

## Quantitative and qualitative evaluation of saffron (*Crocus sativus* L.) for genetic variability, character association and path analysis

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### Abstract

Different accessions of saffron were studied to analyze genetic diversity and heritable component of variation in yield and yield related traits. Dry pistil weight, fresh pistil weight, fresh flower weight corm<sup>-1</sup> line<sup>-1</sup>, number of flowers corm<sup>-1</sup> line<sup>-1</sup> and big corm index, all had high genotypic coefficient of variation, heritability and genetic advance. The traits included in the selection scheme and correlation among traits (floral and agronomic) are important as varieties must have high yield associated with exemplary quality parameters. At both phenotypic and genotypic levels, the association was found significant among the traits. Stigma length and fresh flower weight had strong direct effect with respect to dry pistil weight followed by number of flowers corm<sup>-1</sup> line<sup>-1</sup>, fresh pistil weight and big corm index. Therefore, these parameters can be taken as criteria for selection.

**Keywords:** Saffron, coefficient of variation, correlation, genetic diversity, heritability, path analysis

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### Introduction

Saffron (*Crocus sativus* L.) belongs to the family Iridaceae. It is widely recognized as the "Golden condiment" and is known for its high cost. Saffron is a well-known crop that is cultivated and consumed all over the world. Since ancient times, this spice has been highly valued for its aromatic properties, ability to add color to dishes, and medicinal benefits (Plessner *et al.* 1989). Identification of best accessions having

considerable superiority in yield and corm traits is crucial for the improvement and development of high yielding saffron varieties. This process will greatly benefit the saffron industry worldwide, particularly in India, where the national demand for saffron is approximately 100 metric tons (MT), while the current production stands at a mere 16 MT. India, with its rich history and cultural significance attached to saffron, holds tremendous potential for

increasing its production to meet the growing demand. However, the limited yield and quality of saffron in India pose a significant challenge. To overcome this challenge and to bridge the gap between demand and supply, it is imperative to identify the best accessions with superior yield and corm traits. Through careful evaluation and selection, accessions showing remarkable superiority in terms of yield and corm traits can be singled out. These accessions, with their exceptional performance, serve as a valuable resource for further research and development. By incorporating the genetic characteristics of these superior accessions into breeding programs, the saffron production and quality can be enhanced.

The combination of genetic variability analysis, correlation analysis, and path analysis provides a comprehensive understanding of the genetic architecture of a population. This knowledge is essential for effective selection in plant breeding programs. By utilizing these techniques, breeders can make informed decisions and accelerate the development of new varieties with improved traits. They enable breeders to understand the genetic diversity within a population, identify trait relationships, and prioritize traits for improvement. The interaction between characters, as well as their direct and indirect effects on yield, specifically the dry pistil weight, is of utmost importance. This variable, which serves as the dependent variable, is regulated by several independent variables. Understanding the intricate relationship between these characters and their impact on yield is crucial in the field of crop improvement. By considering both direct and

indirect effects, breeders can identify and manipulate specific traits that positively influence the dry pistil weight, ultimately leading to superior crop varieties. This study aims to explore the potential of clonal selection from existing germplasm as a strategy to boost saffron cultivation and address the growing market requirements. Implementing clonal selection techniques requires a careful evaluation of existing germplasm, rigorous selection criteria, and efficient propagation methods.

### **Materials and methods**

The current investigation was carried out at Advanced Research Station for Saffron and Seed Spices (ARSSSS), Dusso Konibal, Pampore, SKUAST-Kashmir during cropping season 2017-18. The research area was located at 34°N latitude, 74°E longitude and approximately 1650 masl. Pedigree detail of all 50 accessions was gathered from various saffron cultivating regions of valley and abroad was recorded. The accessions were sown in Augmented Block Design (ABD) having row length of 3m, width 2m and inter and intra-row spacing of 20 and 10 cms, respectively. Data was collected for various attributes of the plants, specifically stigma length, style length, leaf length, number of flowers corm<sup>-1</sup> line<sup>-1</sup>, total flower weight corm<sup>-1</sup> line<sup>-1</sup>, big corm index, fresh pistil weight, and dry pistil weight. This data was gathered from a total of 10 randomly selected competitive plants from each line as shown in Fig. 2. By examining these attributes, we can gain insights into the characteristics and performance of the plants. Mean value of the selected traits was evaluated for analysis of variance, as described in the

studies conducted by Verma *et al.* (1987) and Singh and Chaudhary (1985). These studies aimed to assess the average values of different traits and their variations within a population. By analyzing the mean data, researchers were able to determine the significance of differences among the traits and their contribution to overall variability. Furthermore, the relationship between traits was investigated at both the genotypic and phenotypic levels, as discussed by Al Jibouri *et al.* (1958). The evaluation of mean data of traits through analysis of variance allows researchers to understand the significance of trait variations within a population. Additionally, investigating the relationship between traits at the genotypic and phenotypic levels provides insights into the genetic basis and observable characteristics of these traits. The studies conducted by Verma *et al.* (1987), Singh and Chaudhary (1985) and Al Jibouri *et al.* (1958) have contributed to our understanding of trait analysis and relationship assessment. In this study we employed statistical procedures proposed by Burton (1952) for variability and Lush (1949) for heritability.

