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GENETIC COMPONENTS ANALYSIS OF F$_2$ POPULATIONS FOR QUANTITATIVE TRAITS IN FENNEL (*FOENICULUM VULGARE* MILL.)

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ABSTRACT

Fennel, an ancient seed spice cultivated in India, holds significant importance. Renowned for its unique flavor, it finds applications not only in the realms of food and cosmetics but also in the pharmaceutical industry, owing to its medicinal properties. Consequently, there is a growing demand for it, necessitating the development of new cultivars with enhanced yield potential through hybridization. This process can result in the generation of novel segregants showcasing key yield-related traits. Accurate assessments of genetic diversity within the attributes are essential for efficient population selection. Therefore, from November 2022 to April 2023, the F$_2$ populations of the fennel cross HF-33 × HUBFC-2 that were laid out in an Augmented Block Design at the College of Horticulture, Bagalkot, were the subject of the current investigation, which analysed genetic variability parameters. Based on the coefficient of variations, it was found that sufficient amount of genetic variability and high to moderate heritability with high genetic advance were present in the populations for the traits *viz.*, plant height, primary and secondary branches per plant, days to first and 50 % flowering, days to maturity, number of umbels per plant, number of umbellets per umbel, test weight, seed length, seed width, number of ridges per seed, root length, root width and seed yield per plant indicates the presence of additive gene action, which can be improved by simple selection in the earlier generations. Hence, the good segregants could be selected from the F$_2$ populations for yield improvement.

Key words : Fennel, F$_2$ population, Variability, Heritability, Genetic Advance.

Introduction

Fennel (*Foeniculum vulgare* Mill.), belongs to family Apiaceae with chromosome number, $2n = 22$ and native of Mediterranean region (Agarwal *et al.*, 2003). It's mainly cultivated for its seeds in the state of Rajasthan and Gujarat.

Fennel fruits have peculiar aromatic and pleasant taste. The aroma is due to the volatile oil content in seed (0.7 -1.2%). The volatile oil contains anethole, fenchone and trace amount of pinene, camphene, diphetene and others. It is used in folk medicine for its balsamic, cardiotonic, digestive, lactogogue and tonic properties (Choudhary *et al.*, 2017). The fruits have carminative, antispasmodic, antifungal, antimicrobial, antibacterial, anti-inflammatory, diuretic properties, prevents the accumulation of fat in the liver, involved in the transportation of fat and cholesterol in blood stream (Badgujar *et al.*, 2014). The fruits as well as its oil are widely used in flavouring the culinary preparation, pharmaceuticals and cosmetic preparation (Rather *et al.*,

2016).

Fennel being one of the important seed spice crop of India with nutritional and pharmacological properties, development of cultivars with improved productivity and other economic traits are major crop breeding objectives. Thus, the main factor for improving production is the introduction of new, high-yielding cultivars. Through hybridization, new diversity will be created, leading to the production of novel segregants for significant yield-related characteristics. If the qualities have good estimates of genetic variability, the population selection process will be effective (Reni *et al*., 2013). In this investigation, hybridization produced diversity, and F_2 segregating populations were produced. To establish appropriate selection criteria, the genetic variability of 200 F_2 population of fennel was examined. This involved calculating the genetic coefficient of variation, heritability estimates, and expected genetic advance of various biometric traits. Additionally, checks were made to identify superior segregants (Rani *et al*., 2016).

Materials and Methods

The experiment was evaluated in Augmented Block Design with 7 blocks, 200 treatments (F_2 population) of fennel include 3 checks (HF-33, HUBFC-2 and F_1). The analysis was performed in R studio (version 3.5.2). *(https://aravind- j.github.io/augmented RCBD/)* at Department of Plantation, Spices, Medicinal and Aromatic crops, College of Horticulture, Bagalkot, Karnataka, India. The centre lies in the northern dry zone of Karnataka having laterite soil and positioned at 16°12′ N, 75°45′ E the average elevation in this area reaches approximately 610 m. The climate is warm and dry throughout the year and rainfall is scarce with an average annual rainfall of 318 mm.

The cross HF-33 × HUBFC-2 made during *rabi*, 2021 and the F_1 plants were also raised along with parents. The differing morphological characteristics of the individual parents were used to identify the actual hybrid plants, and the individual plants were passed on to the F_2 generation at $60 × 40$ cm. A recommended package of practices and plant protection measures were implemented to establish a good crop stand as needed. Twenty quantitative traits *viz*., plant height (cm), number of primary and secondary branches per plant, days to first and 50% flowering, days to maturity, number of umbels per plant, number of umbellets per umbel, test weight (g), seed length (cm), seed width (cm), number of ridges per seed, root length (cm), root width (cm) and seed yield per plant (g) were recorded for all 200 plants in the F_2 population of HF-33 × HUBFC-2 cross.

