**; NUPU:** Number of Umbellets Per Umbel**; NSPU:** Number of Seeds Per Umbel**; SYPP:** Seed Yield Per Plant (g/plant)**; SYPH:** Seed Yield Per Hectare (q/ha)**; SI:** Seed Index (g) [1000 seed weight]**; HI:** Harvest Index (%).

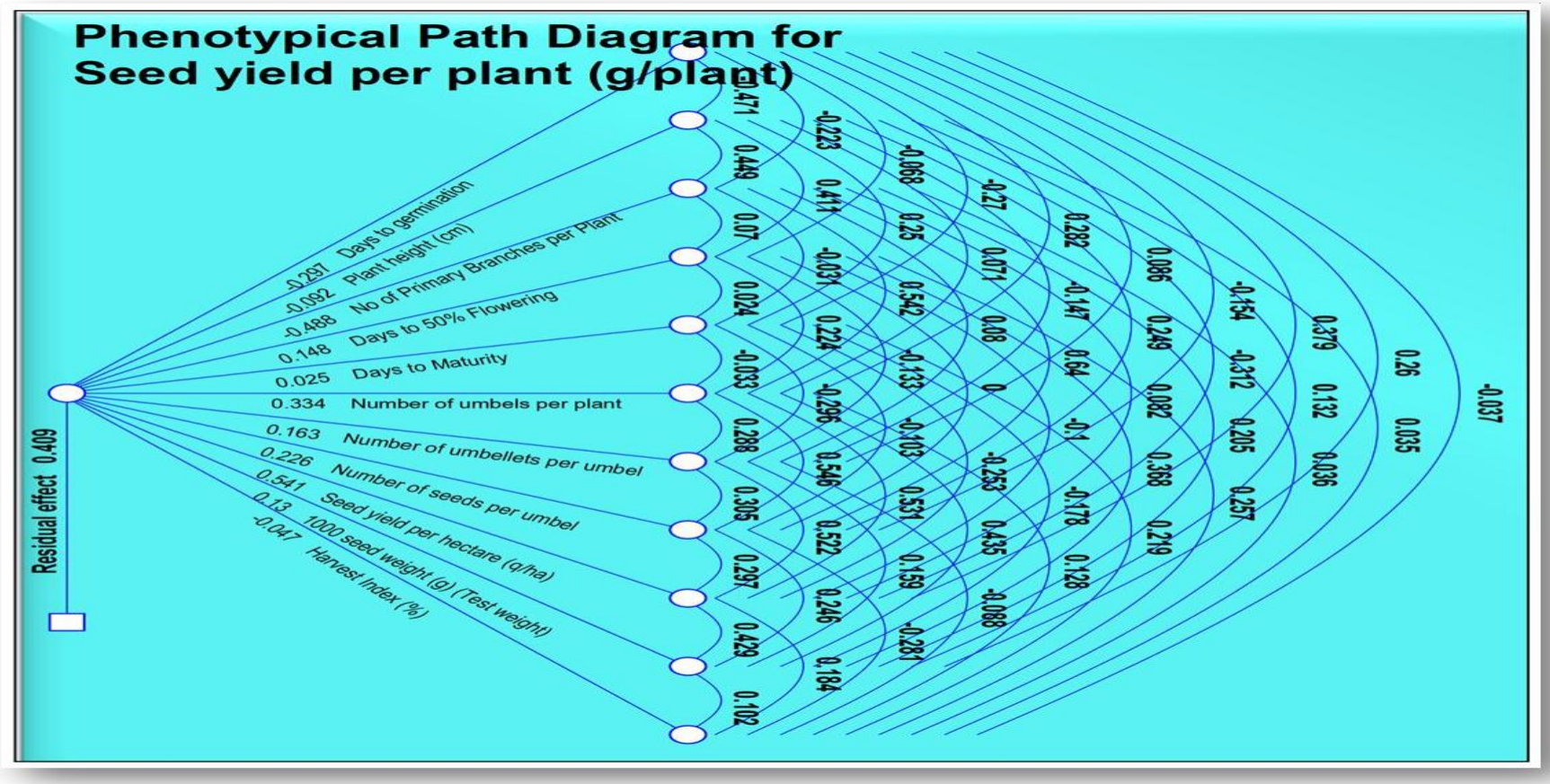

Figure 3.2. Phenotypic Path Diagram for seed yield per plant (g)

