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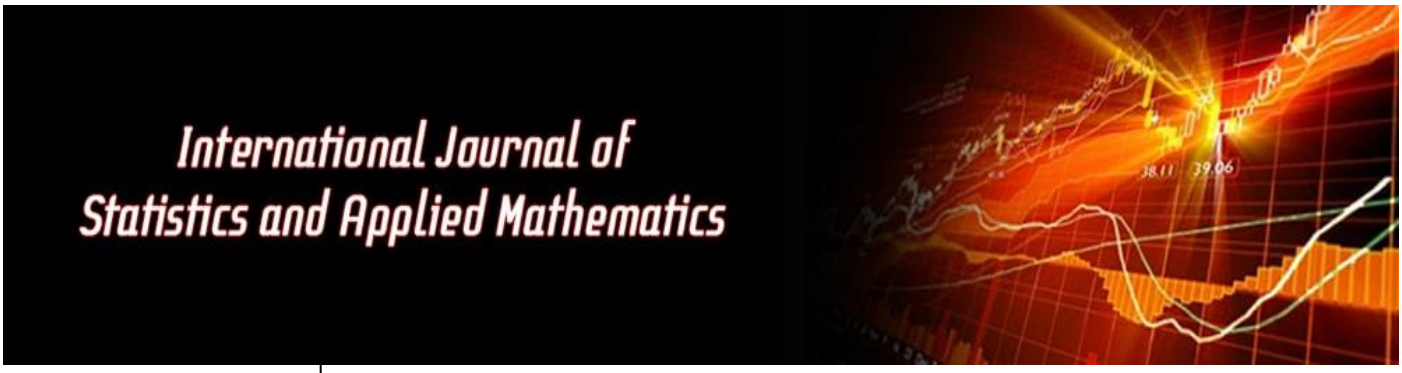

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Study on genetic diversity in Hibiscus (*Rosa-sinensis* L)

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Abstract
Genetic diversity of twenty genotypes of Hibiscus were analysed for various growth and flowering traits. Analysis of variance revealed significant differences among the genotypes for all the morphological traits studied. The twenty genotypes of hibiscus were grouped into six clusters by using Tocher method. Cluster I and II were the largest groups comprising of nine and seven genotypes respectively, while cluster III, IV, V and VI are monogenic clusters i.e. these clusters showed zero intra-cluster. The maximum intra-cluster distance was observed for cluster II (36.77) followed by cluster I (35.40). The highest inter cluster distance was observed between cluster V to cluster VI (D^2 = 153.74), followed by between cluster III and cluster V (D^2 = 130.20) and minimum inter-cluster distance was recorded between cluster III and IV (39.71). The relative contribution of number of secondary branches per plant at 360 days after planting was maximum to divergence (76.32%) followed by number of primary branches per plant (13.16%) indicating that these characters were considerably responsible for total divergence in the material under study. On the basis of divergence classes analysis, the genotypes HCH-15-001, HCH-15-004, HCH-15-005, HCH-15-008, HCH-15-011 and HCH-15-015 were suggested for further breeding programme.

Keywords: Hibiscus, genotypes, clusters, diversity

Introduction
Hibiscus rosa-sinensis Linn. is an ornamental flowering shrub widely cultivated in the tropics as an ornamental plant and has several forms with varying colours of flowers and grouped under minor flower crops. Accordingly, in Hindu Mythology Hibiscus grabbed the top position as they widely used in the worship of Hindu deities, especially Goddess Durga / Kali Jijji *et al.* (2019) [4]. In the Indian literatures the glory of the rising sun is often compared to the resplendently beautiful flower. The flowers are not mere confined to the literature and worship, instead they ruling the international flower market. It may be cut flowers or loose flowers; they both have got immense value for their aesthetic value. Hibiscus is one of the most important indigenous flower and medicinal plant. It is one of the few flower crops which used as loose flower, hedge planting, pot culture, specimen planting, shrubbery, anthocyanins extraction, shampoo preparation, sweet and confectionary usages. The flowers of Hibiscus possess immense medicinal value. Petals of hibiscus are a rich source of anthocyanin. On accounting the phytochemical constituent in its flower petals, it has the potential to be utilised as neutraceutical, food and textile colourant.
Today, various new varieties have been cultivated and developed through cross breeding. These new cultivars bear all the blended characteristics and are increasing popularity as well. Different cultivars and hybrids have been produced and developed with flowers ranging in colours and other features. The best way to understand the potential of the available germplasm is by analysing its genetic diversity. For an outstanding breeding programme in the crop improvement, diversity analysis greatly helps the breeder in the identification and proper choice of parents for specific breeding objectives. The present study was to assess the genetic diversity among germplasm of hibiscus.

Materials and Methods
The experiment was conducted in a randomized block design with two replications. Each plot contains six plants spaced at 1.8 X 1.0 m at Modibaug, Horticulture section, College of Agriculture, Shivajinagar, Pune -5 (M.S) during year 2015 to 2017.