Genetic variability characteristics, or second order statistics, were estimated using the F_2 data. Using the formulas provided by Burton 1952, the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) for fifteen traits were determined. Sivasubramanian and Madhavamenon (1973) classified these estimations into three categories: low (<10%), moderate (10–20%), and high (>20%). Broad sense heritability (h^2) was measured as the ratio of genotypic variation to phenotypic variance (Lush *et al*., 1940) to determine the heritable fraction of variability. It was then classified as low (<30%), moderate (30-60%) and high (>60%). Johanson *et al*. (1955) computed the genetic advance and expressed it as a percentage of mean (GAM). Three categories were established for the GAM values: low (<10%), moderate (10–20%) and high (>20%).

Results and Discussion

Verification of F_1 hybridity

Morphological characteristics that differed between the parents were used to confirm the hybrid in the cross. In the cross HF-33 × HUBFC-2, the parents were contrasting for plant height (medium in HF-33 and high in HUBFC-3), days to maturity (early in HUBFC-2 and late in HF-33), number of umbels per plant (more in HF-33 and medium in HUBFC-2), umbellets per umbel (more in HUBFC-2 and medium in HF-33), seed shape (elongated in HUBFC-2 and oval to oblong in HF-33), seed size (lengthy in HUBFC-2 and shorter in HF-33), umbel diameter (wider in both case) and seed yield per plant (high in HUBFC-2 and medium in HF-33). The true F_1 plants were identified with the expression dominant trait *i.e.,* greater plant height, early maturing, greater number of umbellets per umbel, with elongated seed with high yield which are the characteristics of male parent, HUBFC-2.

Mean and range for seed yield per plant

A diverse array of fluctuations was noted across all characteristics within the F_2 populations, warranting additional scrutiny for genetic variability metrics in determining selection criteria. Among the characteristics observed, the plant height exhibited a range of 41.00 cm to 195.00 cm, with an average of 122.76 ± 1.99. Similarly, the primary branches per plant varied from 3.00 to 10.00, with a mean of 4.85 ± 0.11. The range for secondary branches spanned from 6.00 to 28.00, with a mean of 10.78 ± 0.27. In addition, the days to first flowering ranged from 25.00 to 117.00, with an average of 61.81 ± 1.47. Furthermore, the days to 50% flowering varied from 39.00 to 145.00, with a mean of 85.94 ± 1.9, while the days to
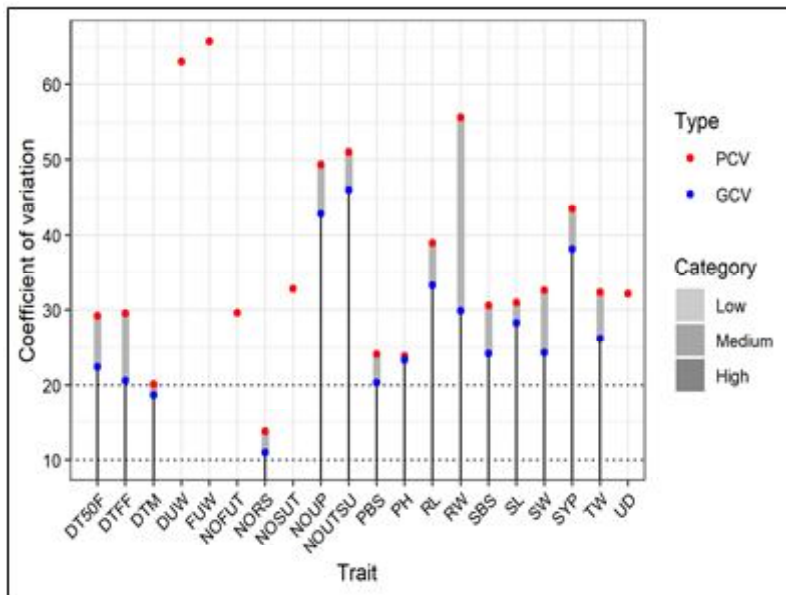
Fig. 1 : Phenotypic and Genotypic Coefficient of variability for F$_2$ population for yield and yield associated trait. **DT50%F:** Days to 50 % flowering, **DTFF:** Days to first flowering, **DTM:** Days to maturity, **DUW:** Dry umbel weight, **FUW:** Fresh umbel weight, **NOF/Ut:** Number of flowers/ umbellet, **NOR/S:** Number of ridges/ seed, **NOS/ Ut:** Number of seeds/ umbellet, **NOUs/P:** Number of umbels/plant, **NOUts/ U:** number of umbellets/umbel, **PBS:** Number of primary branches, **PH:** Plant height (cm), **RL**: Root length, **RW:** Root width, **SBS:** Number of secondary branches, **SL:** Seed length, **SW:** Seed width, **SY/P:** Seed yield per plant, **TW:** Test weight and **UD:** Umbel diameter.