In addition, we have considered the statistical procedures proposed by Lush (1949) to determine the heritability of certain traits. By using Lush's procedures, we have been able to estimate the heritability of specific traits as a percentage of the mean. This allows us to quantify the genetic influence on these traits and understand their potential for inheritance. By incorporating these statistical procedures into our research analysis, we have gained valuable insights into the variability and heritability aspects of our study. According to Johnson *et al.*

(1955), the surveillance technique involves analyzing individual plants at the time of harvesting to evaluate various parameters such as the coefficient of variation, heritability, genetic progress, association, and path analysis. Further cataloging of approximation was done based on Sivasubramanian and Madhavamenon (1973) for variability and Johnson *et al.* (1955) for heritability. By calculating this parameter on a single plant basis, researchers can gain insights into the consistency of yield across different plants in a given population. This information is valuable for determining the stability and reliability of the crop's performance.

Genetic progress, on the other hand, focuses on the improvement of desirable traits over successive generations. Through biometrical yield surveillance, researchers can monitor the rate of genetic progress in terms of yield-related traits. This data aids in the selection of superior plants for future breeding or cultivation purposes. In addition to these factors, association and path analysis are also important aspects of biometrical yield surveillance. An approach given by Dewey and Lu (1959) was utilized for segregation of genotypic and phenotypic associations into path analysis.

### **Results and discussion**

Substantial differences were shown by the genotypes under study for all the traits. Genetic Coefficient of Variation (GCV) combined with heredity, according to Johnson *et al.* (1955), would indicate the proportion of development to be anticipated from the selection. High heritability, GCV, PCV and genetic advance were noticed for dry pistil weight, fresh pistil weight,

number of flowers  $\text{corm}^{-1} \text{ line}^{-1}$ , fresh flower weight  $\text{line}^{-1}$ , big corm index (Table 1). This indicates good opportunity for crop improvement by selection and these findings were consistent with Bekavac *et al.* (2007, 2008) and Mahdi *et al.* (2016). High genetic variability of studied traits responds effectively and therefore can be utilized for selection for better crop improvement.

Correlation studies gives an indication that genotypic correlation was stronger than phenotypic correlation in majority of cases, showing that environmental factors were not significant enough to change the degree of relationship between all of traits (Fig. 1). A substantial positive relationship was found for number of flowers  $\text{corm}^{-1} \text{ line}^{-1}$  with all other yield-related parameters, particularly fresh flower weight  $\text{corm}^{-1} \text{ line}^{-1}$ . All other yield attributing factors showed a weaker positive association with style length. The relationship between the number of flowers  $\text{corm}^{-1} \text{ line}^{-1}$ , fresh flower weight  $\text{corm}^{-1} \text{ line}^{-1}$ , fresh pistil weight, dry pistil weight with saffron yield was found to be extremely significant. As a result, a strong positive correlation with all yield related variables was shown by pistil weight on fresh weight basis. Except for style length, the big corm index demonstrates a highly substantial positive correlation with all other yield attributing traits. Similarly, except for leaf length and style length, dry pistil weight had a substantial correlation with all yield-related parameters. These results agree with the previous findings of Gresta *et al.* (2009) who found that traits have high positive phenotypic and genotypic correlation with each other.

