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Seed yield and its characteristics studies variability correlation and a path coefficient ajwain (*Trachyspermum ammi* L.)

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Abstract
At the Sardar Krushinagar Dantiwada Agricultural University's Agronomy Instructional Farm in Dantiwada during the rabi 2019–20, forty ajwain genotypes were assessed. On the mean sum of squares, each attribute has a significant effect. The GCV and PCV were modest for the number of branches plant^{-1}, umbels plant^{-1}, umbelletes umbel^{-1}, seeds umbel^{-1}, seeds plant^{-1}, biological yield plant^{-1}, test weight, and volatile oil. The number of branches plant^{-1}, the number of umbels plant^{-1}, the number of umbelletes umbel^{-1}, the number of seeds umbel^{-1}, the number of seeds per plant^{-1}, the test weight, and the volatile oil all showed high heritabilities when combined with GAM. Plant height, number of branches, umbels, umbelletes, number of seeds, biological yield plant^{-1}, harvest index, test weight, and volatile oil are all significantly and positively connected with seed yield plant^{-1}. The path analysis identified favourable direct impacts on seed yield per plant for days to maturity, plant height, number of umbels, number of umbelletes per umbel, biological yield per plant, harvest index, and test weight.

Keywords: Ajwain, variability, correlation coefficient, path coefficient

Introduction
Ajwain is planted for its seeds, volatile oil, and herb; it is also referred to in English as Carum and bishop's weed. Through insect and protandrous cross-pollination in flowers. Laxative, healing, and digestive system and indigestion relief benefit. The seed's (2–4%) yellow-brownish volatile oil is present (Bairwa *et al*., 2012) [2]. Ajwain (*Trachyspermum ammi* L.) diploid chromosome number 18, family Apiaceae and center of origin Egypt. It is an aromatic, annual, profuse, and herbaceous plant. The plant is soft fine hair, feather-like leaves, branched leafy stems, and terminal and compound flowers. Fruits are cremocarp, ovoid, and small 2-3 mm grayish brown compressed mericarps (Malhotra and Vijay., 2004) [8]. It is grown in India, Afghanistan, Iran, and Iraq. It is grown in the Indian states of Telangana, Bihar, Madhya Pradesh, Rajasthan, Gujarat, and Madhya Pradesh. Any programme focused at enhancing crops must have access to genetic diversity within a species' germplasm collection. A breeding programme must be effective and have a thorough awareness of both nature and the degree of genetic variability in the breeding stock. Knowledge of factors like the genotypic and phenotypic coefficient of variation, heritability, and genetic progress is necessary to comprehend the nature of the inheritance of different traits. To overcome genetic yield obstacles, it is vital to investigate diverse features and how they relate to one another. While correlation studies assist in identifying the component of a complicated feature, such as seed yield. They do not, however, give an accurate figure for the direct and indirect yield. In order to divide the correlation coefficient into the direct and indirect effects of the independent factors on the dependent variables, path coefficient analysis is an important technique.

Material and Method
Ajwain, the experimental plant, underwent a randomised block design (RBD) design, which used three replications of the 40 genotypes that were investigated. The study material was planted in the field at the Agronomy Instruction Farm during the rabi season of the 2019–20 academic year at Sardarkrushinagar Dantiwada Agricultural University. With a 45 cm gap between each pair of rows and 10 cm between plants. In a single row plot measuring 4.0 metres in length, two rows of each genotype were sowed.

Each replication's plots received a random assignment of genotypes. For the effective raising of the crop, all advised agronomic procedures as well as required plant protection measures were timely implemented. These five randomly chosen plants were observed for the following characteristics: days to flowering, days to maturity, plant height (cm), number of branches per plant, number of umbels per plant, number of umbelletes per umbel, number of seeds per umbel, seed yield per plant (g), biological yield per plant (g), harvest index (%), test weight (g), and volatile oil (%). According to Panse and Sukhatme's descriptions, the data of different characters were examined (1978). By Burton (1952) [3], GCV and PCV. The proportion of phenotypic variation is dictated by genetically. It was calculated in percent using the Allard formula (1960) [1]. Following Hazel's (1943) [6] advice, the genotypic and phenotypic correlations were calculated (1943). Analysis of path coefficients was performed using the Wright (1921) [17] recommended methodology.