maturity ranged from 74.00 to 179.00, with an average of 131.4 ± 1.79. The number of umbels per plant showed a range of 10.00 to 154.00, with a mean of 63.22 ± 2.36, and the number of umbellets per umbel ranged from 10.00 to 96.00, with a mean of 37.94 ± 1.36. Moreover, the test weight varied from 2.50 (g) to 18.00 (g), with an average of 9.87 ± 0.23. Similarly, the seed length ranged from 1.00 cm to 18.00 cm, with a mean of 6.89 ± 0.16 cm, and the seed width showed a range from 0.20 cm to 4.80 cm, with an average of 2.53 ± 0.06 cm. The number of ridges per seed ranged from 7.00 to 16.00, with a mean of 10.82 ± 0.12, while the root length varied from 5.00 cm to 72.00 cm, with a mean of 34.24 ± 1.02 cm. Additionally, the root width ranged from 2.00 cm to 74.00 cm, with an average of 28.96 ± 1.26 cm, and the seed yield per plant spanned from 6.00 (g) to 154.00 (g), with a mean of 77.38 ± 2.38 (g). This notable diversity observed among the traits and the presence of promising segregants offer significant opportunities for enhancing yield through meticulous selection procedures (Aziz and Masmoudi, 2024).

Coefficient of variations

In every breeding program, the process of selection plays a crucial role in enhancing the traits effectively. The presence of variation is a fundamental requirement for conducting selection, enabling the identification and advancement of desirable plants. Consequently, the assessment of variation extent involved the computation of phenotypic and genotypic coefficients of variations (Tesfaye, 2021). The phenotypic coefficient of variation exhibited higher values in both F$_2$ populations compared to the genotypic coefficient of variations, as indicated in Table 1 and Fig. 1, showing a minimal difference between them. This observation implies that genetic factors have a more substantial impact on population diversity than environmental factors (Liu *et al.,* 2013).

The quantitative traits, such as the number of umbellets per umbel (51.01% and 46.03%), the number of umbels per plant (49.39% and 42.87%), root width (55.75% and 29.88%), seed yield per plant (43.6% and 38.13%), root length (38.95% and 33.24%), seed width (32.61% and 24.29%), test weight (32.3% and 26.17%), secondary branches (30.56% and 24.12%), seed length (30.94% and 28.2%), days to 50% flowering (29.23% and 22.35%), days to first flowering (29.56 % and 20.58%), primary branches (24.05 % and 20.29 %), and plant height (23.79% and 23.29%), exhibited higher estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) in the F$_2$ populations, suggesting a greater diversity in these characteristics. Certain attributes, like days to maturity (20.08% and 18.67%) and the number of ridges per seed (13.82% and 10.98%), displayed moderate PCV and GCV in the F$_2$ population. The presence of high GCV and PCV values coupled with minimal variances signifies a wide genetic foundation within the population. It seems that these traits demonstrate consistent genotype expression, implying that a simple selection process could potentially enhance these characteristics. Comparable results were also observed by Singh and Mittal (2002), Patel *et al*. (2008) and Rawat *et al.* (2013).

Heritability and genetic advance

Heritability, a significant parameter for breeders, holds immense importance as it signifies the degree to which a genotype can be distinguished based on its phenotypic manifestation. Johanson *et al*. (1955) emphasizes that for a more accurate evaluation of

Table 1 : Estimation of genetic variability parameters for yield and associated traits of F$_2$ population cross HF-33 × HUBFC-2.

