**Genetic divergence of saffron germplasm for morphological and corm attributes.**

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**Abstract**

The Present Investigation was carried out at Saffron Research Station Pampore, (SKUAST-K) during Rabi season 2017-18. Observations were recorded on 10 randomly selected and tagged competitive plants for eighteen (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-1line-1, number of days to 50% sprouting, big Corm Index, multiplication index. Saffron (*Crocus sativus* L.) study was undertaken to generate information on the phenotypic and genotypic variability for morphological and corm attributes. Genetic divergence among selected lines was studied thoroughly for identification of elite divergent traits showing economic gains for morphological and corm attributes, along with their contribution towards yield components. Extent of divergence was observed in most of the genotypes among one hundred forty (140) saffron germplasm collected from different saffron growing areas of Kashmir and rest of world. Observations were recorded on morphological, floral and corm attributes and significant variations among populations were observed for all the traits indicating presence of high level of variability and therefore imply considerable scope for saffron improvement through clonal selection. It is vital to have better understanding of the nature and magnitude of genetic variability, character association and their direct and indirect effects on yield and other traits. Divergence studies grouped the genotypes into eleven clusters with cluster I having maximum number of genotypes (84) followed by cluster II with 23 genotypes and cluster IV with 18 genotypes. Percentage contribution of different characters towards total divergence revealed that fresh pistil weight contributes (21%) followed by multiplication index (18%), total flower weight corm-1 (13.52%) and number of leaves corm-1 line-1 (13.27%) and big corm index (5%). Therefore, such characters can be taken as criteria in selection for divergent lines of paramount in understanding the extent of variability and possibilities of its future utilization in subsequent breeding programme.

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

**Introduction**

Saffron (*Crocus sativus* L.) belongs to family *Iridaceae* and is the most expensive spice in the world. 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 family *Iridaceae* embraces about 60 genera and 1,500 species. The genus *Crocus* is especially well represented in arid countries of south-eastern Europe, Western and Central Asia. Among the 85 species belonging to the genus *Crocus*, Saffron (*C*. *sativus* L.) is the most fascinating and intriguing species (Fernández, 2004). Dried stigmas of saffron flowers compose the most expensive spice which is famous for its odoriferous, coloring, and medicinal properties (Plessner *et al*., 1989). A relatively low water use, growth and development during fall and winter and a very low harvesting index are some remarkable characteristics of saffron. Kashmir region in India produces between 5 to 6 tonnes mostly dedicated to India’s self consumption. Saffron export from India declined because sterility of saffron limits the application of conventional breeding approaches for its further improvement resulting in a low productivity (Ahmad *et al*., 2013). 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 natural propagation rate of most geophytes including saffron is relatively low. Besides conventional methods of propagation, biotechnological approaches such as *in vitro* cultural methods contribute to the propagation of many important and economic plants. The estimation of heritable variability especially its genetic component in breeding material from different sources is a matter of considerable interest to the breeders. The knowledge about the nature and magnitude of the components of genetic variation and genotype x environment variation can greatly help the plant breeders in formulating the breeding programme. Genetic diversity ensures a wide genetic base for the crop enabling thereby incorporation of a number of genes for disease resistance, varietal adaptability and effective selection. When uniformity becomes the cause of genetic vulnerability, genetic diversity is the only insurance against it. To overcome the menace of this uniformity, it is essential that genetic diversity present in the cultivated crop is systematically exploited and used to generate new gene complexes for improvement in quantitative and qualitative traits.

**Material 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 340N latitude, 740E 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 collected from different saffron growing areas of Kashmir and abroad. The pedigree details of all the 140 corm lines 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. The observations were recorded for all the traits (floral, vegetative and corm attributes).