Result and Discussion

The findings of the analysis of variance showed that there is adequate diversity among the 40 genotypes because the mean square of the investigated genotypes showed extremely significant variances. The majority of the studied traits had genotypic coefficients of variation that were marginally greater when compared to phenotypic coefficients of variation. This result suggests that the environment has a lesser influence on how the traits are expressed. Inter-trait correlations can speed up or slow down the selection process. A positive connection means that increasing one or more components would occur simultaneously with improving one of the yield components. The progress of selection may be accelerated or slowed down by correlations between inter-traits. Rise in one or more components would occur simultaneously with the improvement of the chosen yield component, according to a positive association. The genotypic correlations for each of the studied features were much higher than the corresponding phenotypic correlations. This showed a strong genotypic correlation between the two variables, which was hindered in its phenotypic expression by the influence of environmental conditions. It also demonstrated the significance of these features in increasing seed yield per plant.

The enormous diversity present across all the traits is indicated by the mean square sum, which for all the qualities was found to be highly significant. Moderate values of the genotypic and phenotypic coefficient of variation were discovered for Singh *et al*. (2019) [14], Nagar *et al*. (2018) [11], Subramaniyam *et al*. (2018) [16], and Ghanshyam *et al*. (2015) [5] in the number of branches per plant, number of umbels per plant, number of umbelletes per umbel, number of seeds per umbel, seed yield per plant, biological yield per plant, test weight, and volatile oil (Table.1, Fig.1). The traits with the highest heritability and genetic advance as a percentage of mean were the number of branches per plant, number of umbels per plant, number of umbelletes per umbel, number of seeds per umbel, number of seeds produced per plant, test weight, and volatile oil (Table.1, Fig. 2), indicating the dominance of additive genes and indicating that If selection could make these characters better, that would be rewarded. Therefore, it is evident that additive genetic variance greatly contributes to the manifestation of these traits; consequently, these attributes may be enhanced through effective selection. The correlation coefficient revealed a strong and favourable association between seed yield per plant and genotype at both the phenotypic and genotypic levels for plant height, number of branches per plant, number of umbels per plant, number of umbelletes per umbel, number of seeds per umbel, biological yield per plant, harvest index, test weight, and volatile oil, indicating that these atributing traits had a greater impact on the seed yield in ajwain and were, therefore, considered to be important. Seed yield per plant was discovered to be positively and very substantially connected with, according to Singh *et al*. (2019) [14], Sandhu *et al*. (2018) [13], Subramaniyam *et al*. (2018) [16], Meena *et al*. (2016) [9], and Shravanthi *et al*. (2014) [15] for days to flowering, plant height, number of branches per plant, number of umbels per plant, number of seeds per umbel, biological yield per plant, harvest index, test weight, and volatile oil. Days to maturity and seed yield per plant showed a Positive and non significant favourable correlation. Singh *et al*. (2019) [14] came to a similar conclusion regarding genotypic level. In the current study, the genotypic correlations between the trait pairings were larger than the phenotypic correlations that went along with them. This larger value of genotypic correlations may be the result of surroundings' masking or moderating effects on how these traits are associated. This showed that although there was a strong genetic correlation between the two variables, the impact of environmental factors on phenotypic expression reduced it. For ajwain seed yield and yield components, Singh *et al*. (2019) [14], Subramaniyam *et al*. (2018) [16], Meena *et al*. (2016) [9], Chauhan *et al*. (2019) [4], Sandhu *et al*. (2018) [13], Nagappa *et al*. (2017) [10], and Sravanthi *et al*. (2014) [15] have all seen that estimations of genotypic correlations frequently exceed the corresponding phenotypic correlations (Table. 2). Days to maturity, plant height, number of umbels per plant, number of umbelletes per umbel, biological yield per plant, harvest index, and test weight were determined to be the most significant yield attributing factors and to have a substantial and favourable impact directly on seed yield per plant. Similar results for days to flowering have been reported by Subramaniyam *et al* (2018) [16]. According to research by Singh *et al*. (2019) [14], days to maturity have a favourably impacting seed yield directly. Meena *et al*. (2016) [9] obtained a similar result in relation to plant height. The number of branches per plant had a directly detrimental impect on seed yield per plant, according to studies by Ghanshyam *et al*. (2015) [5] and Subramaniyam *et al*. (2018) [16]. While Ghanshyam *et al*. (2015) [5] and Subramaniyam *et al*. (2018) [16] reported identical results for the number of umbels per plant, Ghanshyam *et al*. (2015) [5] found similar results for the number of umbelletes per umbel. An earlier study by Subramaniyam *et al*. (2018) [16] found that the number of seeds per umbel had a negatively direct impact on the seed yield per plant (2018). Similar outcomes for biological yield per plant components were found by Meena *et al* (2016) [9]. When compared to earlier studies by Sandhu *et al*. (2018) [13] and Shrivanthi *et al*. (2014) [15], the harvest index showed a favourable direct impect on the seed yield per plant. Singh *et al*. (2019) [14] observed that test weight had a favourable direct impact on seed yield per plant (Table. 3, Fig.3).

