Original Research Article

Evaluation Study of the Genetic Variability of Saffron (*Crocus sativus* L.) for morphological and corm attributes

Abstract

The present investigation was carried out at Saffron Research Station Pampore, SKUAST-Kashmir during 2017-18. Observations were recorded on 10 randomly selected and tagged competitive plants for 18 morphological, floral and corm traits viz, number of flowers line^{-1}, number of days to 50% flowering, total flower weight corm^{-1}, inner tepal length, outer tepal length, inner tepal width, outer tepal width, anther length, anther width, style length, stigma length, fresh pistil weight line^{-1}, leaf length, dry pistil weight line^{-1}, number of leaves corm^{-1}line^{-1}, number of days to 50% sprouting, Big Corm Index, Multiplication Index. The study was undertaken to generate information on the phenotypic and genotypic variability for morphological, floral and corm attributes. Genetic divergence among selected lines was studied thoroughly for identification of elite divergent traits showing economic gains for morphological, floral and corm attributes, along with their contribution towards yield components. Significant variations among populations were observed for all the traits, number of flowers per corm (0.90-1.98), fresh pistil weight (31.0- 69.46), stigma length (2.55-4.18), leaf length (16.12-37.10), multiplication index (3.0-4.1), number of leaves corm^{-1}line^{-1} (6.00-11.33), total flower weight corm^{-}1 (1.80-14.31) indicating presence of high level of variability and therefore imply considerable scope for saffron improvement through clonal selection. Estimates of phenotypic variance were higher than the corresponding estimates of genotypic variance, thereby revealing influence of environment in the expression of the traits studied. High values of heritability were recorded for all the traits. Divergence studies are paramount in understanding the extent of variability and possibilities of its future utilization in subsequent breeding programme.

Keyword: *Crocus sativus* L., cluster, correlation, divergence, genetic, variability.

Introduction

Saffron (*Crocus sativus* L.) which belongs to family *Iridaceae* is the most expensive spice in the world and is popularly known as the "Golden Condiment". In India it is a legendary crop of Jammu and Kashmir, produced on well drained karewa soils, where ideal climatic conditions are available for good shoot growth and flower production. The genus *Crocus* includes native species from Europe, North Africa and temperate Asia, and is especially well represented in arid countries of south-eastern Europe and Western and Central Asia. Dried stigmas of saffron flowers compose the most expensive spice which has been valuable since ancient times for its odoriferous, coloring and medicinal properties (Plessner *et al*., 1989). Saffron is a sterile triploid plant that is propagated by corms as the propagation through seed is impossible due to non setting of seeds. The possibility of saffron genetic improvement is indicated through clonal selection from the available germplasm resources. Identification of these elite genotypes with distinct superiority in yield and corm attributes can be used as a source for further improvement and development of high yielding varieties which would be beneficial for saffron industry in Jammu and Kashmir. Development of varieties from the identified germplasm resources, exhibiting high yielding potential and quality will boost the production and productivity of saffron in Jammu and Kashmir and improve the socio-economic condition of the people associated with this important commercial crop. Development of varieties from the identified germplasm resources, exhibiting high yielding potential and quality will boost the production and productivity of saffron in Jammu and Kashmir and improve the socio-economic condition of the people associated with this important commercial crop.

Materials and methods

Saffron corms weighing 5g to 16g were planted in Augmented Block Design, for daughter corm production under annual planting cycle. Corms were planted under each category supplemented with adequate nutrients as per the recommendations of SKUAST-K, Shalimar. The present investigation was carried out at Saffron Research Station Konibal Pampore, a constituent Research Station of Sher-e-Kashmir University of Agricultural Sciences and Technology Kashmir. The experimental site is located at 34^0_N latitude, 74^0_E longitude and about 1650 m a.s.l and 29 km away from main campus of the University at Shalimar, Srinagar. The material for study comprised of 140 saffron germplasm lines collected from different saffron growing areas of Kashmir and abroad. The pedigree details of all the 140 corm samples was recorded and subsequently planted in Augmented Block Design with a row length of 3m, width 2m and inter and intra-row spacing of 20 and 10 cms, respectively. Observations were recorded on 10 randomly selected and tagged competitive plants from each line for all the traits during the crop year 2017-2018.

Floral attributes: Number of flowers corm^{-1}line^{-1}, Number of flowers corm^{-1} line^{-1}, Total flower weight corm^{-1}, Outer tepal length, Inner tepal length (cm), Outer tepal width (cm), Inner tepal width (cm), Anther length (cm), Anther width (mm), Style length (cm), Stigma length (cm), Fresh pistil weight per line (mg), Dry pistil weight per line (mg).

Vegetative parameters : Leaf length (cm), No. of leaves per line

Corm attributes : No. of days to 50% sprouting, Big Corm Index, Multiplication Index.

Mean values for all the characters were estimated for analysis of variance (Verma *et al.* 1987; Singh and Chaudhary, 1985) and Character association at genotypic and phenotypic level (Al Jibouri, 1958).