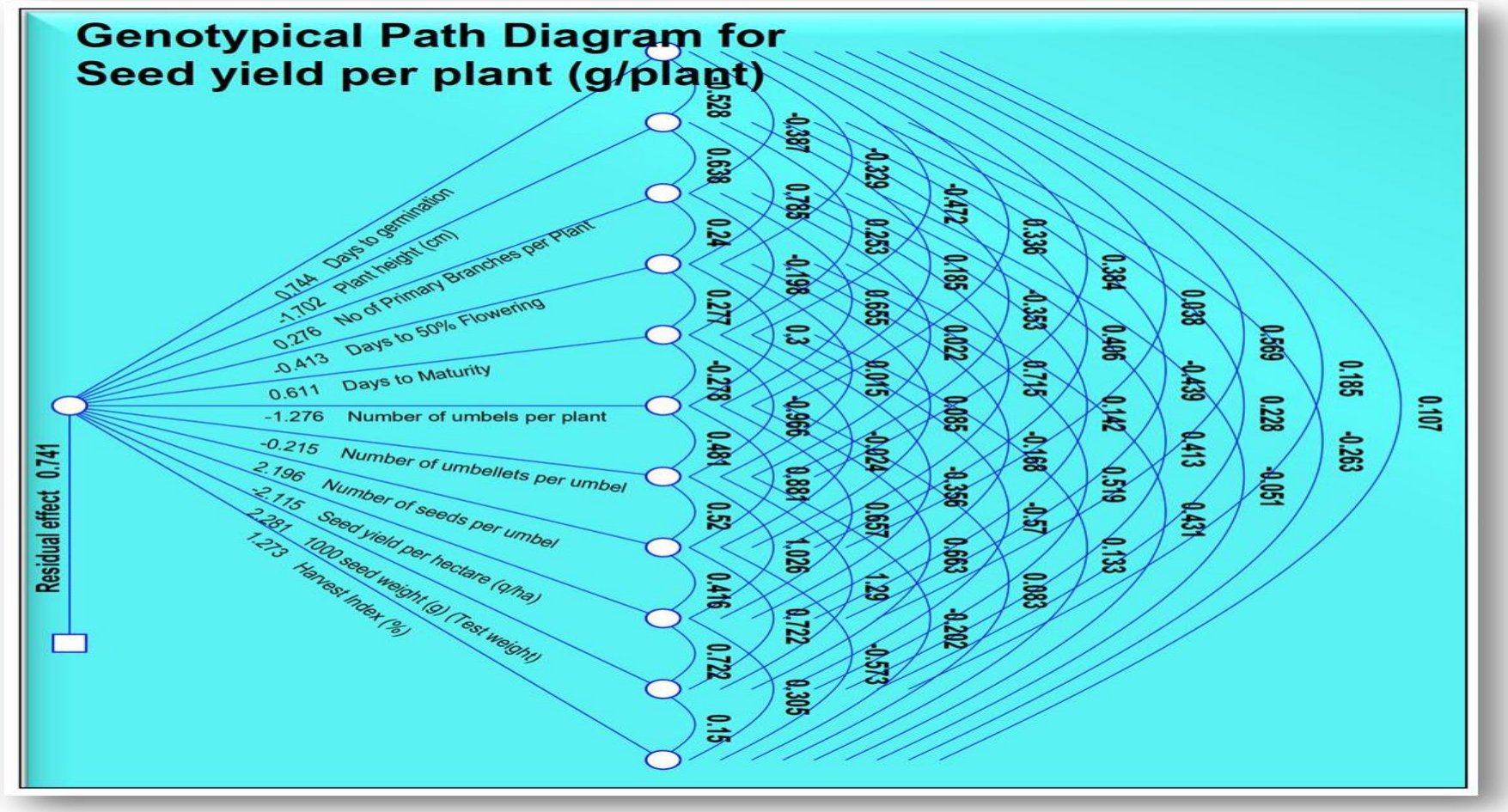

Figure 3.3. Genotypic Path Diagram for seed yield per plant (g)

4. CONCLUSION

From the present investigation it is concluded that among 10 genotypes of fennel on the basis of mean performance 2 genotypes viz. Sugandha-111 and Surbhi possessed maximum seed yield per plant over the check variety Kalyan. Sugandha-111 also had highest number of umbellets per umbel and number of seeds per umbel. Number of primary branches per plant and seed yield per hectare exhibited moderate estimates of GCV and PCV and also High estimates of Heritability (Broad-sense). Therefore, these characters should be given priority during selection for improvement in fennel.

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