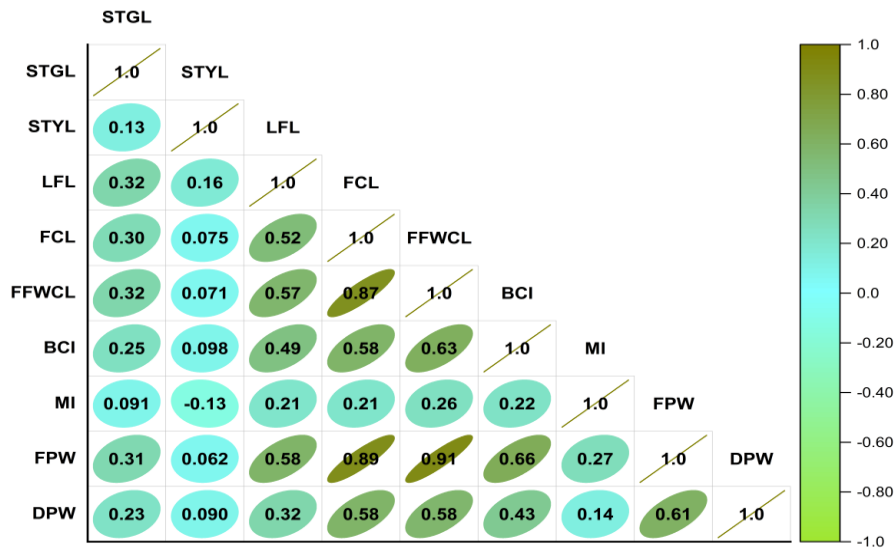
Path coefficient analysis indicates the strong positive direct effect of stigma length (0.945) over dry pistil weight, contributing to the substantial association. The dry pistil weight is an important characteristic that can be influenced by various factors. Among these factors, the stigma length, fresh flower weight, number of flowers  $\text{corm}^{-1} \text{ line}^{-1}$  and big corm index have been found to have a direct and positive impact. Firstly, the stigma length plays a significant role in determining the dry pistil weight. A longer stigma is generally associated with a higher dry pistil weight. This suggests that the length of the stigma is directly related to the reproductive potential of the flower and its ability to produce a greater amount of dry pistil weight. Secondly, the fresh flower weight is another factor that affects the dry pistil weight. Flowers with a heavier weight tend to have a higher dry pistil weight. This indicates that the overall size and mass of the flower are indicative of its reproductive capacity and the amount of dry pistil weight it can produce. Furthermore, the number of flowers  $\text{corm}^{-1} \text{ line}^{-1}$  also contributes to the dry pistil weight. A greater number of flowers  $\text{corm}^{-1} \text{ line}^{-1}$  leads to an increase in the overall dry pistil weight. This suggests that the more flowers a plant produces, the greater the potential for dry pistil weight accumulation. Lastly, the big corm index is an important factor in determining the dry pistil weight. The big corm index refers to

the size and weight of the corm. A higher big corm index is associated with a greater dry pistil weight. This indicates that the size and weight of the corm directly influence the reproductive potential of the plant and its ability to produce dry pistil weight. The dry pistil weight is directly and positively influenced by the stigma length, fresh flower weight, number of flowers corm<sup>-1</sup> line<sup>-1</sup>, and big corm index. Understanding and manipulating these factors can be beneficial in optimizing the dry pistil weight in plants. The residual variance of 0.61 indicated by path coefficient analysis, suggests that 89 percent of variance is accounted by path analysis. The purpose of this study was to identify the contribution of various traits to the dry pistil weight in plants. Specifically, the focus was on stigma length, fresh flower

weight, and number of flowers corm<sup>-1</sup> line<sup>-1</sup>, fresh pistil weight, and the big corm index. Study conducted by Sheikh *et al.* (2014) provided valuable insights into the associations between the mentioned traits and the dry pistil weight. Stigma length, fresh flower weight, number of flowers corm<sup>-1</sup> line<sup>-1</sup>, fresh pistil weight and the big corm index have all been indicated as important factors determining dry pistil weight. The contribution of stigma length, fresh flower weight, and number of flowers corm<sup>-1</sup> line<sup>-1</sup>, fresh pistil weight, and big corm index to the dry pistil weight has been determined (Table 2). These traits have been found to have a significant relationship with the dry pistil weight, as reported by Sheikh *et al.* (2014).

**Table 1.** Mean, range, coefficient of variation, heritability and genetic advance for different characters of saffron (*Crocus sativus* L.)

S. no.	Character	Mean	Range	Phenotypic coefficient of variation (PCV)	Genotypic coefficient of variation (GCV)	Heritability	Genetic advance (GA)
1	Dry pistil weight (DPW)	114.71	25.95- 976.25	64.97	87.61	0.99	127.25
2	Fresh pistil weight (FPW)	483.91	104.84- 1207.38	45.25	45.53	0.98	118.76
3	Fresh flower weight corm <sup>-1</sup> line <sup>-1</sup> (FFW/C/L)	7.23	1.80-14.31	41.61	43.29	0.96	108.10
4	Number of flowers corm <sup>-1</sup> line <sup>-1</sup> (F/C/L)	15.33	4.00-35.33	36.79	37.83	0.95	94.50
5	Multiplication index (MI)	3.80	3.00-5.00	10.43	29.03	0.13	9.89
6	Big corm index (BCI)	10.42	6.00-15.33	22.20	25.49	0.75	51.05
7	Stigma length (STGL)	3.60	2.55-4.18	12.60	11.92	0.89	29.76
8	Style length (STYL)	4.31	2.34-7.35	16.59	16.47	0.55	43.7
9	Leaf length (LFL)	27.73	16.12-37.10	12.84	12.27	0.91	30.97