Results and Discussion

Genetic variability assists a great deal in detecting the range of genetic diversity for various traits in population (Singh *et al*., 2004). Components of phenotypic and genotypic variability indicated that a wide range of variability existed for all the traits studied. Outer tepal length ranged from (3.13-4.55cm) with a mean value of 4.25, inner tepal length (3.46-3.96cm), with a mean value of 3.69, outer tepal width (3.45-3.95cm) with a mean value of 3.70 , inner tepal width (1.55-2.03cm) with a mean value of 1.84, stigma length (2.55-4.18cm) with a mean value of 3.60, style length (2.34-7.35cm) with a mean value of 4.31, leaf length (16.12-37.10cm) with a mean value of 27.73, number of leaves corm^{-1}line^{-1} (6.00-11.33) with a mean value of 8.93, number of flowers line^{-1} (4.00-35.33) with a mean value of 15.33, total fresh flower weight corm^{-1} (1.80-14.31g) with a mean value of 7.23, big corm index (6.00-15.33) with a mean value of 10.42, multiplication index (3.00-5.00) with a mean value of 3.80, fresh pistil weight (104.84-1207.38mg) with a mean value of 483.91, dry pistil weight (25.95-976.25mg) with a mean value of 114.71, anther length (1.34-2.37cm) with a mean value of 1.90, anther width (1.26-3.74mm) with a mean value of 2.40, 50% flowering (68.66-76.66) with a mean value of 73.10 and 50% sprouting (22.00-134.00) with a mean value of 128.16 (Table 1-4). Results are in conformity with the reports of Sheikh *et al* (2014), Latto and Dhar (1999), Zargar (1999), Gohill (1999), Zargar (2002) and Makhdoomi *et al*. (2010). The study suggests that there is an ample scope for saffron genetic improvement through selection of superior genotypes from the heterogeneous saffron populations. For floral attributes viz, outer tepal length, inner tepal length, outer tepal width, inner tepal width, anther length, anther width indicates less range of variability. The estimates of phenotypic variances were higher than the corresponding estimates of genotypic variances thereby revealing a strong influence of environment in the expression of the traits studied. *Per se* performance of genotypes under evaluation revealed a gross fresh pistil weight of 40.24 mg per corm from 1.21 flowers per corm resulting in 3 kg lachha saffron per hectare with planting density of 5 lakh corms per hectare showing an increase of 25% over state average. Estimates of phenotypic and genotypic correlation coefficient among the characters have been found useful in planning and evaluating breeding programme (Johnson *et al*., 1955; Al-Jibouri *et al*., 1958). Genotypic correlation coefficient provide a measure of genetic association among the characters and gives an indication of characters that could be useful as to identify more important ones during a selection programme. At phenotypic and genotypic level, dry pistil weight (economic product) exhibited a significant positive correlation with all the traits. The results clearly reveal a scope for simultaneous improvements of this important trait through selection. Interrelationship among various floral, vegetative and yield contributing traits was observed to be significant both at genotypic and phenotypic levels. Yield is influenced by environmental conditions and is a complex mode for inheritance and low heritability (Bo´canski *et al*., 2009). However, most of the yield components which naturally leads to using some other trait that is highly correlated with yield and has a much higher heritability through selection of the best progenies for more reliability (Bekavac *et al*., 2008, Vasic *et al*., 2001). In this study, to assess the phenotypic and genotypic relationships between studied traits, correlation coefficients based on phenotypic and genotypic values were calculated (Table 5). Results showed that the saffron yield had positive and significant phenotypic and genotypic correlations with all traits. These findings are in conformity with Gresta *et al.,* 2009. Therefore, any increase in the yield components improved saffron yield directly and indirectly. It was notable in this study that in most cases the genotypic correlation coefficients were larger than the phenotypic correlation coefficients. This finding is in agreement with the results of previous studies of Singh *et al*. (2003, 2004). Saffron under temperate conditions of Kashmir Valley reported wide spectrum of variability for floral, vegetative and corm attributes and the results implied a great scope for saffron improvement. Flower size, number of flowers per corm and saffron recovery per flower were observed to help as selection index for increasing saffron yield. Valley exhibited highest range of variability in saffron germplasm. From natural population flowers completely devoid of style and anthers, some flowers with 4 and 5 stigmas were observed. The presence of higher number of stigmas per flower results from physiological or developmental irregularities leading to 4-5 stigmas. These results are in conformity with Nehvi *et al.* (2003, 2004 and 2006). The phenotypic and genotypic variations between different saffron ecotypes and the phenotypic/genotypic relationships between yield and yield components of saffron were measured such as: Fresh pistil Weight, Dry pistil Weight and Stigma Length. The results showed that genetic variances were much higher than phenotypic variances for most of the traits. And also these traits show highest genetic diversity. Results of the correlation coefficients showed that the phenotypic correlations were higher than the genotypic correlations for almost all of the traits like big corm index (0.72), number of flowers per line (0.62), flower weight (0.89) and fresh pistil weight (0.910) had the highest genotypic correlation with dry stigma yield. In general, with the purpose of the study and assessments to genotypic correlation coefficients, genetic parameters and genotypic direct and indirect effects, we can conclude that traits like, big corm index, number of flowers per line, flower weight, fresh pistil weight were the most effective traits and had the highest positive impacts on the saffron yield. Therefore, with the phenotypic selection of saffron ecotypes in respect of these traits the saffron yield can be increased. These findings are in agreement with the results of previous studies of Bayat *et al.* (2016)

Table 1. Estimates of Phenotypic variance (δ^2 p), genotypic variance(δ^2 g), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) for morphological and corm attributes of Saffron (*Crocus sativus* L.)