Traits	Mean ± S.Em	Range		GCV (%)	GCV category	PCV (%)	PCV category	h²$_{bs}$ (%)	GAM (%)	GAM category
		Min	Max							
Plant height	122.76±1.99	41.00	195.00	23.29	High	23.79	High	95.89	47.05	High
Primary branches	4.85±0.11	3.00	10.00	20.29	High	24.05	High	71.18	35.32	High
Secondary branches	10.78±0.27	6.00	28.00	24.12	High	30.56	High	62.28	39.27	High
Days to first flowering	61.81±1.47	25.00	117.00	20.58	High	29.56	High	48.44	29.55	High
Days to 50% flowering	85.94±1.9	39.00	145.00	22.35	High	29.23	High	58.43	35.24	High
Days to maturity	131.4±1.79	74.00	179.00	18.67	Medium	20.08	High	86.49	35.82	High
Number of umbels/ plant	63.22±2.36	10.00	154.00	42.87	High	49.39	High	75.35	76.77	High
Number of umbellets/ umbel	37.94±1.36	10.00	96.00	46.03	High	51.01	High	81.44	85.7	High
Number of flowers/ umbellete †‡	30.44±0.89	13.00	57.00	-	-	29.59	High	-	-	-
Number of seeds/ umbellete†‡	26.06±0.86	8.00	52.00	-	-	32.76	High	-	-	-
Umbel diameter †‡	15.31±0.42	4.20	32.00	-	-	32.16	High	-	-	-
Fresh umbel weight †‡	23.77±1.34	1.30	84.60	-	-	65.74	High	-	-	-
Dry umbel weight †‡	9.64±0.5	0.13	35.24	-	-	63.06	High	-	-	-
Test weight	9.87±0.23	2.50	18.00	26.17	High	32.3	High	65.66	43.76	High
Seed length	6.89±0.16	1.00	18.00	28.2	High	30.94	High	83.09	53.03	High
Seed width	2.53±0.06	0.20	4.80	24.29	High	32.61	High	55.47	37.31	High
Number of ridges/ seed	10.82±0.12	7.00	16.00	10.98	Medium	13.82	Medium	63.17	18.01	Medium
Root length	34.24±1.02	5.00	72.00	33.24	High	38.95	High	72.84	58.53	High
Root width	28.96±1.26	2.00	74.00	29.88	High	55.75	High	28.73	33.05	High
Seed yield/ plant	77.38±2.38	6.00	154.00	38.13	High	43.6	High	76.49	68.79	High

† P-value for "Treatment: Test'' is > 0.05. Genetic variability analysis may not be appropriate for this trait.
‡ Negative GV detected. GCV, GCV category, h²$_{bs}$, GA, GAM and GAM category could not be computed.
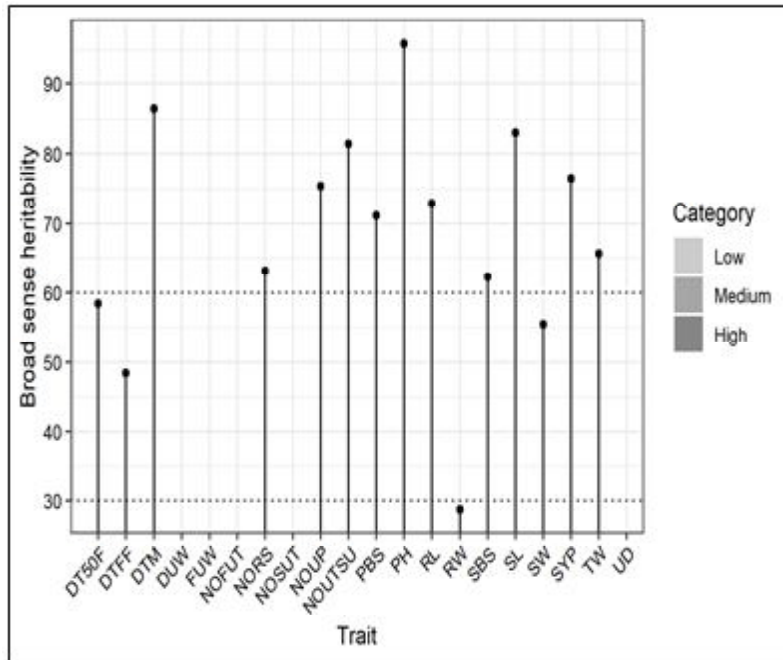
Fig. 2 : Broad sense heritability for F$_2$ population for yield and yield associated traits. **DT50%F:** Days to 50 % flowering, **DTFF:** Days to first flowering, **DTM:** Days to maturity, **DUW:** Dry umbel weight, **FUW:** Fresh umbel weight, **NOF/ Ut:** Number of flowers/ umbellet, **NOR/S:** Number of ridges/ seed, **NOS/ Ut:** Number of seeds/ umbellet, **NOUs/P:** Number of umbels/plant, **NOUts/ U:** number of umbellets/umbel, **PBS:** Number of primary branches, **PH:** Plant height (cm), **RL**: Root length, **RW:** Root width, **SBS:** Number of secondary branches, **SL:** Seed length, **SW:** Seed width, **SY/P:** Seed yield per plant, **TW:** Test weight and **UD:** Umbel diameter.