Table 1: Seed yield genetic variation factors and their contributory traits

Sr. No.	Characters	Range	Mean	GCV (%)	PCV (%)	h2(b.s) (%)	GA (%)	GA as percent of mean (%)
1	Days to flowering	65.33-94	80.60	6.59	9.26	50.60	7.78	9.65
2	Days to maturity	129.00-164.33	143.62	4.43	5.54	63.93	10.47	7.29
3	Plant height	66.93-91.07	80.60	7.04	7.77	82.18	10.60	13.16
4	Number of branches per plant	6.67-13.20	9.64	18.92	19.68	92.41	3.61	37.47
5	Number of umbels per plant	63.20-117.07	83.69	16.34	16.91	93.41	27.23	32.53
6	Number of umbelletess per umbel	8.13-17.40	13.39	16.16	17.65	83.84	4.08	30.48
7	Number of seed per umbel	189.93-378.67	281.02	18.11	19.23	88.68	98.71	35.12
8	Seed yield per plant	3.57-6.65	4.99	13.49	14.32	88.68	1.31	26.17
9	Biological yield per plant	14.82-23.33	18.52	10.99	12.53	76.97	3.68	19.87
10	Harvest index	22.80-35.42	26.98	7.27	9.12	63.56	3.22	11.94
11	Test weight	0.97-2.16	1.51	19.11	19.21	98.95	0.59	39.15
12	Volatile oil	4.87-6.08	4.79	12.25	12.95	89.48	1.14	23.87

Where,
GCV (%) and PCV (%) are genotypic and phenotypic coefficient of variance, respectively.
$h^2_{(b.s)}$ (%), GA and GAM are broad sense heritability, genetic advance and genetic advance expressed as percent of mean, respectively.

