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Genetic diversity in saffron (*Crocus sativus* L.)

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Abstract

Two hundred saffron genotypes collected from saffron growing areas of Kashmir subjected to Mahalanobis D^2 analysis revealed high amount of diversity. Out of 200 genotypes, 171 genotypes were grouped in cluster I, 9 in cluster V and 7 in cluster VI whereas the other 13 clusters were monogenotypic. Maximum intracluster distance (6.50) was recorded for cluster V accommodating SH-21, SH-123, SH-200, SH-51, SH-30, SH-81, SH-69, SH-03, SH-98 genotypes collected from Kushbal, Wuyan, Khrew, Kashbal, Wulan nadh, Kruncho, Dusso, Tang and Darbagh. Maximum intercluster distance (18.14) was recorded between cluster XV and XVI showing maximum genetic divergence among the population for SH-67 collected from Chandhara and SH- 89 collected form Khrew area of Kashmir valley. Fresh stamen weight (20.86%) followed by plant height (17.77%), fresh flower weight (15.31%) and pistil length (9.98%) had contributed significantly towards diversity.

Keywords: clustering, diversity, mahalanobis, saffron

Saffron (*Crocus sativus* L.), the legendary crop of Kashmir belongs to the family Irridaceae and genus *Crocus*, of which about 80 species are known so far. It is thought to have originated in Greece, Asia minor and Persia, spreading eastwards to Kashmir and China. Saffron is a cormose triploid geophyte (2n = 3x = 24), unknown in wild state (Mathew 1983). The plant is characterized by a biological cycle with a long pause in the summer and active growth period in the autumn. Iran, India and Spain are the major saffron producing countries of the world. Iran occupies the maximum area of 47,000 ha with a total production of 238 MT contributing above 90% of the total world's saffron production. Though India (Jammu & Kashmir) occupies the 2nd highest area of 3,785 ha the production is only 9.462 MT with an average productivity of 2.50 kg ha^{-1}. Spain with 600 ha of land under saffron cultivation produces 4.70 MT of saffron with an average productivity of 7.84 kg ha^{-1} which is the highest among the major saffron producing countries of the world (Nehvi 2010). In Jammu & Kashmir, Pulwama district, commonly known as Saffron bowl of Kashmir, is the main contributor to saffron production followed by Budgam, Srinagar and Kishtiwar districts.

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Due to sterility imposed by triploidy, clonal selection offers ample scope to ameliorate the productivity constraints. The natural population of saffron in Jammu and Kashmir has been under cultivation for so many centuries. The heterogeneity found in natural population for morphological, developmental and yield component traits are due to genetic and environmental factors. Initiation of coherent breeding programmes on sound scientific lines necessitates generation and application of basic information on various genetic parameters that pragmatically help in achieving breeding goals. To overcome the menace of uniformity, it is essential that genetic diversity present in the cultivated crop be systematically exploited and used to generate new gene complexes for improvement in quantitative and qualitative traits and resistance to biotic and a biotic stresses. Therefore, the present study was carried out to generate information on the extent of genetic variability prevailing in the temporal sub-population of saffron and possibilities of utilizing this variability in developing gene repositories for identification of high yielding varieties. Attempts were also made to study the nature and magnitude of interrelationship among the components of economic worth so as to devise a selection criterion in the clonal selection of saffron.

Exploratory survey was carried out during August 2006 and 2007 in prominent saffron growing areas of Kashmir *viz.*, Zeevan, Khrew, Wuyan, Ladhoo in Srinagar district; Dusso, Namlabal, Konibal, Chandar, Pampore, Barsu, Lathipora in Pulwama district and Chadora, Chararisharief, Kakawring, Hapatnar in Budgam district, located at an altitude of 1686, 1644, 1597, 1730 above MSL, respectively. Two hundred saffron genotypes (each sample of 60 corms in number) of uniform weight and size (>10.0g /3.5 cms) were collected from each location. The pedigree details of all the 200 corm samples were recorded and subsequently planted in a randomized block design at Lethpora district Pulwama during September 2006 and 2007. Each sample of 60 corms were replicated twice in two row experimental plot of 1.5 m row length with inter and intra-row spacing of 20 cm and 10 cm, respectively. All the recommended package of practices was followed to raise a good crop. Observations were recorded on 10 randomly selected competitive plants from each experimental plot in each replication during the crop year 2006 (Y_1) and 2007 (Y_2) for 19 characters *viz.*, number of flowers per corm, fresh flower weight per corm, fresh pistil weight per corm, fresh stigma weight per corm, fresh style weight per corm, fresh stamen weight per corm, stigma length, style length, pistil length, dry flower weight per corm, dry pistil weight per corm, dry stigma weight per corm, dry style weight per corm dry stamen weight per corm, number of daughter cormels per mother corm, average weight of daughter cormels per mother corm, leaf length, number of radical leaves per corm and dry leaves weight per corm. The year wise data was subjected to various statistical/biometrical analysis (Mahalanobis 1936) for drawing the inferences and pooled data over years are presented.