S. No.	Characters	Phenotypic variance (δ^2 P)	Genotypic variance (δ^2g)	Phenotypic coefficient of variation (PCV)	Genotypic coefficient of variation (GCV)
1	**Outer tepal length**	**0.015**	**0.058**	**2.88**	**5.65**
2	**Inner tepal length**	**0.013**	**0.015**	**3.04**	**3.10**
3	**Outer tepal width**	**0.013**	**0.014**	**3.11**	**3.15**
4	**Inner tepal width**	**0.012**	**0.013**	**5.97**	**6.08**
5	**Stigma length**	**0.18**	**0.25**	**12.60**	**11.92**
6	**Style length**	**0.51**	**0.51**	**16.57**	**16.59**
7	**Leaf length**	**11.59**	**12.69**	**12.27**	**12.84**
8	**Number of leaves per corm**	**0.95**	**2.971**	**10.72**	**19.28**
9	**Number of flowers per corm per line**	**31.83**	**33.663**	**36.79**	**37.83**
10	**Fresh Flower weight corm^{-1} line^{-1}**	**9.055**	**9.353**	**41.61**	**42.29**
11	**Big corm index**	**5.35**	**7.064**	**22.20**	**25.49**
12	**Multiplication index**	**-0.15**	**1.223**	**10.43**	**29.03**
13	**Fresh pistil weight**	**47967.17**	**48544.88**	**45.25**	**45.53**
14	**Dry pistil weight**	**5556.44**	**10101.17**	**87.61**	**64.97**
15	**Anther length**	**0.092**	**0.092**	**15.92**	**15.95**
16	**Anther width**	**0.33**	**0.360**	**24.07**	**25.06**
17	**50% flowering**	**2.29**	**4.680**	**2.29**	**2.95**
18	**50% sprouting**	**2.44**	**11.17**	**2.44**	**2.60**

Table 2. Magnitude of variability for different morphological and corm attributes in saffron (*Crocus sativus* L.).

S. No.	Characters	Range	Mean	C.V.	S.E.	C.D. at 5%
1	Outer tepal length (cm)	3.13-4.55	4.25	4.85	0.11	0.33
2	Inner tepal length (cm)	3.46-3.96	3.69	0.55	0.01	0.03
3	Outer tepal width (cm)	3.45-3.95	3.70	0.48	0.02	0.02
4	Inner tepal width (cm)	1.55-2.03	1.84	1.14	0.01	0.03
5	Stigma length (cm)	2.55-4.18	3.60	4.08	0.08	0.23
6	Style length (cm)	2.34-7.35	4.31	0.70	0.02	0.04
7	Leaf length (cm)	16.12-37.10	27.73	3.77	0.60	1.68
8	Number of leaves corm^{-1}line^{-1}	6.00-11.33	8.93	16.02	0.82	2.30
9	Number of flowers line^{-1}	4.00-35.33	15.33	8.81	0.78	2.17
10	Fresh Flower weight corm^{-1} line^{-1}	1.80-14.31	7.23	7.55	0.31	0.87
11	Big corm index (g)	6.00-15.33	10.42	12.53	0.75	2.09
12	Multiplication index	3.00-5.00	3.80	30.84	0.67	1.08
13	Fresh pistil weight (mg)	104.84-1207.38	483.91	4.96	13.87	38.63
14	Dry pistil weight (mg)	25.95-976.25	114.71	58.76	38.92	108.35
15	Anther length (cm)	1.34-2.37	1.90	1.01	0.01	0.03
16	Anther width (mm)	1.26-3.74	2.40	6.97	0.09	0.26
17	50% flowering	68.66-76.66	73.10	1.87	0.78	2.19
18	50% sprouting	22.00-134.00	128.16	0.92	0.68	1.89

Conclusion

Based on the results of the investigation, wide range of variability exists in the natural population of saffron as indicated by the magnitude of performance, phenotypic and genotypic coefficient of variation, implying considerable scope for saffron improvement through clonal selection. Number of flowers corm^{-1} and stigma length are the important traits for which due emphasis should be given while selecting for high saffron yield with better quality. Also the percent contribution of different floral, vegetative and corm attributes towards divergence in saffron germplasm revealed strong influence of fresh pistil weight, multiplication index followed by fresh flower weight corm^{-1} line^{-1} and dry pistil weight. Therefore, such characters can be taken as criteria in selection for divergent lines and could be used as a source of elite genetic resource for of new varieties.

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