**Fig. 1.** Correlations among different parameters of saffron under study.

**Table 2.** Direct and indirect effects among their characters towards saffron yield.

Variable	STGL	STYL	LFL	F/C/L	FFW/C/L	BCI	MI	FPW	DPW
STGL	1	0.2019	0.4303	0.3763	0.3763	0.3970	-	0.3873	0.2966
STYL		1	0.1514	0.0847	0.0779	0.1381	-	0.0585	0.1018
LFL			1	0.6099	0.6105	0.6759	0.4646	0.6284	0.4080
F/L				1	0.9152	0.7355	0.5173	0.9247	0.7699
FWT/L					1	0.9132	0.5659	0.9137	0.6604
BCI						1	0.5490	0.7799	0.5575
MI							1	-0.5300	-0.2663
FPW								1	0.6855
DPW									1

STGL= Stigma length, STYL=Style length, LFL=Leaf length, F/C/L=Number of flowers corm<sup>-1</sup> line<sup>-1</sup>, FW/C/L= Fresh flower weight corm<sup>-1</sup> line<sup>-1</sup>, BCI=Big corm index, MI=Multiplication index, FPW=Fresh pistil weight, DPW=Dry pistil weight.

Path analysis is a marked case of structural equation modeling (SEM) method. It is a multivariate statistical tool and is frequently used to examine the interconnections and causes between clearly observable and inherently latent variables, as well as to manage measurement or observation errors.

Discrepancy between the data and the hypothesized model was tested by using comparative fit index (CFI) and its value ranges from 0 to 1, with higher variable data designate better fit and the value was 1 in the present study which suggests that it fits better. Tucker-

Lewis Index, employed in linear mean and covariance structure modeling should have value more than 0.90 for an acceptable fit and the value was 1.012 in the present study which suggests that it is acceptable (Table 3).

**Table 3.** Model test versus baseline model

Comparative Fit Index (CFI)	1.000
Tucker-Lewis Index (TLI)	1.012

Latent variables cannot be measured directly, however, can be detected by their effects on variables that are observable. Here we have 9

different latent variables grouped in two A & B parameters, variances and covariances are and their estimate, standard error, z-value and p value are given in Table 4. Regression

parameters, variances and covariances are presented in Tables 5, 7 and 6 respectively.

**Table 4.** Latent variables

S. No.		Estimate	Standard error	z-value	P(> z )
Group (A)					
1	STGL	1.000			
2	STYL	0.351	0.396	0.887	0.375
3	FFWCL	17.689	4.358	4.059	0.000
4	FCL	31.841	7.873	4.044	0.000
5	FPW	1325.572	325.605	4.071	0.000
Group (B)					
6	LFL	1.000			
7	BCI	0.705	0.097	7.274	0.000
8	MI	0.124	0.039	3.217	0.001

**Table 5.** Regression parameters

S. No.		Estimate	Standard error	z-value	P(> z )
DPW					
1	A	404.307	184.495	2.191	0.028
2	B	5.668	11.556	490	0.624

**Table 6.** Covariances

S. No.		Estimate	Standard error	z-value	P(> z )
1	A				
2	B	0.331	0.098	3.388	0.001

**Table 7.** Variances

S. No.	Parameters	Estimate	Standard error	z-value	P(> z )
1	STGL	0.206	0.025	8.330	0.000
2	STYL	0.515	0.062	8.365	0.000
3	FFWCL	1.030	0.179	5.762	0.000
4	FCL	4.868	0.729	6.673	0.000
5	FPW	3321.023	810.123	4.099	0.000
6	LFL	6.684	0.967	6.910	0.000
7	BCI	2.169	0.372	5.834	0.000
8	MI	0.822	0.100	8.220	0.000
9	DPW	4262.488	538.178	7.920	0.000
	A	0.025	0.013	1.988	0.047
	B	5.262	1.303	4.038	0.000



**Fig. 2.** A= Field layout, B= Saffron flower along with leaves, C= Fresh pistil per corm D=Multiplication index

### Conclusion

Based on the results of the study, it can be concluded that enhancing saffron production through clonal selection is highly desirable. This method involves identifying and selecting specific elite genotypes possessing desired qualities such as higher yield (which have been identified in the present study), better quality, and increased adaptability to different environmental conditions, breeders can effectively use them as donors to develop improved saffron varieties. Utilizing clonal selection as a means of enhancing saffron offers several advantages. It allows preservation and multiplication of the desired traits present in the elite genotypes. By selecting and propagating these genotypes, breeders can ensure the perpetuation of the desirable characteristics in the subsequent generations of saffron. This

targeted approach increases the efficiency and effectiveness of crop improvement efforts. Through these efforts, saffron production can be enhanced, leading to increased yield, improved quality, and greater resilience to environmental challenges.

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