Table 2: Different characters' phenotypic and genotypic correlation coefficients

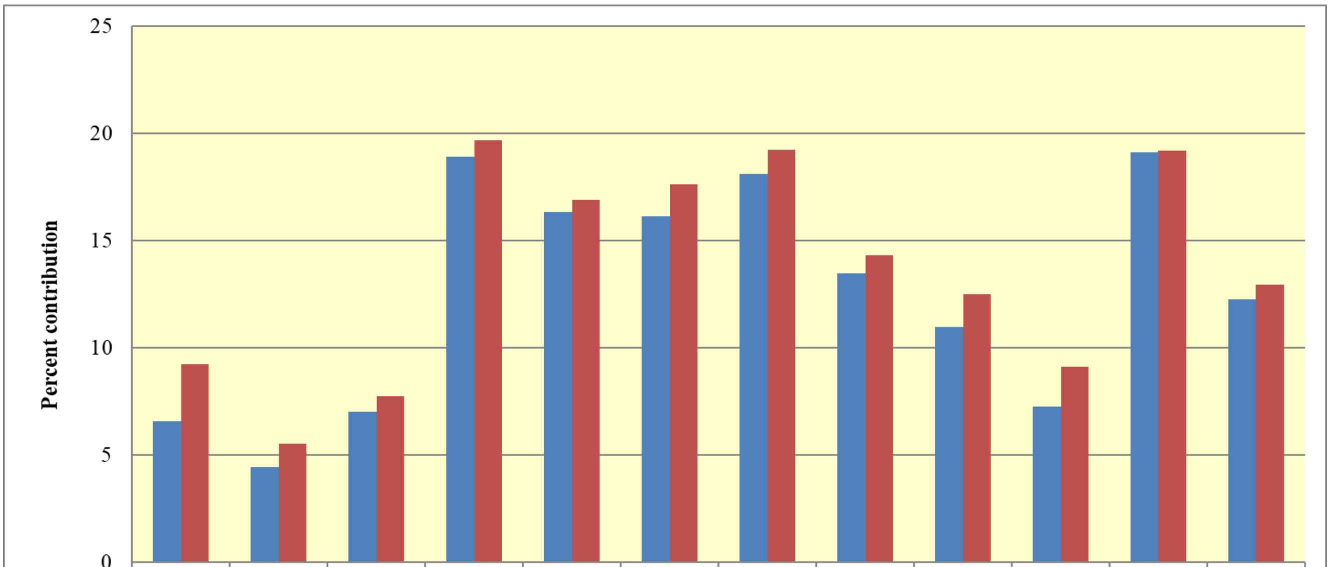
		DF	DM	PH	BPP	UPP	UPU	SPU	BY	HI	TW	VO	SPP
DF	r_g	1.000	1.027**	0.231*	-0.037	0.259**	0.424**	0.247**	0.278**	0.125	0.094	-0.144	0.273**
	r_p	1.000	0.779**	0.152	-0.041	0.192*	0.293**	0.156	0.160	0.068	0.065	-0.141	0.164
DM	r_g		1.000	0.203*	-0.067	0.117	0.237**	0.086	0.138	0.042	0.057	-0.023	0.115
	r_p		1.000	0.147	-0.057	0.100	0.194*	0.028	0.085	0.036	0.046	-0.030	0.082
PH	r_g			1.000	0.247**	0.377**	0.457**	0.490**	0.531**	0.156	0.132	0.324	0.519**
	r_p			1.000	0.301**	0.367**	0.437**	0.472**	0.563**	0.051	0.151	0.302	0.513**
BPP	r_g				1.000	0.422**	0.300**	0.278**	0.323**	-0.130	0.124	0.055	0.200*
	r_p				1.000	0.413**	0.292**	0.286**	0.383**	-0.179	0.137	0.070	0.211*
UPP	r_g					1.000	0.814**	0.806**	0.804**	0.446**	0.409**	0.350	0.879**
	r_p					1.000	0.734**	0.744**	0.699**	0.372**	0.406**	0.328	0.835**
UPU	r_g						1.000	0.887**	0.740**	0.559**	0.401**	0.235	0.881**
	r_p						1.000	0.805**	0.637**	0.424**	0.378**	0.232	0.800**
SPU	r_g							1.000	0.719**	0.584**	0.508**	0.401	0.885**
	r_p							1.000	0.658**	0.429**	0.492**	0.385	0.827**
BY	r_g								1.000	0.103	0.293**	0.270	0.859**
	r_p								1.000	-0.123	0.286**	0.240	0.758**
HI	r_g									1.000	0.403**	0.447	0.595**
	r_p									1.000	0.313**	0.353	0.546**
TW	r_g										1.000	0.462	0.474**
	r_p										1.000	0.439	0.463**
VO	r_g											1.000	0.456**
	r_p											1.000	0.425**
SPP	r_g												1.000
	r_p												1.000