selection impact, heritability estimates in conjunction with genetic advance are more meaningful. The broad sense observation revealed high heritability across all studied traits. Previous studies by Verma *et al*. (2004) and Samadia (2008) also reported high heritability estimates. It is essential to note that heritability estimates alone may not suffice for forecasting the outcomes of selecting specific individuals. The combination of heritability estimates and genetic advance proves to be more beneficial than relying solely on heritability values in predicting the selection of superior individuals (Singh *et al*., 2021). Therefore, this current study delves into the analysis of heritability (Table 1 and Fig. 2) and genetic advance of traits within the F$_2$ population, with the corresponding values presented in Table 1.

Concerning the traits observed in the F$_2$ generation, such as plant height (95.89% and 47.05%), primary (71.18% and 35.32%) and secondary branches (62.28% and 39.27%), days to maturity (86.49% and 35.82%), number of umbels per plant (75.35% and 76.77%), number of umbellets per umbel (81.44% and 85.72%), test weight (65.66% and 43.76%), seed length (83.09%

and 53.03%), root length (72.84% and 58.53%) and seed yield per plant (76.49% and 68.79%), high heritability estimates were obtained in combination with elevated GAM values. This indicates that certain characteristics possess predominantly additive elements, implying that direct selection may prove more effective in improving these traits. Singh and Mittal (2002), Rajput *et al*. (2004), Singh *et al*. (2004) and Meena *et al*. (2013) have noted that these findings exhibit consistency.

With regards to the trait pertaining to the number of ridges per seed, the observations revealed a high heritability of 63.17% and a moderate Genetic Advance for Mean (GAM) of 18.01%. These findings imply that focusing on direct selection may yield better results in improving these characteristics due to the predominance of additive elements for these traits (Singh *et al*., 2021).

Moderate heritability and high GAM were observed for days to first flowering (48.44% and 29.55%), days to 50% flowering (58.43% and 35.24%), seed width (55.47% and 37.31%) and root width (28.73% and 33.05%) respectively. The moderate heritability is due to the environmental influences on these traits, which indicated limited scope for improvement of these characters through direct selection. These, results are accordance with Meena *et al*. (2010), Rawat *et al*. (2013), Yadav *et al*. (2013), Yogi *et al*. (2013), Sengupta *et al*. (2014), Sharma *et al*. (2015), Ghanshyam *et al*. (2015), Dashora and Sastry (2011), Choudhary *et al*. (2017).

Selection of parameters that exhibit a positive correlation with yield contributes to the enhancement of crop productivity by boosting the yield of different genotypes (Choudhary *et al*., 2017). These attributes related to yield facilitate a more effective selection process. Therefore, opting for these highly beneficial characteristics associated with seed yield per plant indirectly assists in identifying plants with significant yields (Dashora and Sastry, 2011).

Negative genotypic variance was observed in other factors such as seeds per umbellet, umbel diameter, fresh umbel weight and dry umbel weight (Table 1). Consequently, it became unfeasible to calculate h$^2_{bs}$, Genetic Advance (GA), or Genetic Advance over Mean (GAM), and conducting a genetic variability analysis may

not be appropriate for these particular traits (Thonta, 2023). This indicates the prevalence of non-additive gene effects and the limited diversity in these aspects within the germplasm. The likelihood of improving these attributes through selection in this manner is exceedingly low (Hoque *et al*., 2024). This implies that these traits possess a restricted genetic basis, necessitating the introduction of variability through mutation breeding, as suggested by Novak and Brunner (1992).

Conclusion

In light of the preceding discussion, it was deduced that selection from the segregating populations in the current study can facilitate the development of high-yielding fennel varieties by enhancing traits such as plant height, primary and secondary branches, days to maturity, number of umbels per plant, number of umbellets per umbel, test weight, seed length, root length, number of ridges per seed, and seed yield per plant.

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