**Floral attributes**: Number of flowers corm-1line-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**

One hundred and forty (140) saffron germplasm lines were evaluated for genetic divergence as per Mahalanobis D2 analysis employing Tocher’s method (Rao, 1952). Based on the performance, the genotypes were grouped into 11 clusters. Cluster I contains maximum number of genotypes (84). Rest of genotypes was grouped in 10 clusters irrespective of the geographical area. Cluster mean of different characters revealed that the number of flowers corm-1 line-1 had maximum cluster mean. Cluster means were generally associated with divergence pattern. Studies in a number of crop species with different breeding systems by means of D2 statistics suggest that genetic diversity need not be directly related with enough genotypic diversity. For development of high yielding saffron varieties enough information regarding genetic diversity is presently not available although the technique has extensively been used by numerous workers in understanding the nature of genetic divergence and for selecting diverse parents for successful hybridization in the breeding populations. In saffron, the basic aim is to study the group of sub populations for their genetic diversity and subsequent utilization of diverse individuals in development of high yielding varieties. Analysis of variance for divergence revealed that value of statistics measuring Wilk’s criterion were high and significant indicating presence of substantial genetic diversity in the material. Similar results have also been reported by Desh and Misra (1993), Arya *et al*., (1999), Desh Raj and Misra (1999) and Nimbalkar *et al*., (2002) in gladiolus. Genotypes were classified into 11 clusters and cluster I accommodated maximum number of genotypes irrespective of geographical area. Data analysis revealed that cluster I accommodated 84 genotypes followed by cluster II (23) and cluster IV (18). Mean intra-cluster and inter-cluster distances (Table 1) which determine the level of divergence, revealed that maximum divergence between genotypes within a cluster was recorded for cluster I (415.78) which accounted for maximum genetic distance between genotype SSR/SD-104 and SSR/SD-107. Maximum inter cluster distance of 10923.91 was recorded between cluster X and cluster XI accommodating genotypes SSR/SD-13 and SSR/SD-62 followed by cluster VIII and cluster X (7598.09) which accommodates genotypes SSR/SD-61 and SSR/SD-13, cluster VII and cluster XI (6977.24)accommodating genotypes SSR/SD-6, SSR/SD-15, SSR/SD-29, SSR/SD-81, SSR/SD-2, SSR/SD-1, SSR/SD-67, SSR/SD-24 and SSR/SD-13. The results clearly indicated that there is potential for identification of diverse genotypes which can act as a source of allelic resources for development of new saffron varieties. Cluster means for different morphological and corm attributes (Table 2) revealed that substantial variability existed for all these traits. Cluster mean of different traits revealed a wide range of variability. Cluster IX revealed high cluster mean for saffron yield, big corm index and stigma length on account of grouping of high yielding genotype SSR/SD-30. Superiority in terms of saffron yield and big corm index was exhibited by cluster IX. Also this cluster IX was observed to record maximum cluster mean for multiplication index. The highest cluster mean for saffron and corm yield was attributed to genotype SSR/SD-30 grouped in cluster IX whereas, maximum cluster mean for floral attribute was exhibited by cluster V which was due to highest mean performance of genotype SSR/SD-7. Genotypes SSR/SD-30, SSR/SD-6, SSR/SD-15, SSR/SD-29, SSR/SD-81, SSR/SD-2, SSR/SD-1, SSR/SD-67 and SSR/SD-24 exhibited high mean performance for saffron yield associated with high mean performance for corm yield also. Percentage contribution of different characters (Table 3) towards divergence revealed that fresh pistil weight (21%) followed by multiplication index (18%), total flower weight corm-1 (13.52%) and number of leaves corm-1 line-1 (13.27%) and big corm index (5%) contributed maximum towards divergence. Therefore, such characters can be taken as criteria in selection for divergent lines. Sardana *et al*., (1997) observed that cluster mean and coefficient of variation represent picture of diversity. Based on findings of present investigation there is possibility of saffron improvement through clonal selection from the available germplasm resources. Identification of 6 elite genotypes with distinct superiority in yield and corm attributes can act as a source for further improvement and development of high yielding varieties which can be beneficial for saffron industry in Jammu and Kashmir, particularly to the marginal and small farmers associated with saffron cultivation by increasing their net returns from saffron, besides encourage farmers from nontraditional areas to take up saffron cultivation. Development of variety from the identified germplasm resources, exhibiting high yielding potential and quality will boost the production and productivity of saffron in Jammu and Kashmir and also improve the socio-economic well being of the people associated with this important commercial crop.