*, ** significant at 0.05% and 0.01% level of significance, respectively
DF- Days to flowering, DM- Days to maturity, PH- Plant height, BPP- Number of branches per plant, UPP- Number of umbels per plant, UPU- Number of umbelletess per umbel, SPU- Number of seed per umbel, BY- Biological yield per plant, HI- Harvest index, TW- Test weight, VO- Volatile oil, SPP- Seed yield per plant

Table 3: Effects of yield component on seed yield direct and indirect

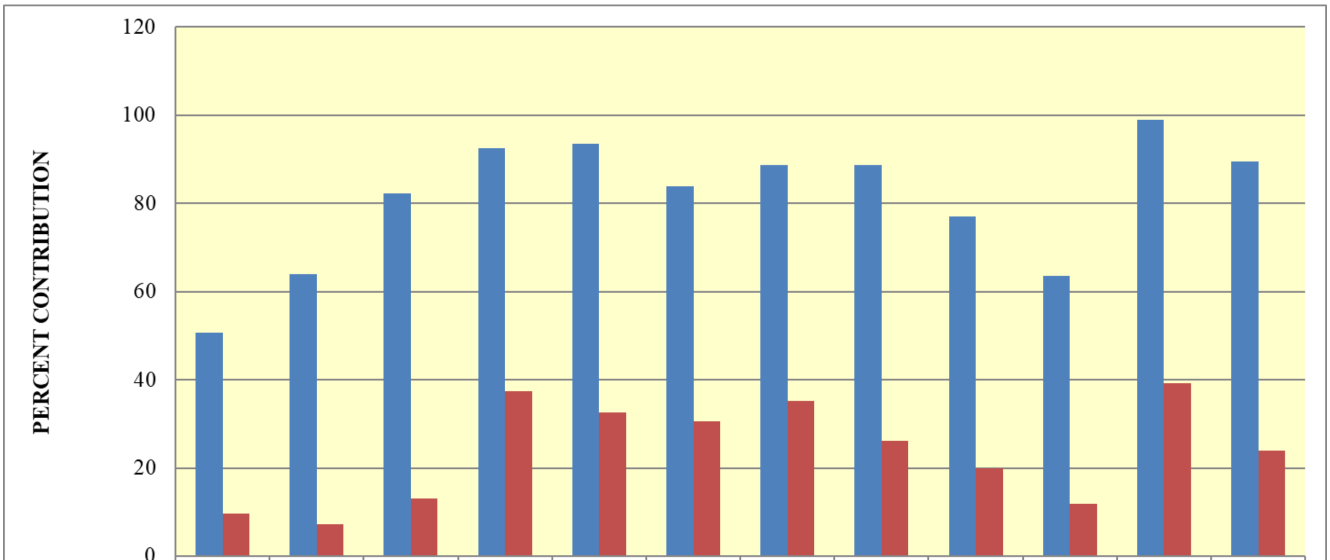
Sr. No	Character	DF	DM	PH	BPP	UPP	UPU	SPU	BY	HI	TW	VO	Genotypic correlation with SPP
1	DF	-0.029	0.005	0.007	0.000	0.005	0.003	-0.002	0.216	0.061	0.004	0.002	0.273**
2	DM	-0.030	0.005	0.006	0.001	0.002	0.002	-0.001	0.108	0.021	0.003	0.000	0.115
3	PH	-0.007	0.001	0.029	-0.002	0.008	0.003	-0.003	0.413	0.077	0.006	-0.004	0.519**
4	BPP	0.001	0.000	0.007	-0.009	0.009	0.002	-0.002	0.251	-0.064	0.006	-0.001	0.200*
5	UPP	-0.008	0.001	0.011	-0.004	0.020	0.005	-0.005	0.625	0.219	0.019	-0.005	0.879**
6	UPU	-0.012	0.001	0.013	-0.003	0.017	0.007	-0.006	0.575	0.274	0.018	-0.003	0.881**
7	SPU	-0.007	0.000	0.014	-0.002	0.017	0.006	-0.007	0.559	0.287	0.023	-0.006	0.885**
8	BY	-0.008	0.001	0.015	-0.003	0.016	0.005	-0.005	0.777	0.050	0.014	-0.004	0.859**
9	HI	-0.004	0.000	0.004	0.001	0.009	0.004	-0.004	0.080	0.491	0.019	-0.006	0.595**
10	TW	-0.003	0.000	0.004	-0.001	0.008	0.003	-0.003	0.228	0.198	0.046	-0.006	0.474**
11	VO	0.004	0.000	0.009	0.000	0.007	0.002	-0.003	0.210	0.220	0.021	-0.014	0.456**