Analysis of variance for dispersion of saffron genotypes revealed that Wilkins criteria was high and significant indicating substantial genetic diversity in the material under study. Similar results have been reported by several workers in gladiolus (Arya & Gupta 1999; Desh & Mishra 1999; Nimbalkar *et al*. 2002) and in saffron (Makhdoomi 2007). Mahalanobis distribution pattern employing Tochers method classified 200 genotypes in sixteen clusters in data pooled over years with 171 genotypes in cluster I, 9 genotypes in cluster V and 7 genotypes in cluster VI and one genotype each in rest of the clusters (Table 1). Genotype SH-192, SH-164, SH-186, SH-139, SH-84, SH-127, SH-174, SH-159, SH-110, SH-78, SH-22, SH-67 and SH-89, were grouped in mono genotypic clusters of cluster II, III, IV, VII, VIII, IX, X, XI, XII, XIII, XIV, XV, XVI. Genotypes SH-21, SH-123, SH-200, SH-51, SH-30, SH-81, SH-69, SH-3, SH-98, were grouped in cluster V, whereas genotypes SH-62, SH-63, SH-64, SH-13, SH-65, SH-14, SH-187 were grouped in cluster VI. Rest of the genotypes were grouped in cluster I. The pattern of group constellation indicated

Table 1. Distribution of different saffron genotypes into clusters based on D^2 statistics– Pooled over years

Cluster	Number of genotypes in the cluster	Number of the germplasm lines
I	171	SH-35,SH-37,SH-38,SH-142,SH-129,SH-138,SH-55,SH-102,SH-137,SH-83,SH-24,SH-131,SH-9,SH-118,SH-41,SH-133,SH-147,SH- 195,SH-146,SH-72,SH-122,SH-185,SH-31,SH-144,SH-160,SH-141,SH-12,SH-90,SH-32,SH-136,SH-88,SH-189,SH-54,SH-56,SH-13,SH- 151,SH-111,SH-128,SH-126,SH-105,SH-120,SH-163,SH-101,SH-45,SH-01,SH-50,SH-48,SH-40,SH-155,SH-154,SH-167,SH-04,SH-178,SH-148,SH-23,SH-18,SH-75,SH-145,SH-16,SH-10,SH-179,SH-182,SH-08,SH-74,SH-198,SH-169,SH-30,SH-150,SH-196,SH-181,SH-180,SH-166,SH-87,SH-134,SH-162,SH-82,SH-114,SH-02,SH-15,SH-152,SH-34,SH-57,SH-73,SH-197,SH-157,SH-135,SH-104,SH-19,SH-176,SH-191,SH-153,SH-163,SH-46,SH-27,SH-36,SH-20,SH-26,SH-17,SH-96,SH-170,SH-11,SH-116,SH-71,SH-124,SH-66,SH-172,SH-156,SH-92,SH-61,SH-173,SH-70,SH-165,SH-99,SH-60,SH-28,SH-112,SH-29,SH-39,SH-158,SH-140,SH-183,SH-132,SH-05,SH-85,SH-59,SH-58,SH-79,SH-168,SH-44,SH-52,SH-190,SH-177,SH-25,SH-188,SH-53,SH-119,SH-107,SH-175,SH-108,SH-47,SH-43,SH-149,SH-143,SH-86,SH-115,SH-100,SH-76,SH-109,SH-07,SH-06,SH-80,SH-68,SH-103,SH-171,SH-125,SH-94,SH-117,SH-33,SH-93,SH-121,SH-193,SH-184,SH-97,SH-199,SH-49,SH-91,SH-194,SH-95,SH-106,SH-77,SH-42
II	1	SH-192
III	1	SH-164
IV	1	SH-186
V	9	SH-21,SH-123,SH-200,SH-51,SH-30,SH-81,SH-69,SH-03,SH-98
VI	7	SH-62,SH-63,SH-64,SH-13,SH-65,SH-14,SH-187
VII	1	SH-139
VIII	1	SH-84
IX	1	SH-127
X	1	SH-174
XI	1	SH-159
XII	1	SH-110
XIII	1	SH-78
XIV	1	SH-22
XV	1	SH-67
XVI	1	SH-89

that geographical diversity was not an essential factor to group the genotypes from a particular source. Similar findings have been reported by Makhdoomi (2007).