 **Table 2 Cluster means for morphological and corm attributes in saffron (*Crocus sativus* L.).**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Cluster | OTL | ITL | OTW | ITW | STGL | STYL | LFL | L/C/L | F/C/L | FWT/C/L | BCI | MI | FPW | DPW | AL | AW | 50%F | 50%S |
| I | 4.24 | 3.71 | 3.73 | 1.83 | 3.63 | 4.26 | 27.11 | 8.69 | 14.16 | 6.58 | 9.94 | 3.77 | 441.42 | 100.26 | 1.88 | 2.31 | 73.25 | 128.43 |
| II | 4.30 | 3.68 | 3.72 | 1.89 | 3.72 | 5.32 | 29.60 | 9.52 | 18.10 | 8.98 | 11.65 | 3.91 | 605.76 | 166.34 | 2.11 | 2.88 | 72.36 | 134.01 |
| III | 4.13 | 3.65 | 3.63 | 1.85 | 3.36 | 3.96 | 31.20 | 10.13 | 10.33 | 5.67 | 9.33 | 3.00 | 314.87 | 74.65 | 1.38 | 1.87 | 72.00 | 133.00 |
| IV | 4.20 | 3.67 | 3.66 | 1.78 | 3.19 | 3.73 | 26.39 | 10.87 | 27.11 | 5.63 | 12.75 | 3.69 | 361.85 | 84.91 | 1.55 | 1.93 | 73.74 | 129.28 |
| V | 4.45 | 3.77 | 3.76 | 1.97 | 4.14 | 3.55 | 31.29 | 10.63 | 22.67 | 11.78 | 14.0 | 4.66 | 674.17 | 157.93 | 2.35 | 3.25 | 73.67 | 127.33 |
| VI | 4.27 | 3.74 | 3.52 | 1.67 | 3.66 | 3.96 | 29.14 | 9.33 | 14.67 | 4.63 | 10.67 | 3.00 | 405.27 | 99.94 | 2.36 | 1.76 | 73.00 | 132.00 |
| VII | 4.30 | 3.71 | 3.73 | 1.84 | 3.89 | 3.14 | 30.13 | 9.75 | 24.21 | 11.53 | 14.23 | 4.73 | 855.37 | 173.69 | 2.24 | 2.74 | 73.33 | 127.17 |
| VIII | 4.43 | 3.64 | 3.95 | 2.03 | 4.13 | 6.34 | 29.07 | 9.33 | 20.33 | 7.88 | 12.67 | 4.00 | 624.22 | 142.53 | 2.26 | 3.26 | 69.67 | 125.00 |
| IX | 4.23 | 3.93 | 3.57 | 1.96 | 4.15 | 7.36 | 34.13 | 10.67 | 26.00 | 13.30 | 14.96 | 4.87 | 904.67 | 188.64 | 2.37 | 3.19 | 70.67 | 132.00 |
| X | 4.22 | 3.69 | 3.65 | 1.75 | 2.83 | 2.34 | 26.16 | 10.00 | 14.00 | 7.21 | 9.00 | 3.00 | 418.10 | 98.18 | 1.37 | 1.84 | 72.67 | 129.33 |

 OTL (Outer tepal length), ITL (Inner tepal length), OTW (Outer tepal width), ITW (Inner tepal width), STGL

(Stigma length), STYL (Style length), LFL (Leaf length), L/C/L (Number of leaves per corm per line), F/C//L (Number of flowers per line), FWT/C/L (Total flower weight per line), BCI (Big corm index), MI (Multiplication index), FPW (Fresh pistil weight), DPW (Dry pistil weight), AL (Anther length), AW (Anther width), 50% F (50 percent flowering), 50% S (50 percent sprouting).

**Summary and conclusion**

Divergence studies grouped all the genotypes in eleven clusters with majority of genotypes 84 in cluster I, 23 in cluster II, 18 in cluster IV and 8 in cluster (VII) whereas, all other clusters were monogenotypic. The highest intra-cluster distance of 415.78 was observed between genotype SSR/SD-104 and SSR/SD-107 grouped in cluster I. Maximum inter-cluster distance of 10923.91 was recorded between cluster X and cluster XI accommodating genotypes SSR/SD-13 and SSR/SD-62 followed by cluster VIII and cluster X (7598.09) accommodating genotypes SSR/SD-61 and SSR/SD-13, cluster VII and cluster XI (6977.24)accommodating genotypes SSR/SD-6, SSR/SD-15, SSR/SD-29, SSR/SD-81, SSR/SD-2, SSR/SD-1, SSR/SD-67, SSR/SD-24 and SSR/SD-13. Cluster mean of different traits revealed a wide range of variability. Cluster IX revealed high cluster mean for saffron yield, big corm index and stigma length on account of grouping of high yielding genotype SSR/SD-30. High cluster mean for floral attributes was observed to be on account of grouping of genotype SSR/SD-30 in cluster IX. High *per se* performing genotypes viz SSR/SD-13, SSR/SD-36, SSR/SD-62, SSR/SD-63, SSR/SD-67 and SSR/SD-140 for yield attributes provide an ample scope for saffron improvement through clonal selection.

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