*, ** significant at 0.05% and 0.01% level of significance, respectively
DF- Days to flowering, DM- Days to maturity, PH- Plant height, BPP- Number of branches per plant, UPP- Number of umbels per plant, UPU- Number of umbelletess per umbel, SPU- Number of seed per umbel, BY- Biological yield per plant, HI- Harvest index, TW- Test weight, VO- Volatile oil, SPP- Seed yield per plant



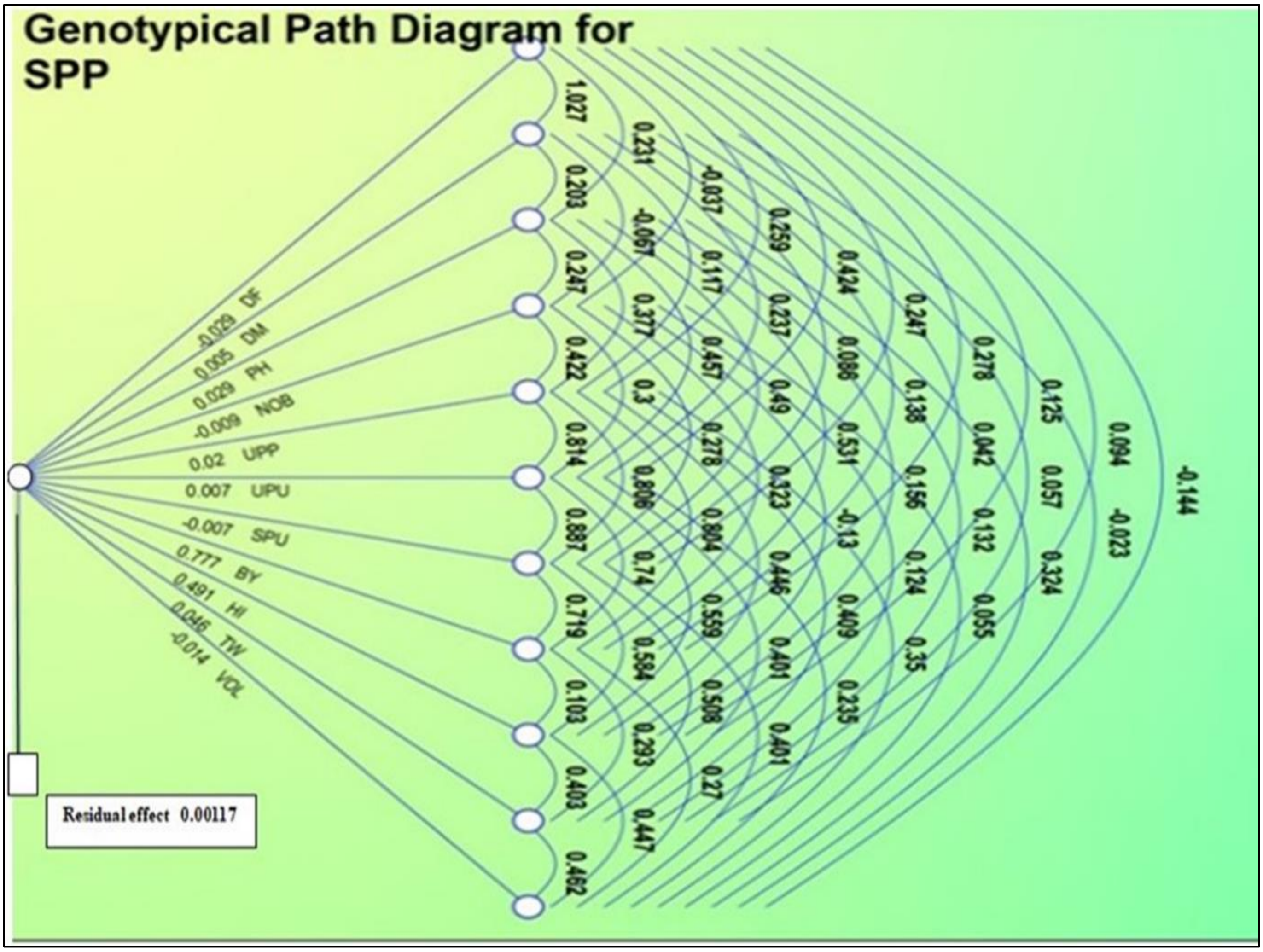
	Days to flowering	Days to maturity	Plant height	Number of branches per plant	Number of umbels per plant	Number of umbelletes per umbel	Number of seed per umbel	Seed yield per plant	Biological yield per plant	Harvest index	Test weight	Volatile oil
GCV%	6.59	4.43	7.04	18.92	16.34	16.16	18.11	13.49	10.99	7.27	19.11	12.25
PCV%	9.26	5.54	7.77	19.68	16.91	17.65	19.23	14.32	12.53	9.12	19.21	12.95