Average intra cluster D^2 that gives us measure of level of divergence among genotypes of same cluster indicated maximum intra cluster D^2 values (6.50) for cluster V followed by cluster VI (5.93) and cluster I (4.67). Maximum intercluster D^2 (18.14) estimates was observed between clusters XV and cluster XVI accommodating genotype SH-67 collected from Chandhara and genotype SH-89 collected from Khrew areas of Kashmir valley. Similar level of high intercluster distance (17.22) was exhibited between cluster V and XVI accommodating genotypes SH-21, SH-123, SH-200, SH-51, SH-30, SH-81, SH-69, SH-3 and SH-98 in cluster V and SH-89 in cluster XVI. The results have indicated that the genotypes present in different clusters were diverse and can be used as a source of allelic resources for development of new saffron varieties (Table 2). Cluster V had highest cluster mean for floral attributes such as fresh pistil weight, fresh stigma weight, fresh style weight and style length. Highest cluster mean was exhibited by cluster XIV for number of flowers, cluster IV for fresh stamen weight and dry stamen weight, cluster III for dry flower weight and fresh flower weight, cluster VI for dry stigma weight and number of radicle leaves, cluster IX for dry pistil weight and cluster XV for pistle length and stigma length. Among corm attributes highest cluster mean was recorded for number of daughter corms in cluster IX, whereas, cluster XII recorded the maximum cluster mean for average weight of daughter corms. Among morphological attributes, cluster XI recorded maximum cluster mean for dry leaves weight, whereas cluster VI and cluster X recorded maximum mean for number of leaves and plant height, respectively. Cluster V exhibiting maximum cluster mean for yield contributing traits was on account of contribution made by genotypes SH-21, and SH-98. Similar pattern of contribution has been reported by Makhdoomi (2007), who observed that the cluster mean and coefficient of variation are interactive pictures of diversity. In case of

Table 2. Average inter-cluster (above diagonal) and intra-cluster (diagonal) distance (D^2 values) among different germplasm lines of saffron -Pooled over years

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X	Cluster XI	Clustr XII	Cluster XIII	Cluster XIV	Cluster XV	Cluster XVI
I	**4.67**	6.79	6.60	7.94	9.71	10.96	7.05	7.64	7.36	6.96	6.96	8.37	7.15	7.59	11.06	10.90
II		**0.00**	2.80	2.32	11.72	11.67	3.47	8.52	10.35	9.65	10.11	7.34	7.90	10.72	11.40	10.65
III			**0.00**	3.98	11.02	11.81	4.84	7.42	10.87	9.75	10.12	7.73	8.20	10.93	11.89	9.60
IV				**0.00**	12.51	11.86	3.70	9.56	10.99	10.90	11.11	8.99	8.71	11.51	12.39	11.69
V					**6.50**	15.09	12.34	12.83	11.36	9.72	12.18	13.37	11.30	11.41	10.85	17.22
VI						**5.93**	11.22	8.72	13.14	14.75	13.67	12.92	11.63	12.55	14.58	13.18
VII							**0.00**	8.13	11.02	10.54	10.11	9.23	7.28	9.91	13.12	10.61
VIII								**0.00**	12.33	11.94	11.09	9.37	9.32	10.86	14.14	6.59
IX									**0.00**	6.31	6.42	10.18	9.73	8.15	10.53	15.01
X										**0.00**	8.19	9.85	9.25	8.00	10.75	14.81
XI											**0.00**	10.73	8.90	8.02	13.67	12.13
XII												**0.00**	10.78	11.40	8.80	10.82
XIII													**0.00**	9.06	12.87	12.43
XIV														**0.00**	12.77	14.04
XV															**0.00**	18.14
XVI																**0.00**

per cent contribution of different traits towards divergence, contribution by fresh stamen weight was maximum (20.86) followed by plant height, fresh flower weight, pistle length and fresh pistle weight. Maximum contribution of fresh pistle weight, stigma length, fresh flower weight and fresh style weight has also been reported by Makhdoomi (2007). Dee & Mishra (1993) reported that traits contributing maximum towards divergence need to be given greater emphasis for deciding on the cluster to be chosen for the purpose of further selection. On this basis, genotypes in clusters III, IV, V, X, XV were considered for divergence studies at molecular level besides promising elite genotypes showing high *per se* performance suggested ample scope of clonal selection in saffron particularly with traits having highest genetic gain. Based on findings of present investigation there is possibility of saffron improvement through clonal selection from the available germplasm resources.

References

Arya S, Kumar R & Gupta K 1999 Genetic divergence in gladiolus cultivars. In: Proc. National Symposium on emerging Scenario in Ornamental Horticulture in 2000 A.D. and Beyond. Indian Agricultural Research Institute, New Delhi, 21–22 July.

Dee L C & Misra R L 1993 Genetic diversity in gladiolus. Ind. J. Pl. Gen. Resources 6: 9–14.

Desh R & Misra R L 1999 Genetic divergence in gladiolus. Ann. Agri. Res. 20: 47–50.

Mahalanobis P C 1936 A preliminary note on inter-varietal correlation in rice plant. Pl. Br. Abstract 4: 545.

Makhdoomi M I 2007 Studies in relation to genetic variability and divergence in saffron (*Crocus sativus* L.) Ph.D Thesis SK University of Agricultural Sciences & Technology of Kashmir, India.

Mathew B 1982 The crocus- A revision of the Genus *Crocus* (Iridaceae). B.T. Batsford Ltd., London.

Nehvi F A 2010 Forthcoming challenges for improving saffron farming system in Kashmir. Acta Horti. 850: 281–85.

Nimbalkar C A, Katwate S M, Patil M T & Desai U T 2002 Genetic divergence and selection of genotypes in gladiolus. In: Misra R L & Sanyat Misra (Eds.), Floriculture research trend in India (pp.100–104), Proc. National Symposium on Indian Floriculture in the new-millenium, 25–27 February, Lal-Bagh, Bengaluru.