The experimental material consisted of 20 genetically diversed genotypes of *Hibiscus rosa-sinensis* L. obtained from different sources. All cultural practices and application of fertilizers were common for all the varieties. The usual cultural practices like weeding, irrigation and plant protection measures were followed and when required during the growth period of the crop. Three plants per treatment were used for recording the weight of flower (gm), pedicel length (mm), style length (mm), weight of flowers per plant (g), days for initiation of flower bud from planting, longevity of flower, diameter of flower (cm), days to anthesis, length of flower bud (cm), number of nodes at which first flower appeared, number of petals / flower, plant height (cm) at 360 dap, plant spread (EW) in cm, plant spread (NS) in cm, number of primary branches per plant, number of secondary branches per plant at 360 days after planting and number of flowers per plant. Multivariate analysis was done utilising Mahalanobis D^2 statistic Mahalanobis (1936) [5] and genotypes were grouped into different clusters by following Tocher's method.

Results and Discussion

The genetic diversity among twenty genotypes was measured by employing D^2 statistics and grouped into six clusters by using Tocher's method was developed by Rao (1952) [7]. Distribution of genotypes in each cluster is presented in Table 1. Cluster I was found largest with nine genotypes followed by cluster II comprising seven genotypes, while cluster III,IV V and VI are monogenic clusters i.e. these clusters showed zero intra-cluster. The inter-cluster and intra-cluster D^2 values were estimated and had been presented in Table 2 and the highest intra cluster distance was observed for cluster II (36.77) followed by cluster I (35.40). The cluster III, IV, V and VI showed no any intra cluster distance.

The highest inter cluster distance was observed between cluster V to cluster VI (D^2 = 153.74), followed by between cluster III and cluster V (D^2 = 130.20) and in between cluster IV and cluster V (D^2 = 124.60), cluster I and VI (D2 = 119.01), cluster II and cluster V (D^2 = 108.57) and cluster I and cluster III (D^2 = 103.15). The minimum inter-cluster distance was recorded between cluster III and IV (39.71). where, cluster IV and VI (D^2 = 44.37); cluster III and cluster VI (D^2 = 47.13), cluster II and cluster III (D^2 = 53.81) and cluster II and cluster IV (D^2 = 58.19) showed relatively low inter cluster distance. Thus, the crossing between the genotypes belonging to cluster pairs separated by very high inter cluster distances, may be helpful to get desirable transgressive segregants. The lowest inter-cluster distance between demonstrated by cluster III and IV which indicates that genotypes belong to these clusters pairs were genetically close to each other. The crosses between genotypes belonging to clusters separated by low inter-cluster distances are unlikely to throw promising recombinants in the segregating generations. Therefore, it is suggested that selection of genotypes based upon large cluster distances from all the clusters may lead to favorable broad spectrum of genetic variation for flower yield improvement. Similar results had also been suggested by Baliyan *et al*. (2014) [1] in chrysanthemum.

All twenty genotypes were spread over 6 clusters and means were scored across the clusters for all the 17 characters, and this is given in Table 3. Among all the clusters, high values of cluster means for weight of flower per plant was recorded in all clusters. The cluster V with only one genotype recorded highest number of flowers per plant (74.00) characterized by number of petals per flower (5.0), maximum plant height (116.53), number of primary and secondary branches per plant (10.16) low flower weight (11.56 g), pedicel length (12.74 mm) and style length (19.23 mm). All these characters appeared to have played important role in determining the yield of this cluster. Cluster VI with single genotype was found second best for number of flowers per plant (43.50), flower weight (113.25 g), pedicel length (65.85 mm), weight of flowers per plant (4925.25), number of petals per flower (37.00) plant height (120.10 cm) and number of primary branches per plant (10.16). Cluster I with maximum genotypes showed maximum days for initiation of flower bud from planting (151.28), indicate that genotypes were late. Cluster II with seven genotypes recorded flowers per plant (39.07), highest style length (57.42 mm) and length of flower bud (3.14 cm), maximum number of node at which first flower appeared (25.29) and plant spread (EW and NS) (63.15 and 61.11 respectively) with second highest pedicel length (59.04 mm) and days for initiation of flower bud from planting (130.36). The genotype from cluster III was found earliest in respect of initiation of flower bud (93.50 days) and node number at which first flower appeared (12.93). Maximum longevity of flower (16.83 hrs) and maximum diameter of flower (9.18 cm) was recorded by genotype from cluster IV. Based on cluster mean values for a given character, highly divergent genotypes from the respective clusters to be used in crossing. Similar results were reported by Riaz *et al*. (2019) [8]; Dudhe *et al*. (2019) [2].

As far as the cluster means are concerned, different clusters have higher mean values for different traits indicating that few of the cluster contained genotypes with most of the desirable characters (Table 3) Therefore, a hybridization programme may be initiated involving the genotypes belonging to diverse clusters with high mean for desirable and qualitative traits. Therefore, based on D^2 analysis, yield contributing characters showed higher value under clusters mean performance need to be given more weightage, while selecting parents for improvement. Giri *et al*. (2019) [3] also observed similar findings when worked on marigold.