Fig 1: Estimates of the coefficient of variation (%) for various genotypic and phenotypic traits



	Days to flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of umbels per plant	Number of umbelletes per umbel	Number of seeds per umbel	Seed yield per plant(g)	Biological yield per plant(g)	Harvest index(%)	Test weight(g)	Volatile oil(%)
H2bs	50.6	63.93	82.18	92.41	93.41	83.84	88.68	88.68	76.97	63.56	98.95	89.48
ga(% mean)	9.65	7.29	13.16	37.47	32.53	30.48	35.12	26.17	19.87	11.94	39.15	23.87

Fig 2: The estimated genetic advance per mean (%) and heritability (%) for several characteristics



DF- Days to flowering, DM- Days to maturity, PH- Plant height, BPP- Number of branches per plant, UPP- Number of umbels per plant, UPU- Number of umbelletes per umbel, SPU- Number of seed per umbel, BY- Biological yield per plant, HI- Harvest index, TW- Test weight, VO- Volatile oil, SPP- Seed yield per plant

Fig 3: Representation of genotypic path analysis in a diagram

Conclusion

The traits with the highest heritability and genetic advance as a percentage of mean were the number of branches per plant, number of umbels per plant, number of umbelletes per umbel, number of seeds per umbel, number of seeds produced per plant, test weight, and volatile oil, indicating the predominance of additive genes and suggesting that effective selection could lead to rewarding improvements in these characters.

The correlation coefficient revealed strong and favorable associations between seed yield per plant and genotype at both phenotypic and genotypic levels for various attributes including plant height, number of branches per plant, number of umbels per plant, number of umbelletes per umbel, number of seeds per umbel, biological yield per plant, harvest index, test weight, and volatile oil. These attributes were found to have a substantial impact on seed yield in ajwain and were considered important. Additionally, days to maturity and seed yield per plant showed a positive but non-significant correlation. The larger genotypic correlations compared to phenotypic correlations suggest that environmental factors may moderate or mask the association between these traits.

Overall, these findings emphasize the significance of genetic factors in influencing the expression of important traits in ajwain and suggest that effective selection could lead to improvements in seed yield and other key characteristics.

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