Out of 17 characters studied, the maximum contribution to divergence was reported in characters number of secondary branches per plant (76.32%) followed by number of primary branches per plant (13.16%), longevity of flower (5.26%), diameter of flower (1.58), number of node at which first flower appeared (1.58), East-West plant spread (1.05%). The least contribution was recorded by style length and number of petals per flower (0.53%). Similar results were reported by Varalakshmi *et al*. (2020) [9]; Radic *et al*. (2021) [6]

Table 1: Distribution of 20 genotypes of Hibiscus (*Rosa-Sinensis* L.) in to different clusters

Cluster	Total no. of genotypes included	Genotypes
I	9	HCH-15-006, HCH-15-020, HCH-15-007, HCH-15-015, HCH-15-012, HCH-15-005, HCH-15-019, HCH-15-010 and HCH-15-018
II	7	HCH-15-009, HCH-15-013, HCH-15-014, HCH-15-002, HCH-15-016, HCH-15-011, HCH-15-017
III	1	HCH-15-001
IV	1	HCH-15-008
V	1	HCH-15-003
VI	1	HCH-15-004

Table 2: Average intra and inter cluster D2 and D (in parenthesis) value of 6 clusters from 20 genotypes of Hibiscus (*Rosa-Sinensis* L.)

Cluster	I	II	III	IV	V	VI
I	35.40 (5.95)	69.25 (8.32)	103.15 (10.16)	94.85 (9.74)	65.94 (8.12)	119.01 (10.91)
II		36.77 (6.06)	53.81 (7.33)	58.19 (7.63)	108.57 (10.42)	72.27 (8.50)
III			0.00 (0.00)	39.71 (6.30)	130.20 (11.41)	47.13 (6.87)
IV				0.00 (0.00)	124.60 (11.16)	44.37 (6.67)
V					0.00 (0.00)	153.74 (12.40)
VI						0.00 (0.00)

Table 3: Mean performance of cluster for 17 characters in *Hibiscus rosa-sinensis*.

Sr. No.	Cluster / Characters	Cluster					
		I	II	III	IV	V	VI
1	Weight of flower (g)	20.82	33.09	65.34	60.28	11.56	113.25
2	Pedicel length (mm)	31.32	59.04	32.93	51.14	12.74	65.85
3	Style length (mm)	40.52	57.42	43.30	34.55	19.23	44.81
4	Number of flowers / plant	25.50	39.07	29.00	24.00	74.00	43.50
5	Weight of flowers / plant (g)	520.38	1283.86	1896.76	1457.01	857.42	4925.25
6	Days for initiation of flower bud from planting	151.28	130.36	93.50	123.50	105.50	96.50
7	Longevity of flowers (Hrs.)	9.47	10.19	14.15	16.83	11.45	15.25
8	Diameter of flower (cm)	7.41	9.13	8.64	9.18	7.42	8.85
9	Days to anthesis from bud initiation	19.52	18.62	22.33	28.17	25.66	22.00
10	Length of flower bud (cm)	2.98	3.14	2.61	3.02	3.11	2.76
11	Number of node at which first flower appeared	20.46	25.29	12.93	15.83	17.96	15.90
12	Number of petals / flower	8.50	7.14	12.00	33.50	5.00	37.00
13	Plant height at 360 days after planting (cm)	99.40	114.53	68.38	76.42	116.53	120.10
14	Plant spread (EW) in cm at 360 days after planting	51.84	63.15	35.53	39.50	62.46	47.53
15	Plant spread (NS) in cm at 360 days after planting	48.47	61.11	37.23	42.94	49.18	47.03
16	Number of primary branches at 360 days after planting	7.94	8.62	6.67	10.00	10.16	10.16
17	Number of secondary branches at 360 days after planting	7.24	6.69	5.67	7.33	10.16	7.33

Table 4: Percent contribution of various characters to divergence

Sr. No.	Characters	Percent Contribution
1	Weight of flower (g)	0.00
2	Pedicel length (mm)	0.00
3	Style length (mm)	0.53
4	Number of flowers per plant	0.00
5	Weight of flowers per plant (g)	0.00
6	Days for initiation of flower bud from planting	0.00
7	Longevity of flowers (Hrs.)	5.26
8	Diameter of flower (cm)	1.58
9	Days to anthesis of flower from initiation of flower bud	0.00
10	Length of flower bud (cm)	0.00
11	Number of node at which first flower appeared	1.58
12	Number of petals per flower	0.53
13	Plant height in cm at 360 days after planting	0.00
14	Plant spread (EW) in cm at 360 days after planting	1.05
15	Plant spread (NS) in cm at 360 days after planting	0.00
16	Number of primary branches at 360 days after planting	13.16
17	Number of secondary branches at 360 days after planting	76.32

Conclusion

The wide spectrum of variation was observed in hibiscus germplasm for growth and flowering traits. Divergence analysis of twenty genotypes of hibiscus was grouped into six clusters. On the basis of divergence classes analysis, the genotypes HCH-15-001, HCH-15-004, HCH-15-005, HCH-15-008, HCH-15-011 and HCH-15-015 were suggested for further breeding programme.

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