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Genetic diversity and morpho-agronomic characterization of Gobhi sarson (*Brassica napus* L) genotypes

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Abstract

The present study was carried out to assess the genetic diversity and to characterize the set of fifty Gobhi Sarson (*Brassica napus* L) lines during Rabi 2019-2020. Extent of diversity was estimated and distinctness among the cultivated varieties was established. Divergence analysis categorised the genotypes in to 8 clusters using Mahalanobis D^2 analysis. Cluster II contained the maximum no. of genotypes i.e. 18 genotypes followed by Cluster III (11 genotypes), Cluster I (9 genotypes), Cluster IV (6 genotype), Cluster V (2 genotype), Cluster VI (2 genotype), Cluster VII (1 genotype) and Cluster VIII (1 genotype). It was observed that seed yield contributed maximum (25.2%) towards divergence, followed by main raceme length (21.9%), no. of seeds silique^{-1} (18.3%), no. of pods plant^{-1} (13.4%), 1000 seed weight (8.5%), oil content (5.5%), days to 50 per cent flowering (4.2%) and days to 80 per cent maturity (2.9%). Since the inter cluster distance between Cluster I and V (154.9), followed by Cluster V and VIII (145.1), was found quite large. Also, all the genotypes were characterized for 24 morphological traits as per DUS Descriptor of PPV&FRA, 2001. A good spectrum of variation was found in the frequency distribution of genotypes for various characters.

Keywords: *Brassica napus, distinctness, diversity, genetic divergence*

Introduction

Brassica species have been exploited by man, among all the different oilseed groups, domesticated and modified to meet the altering needs as a source of vegetable oil for centuries. These crops occupy a leading position in India with a contribution of about 28 per cent of the total oilseeds production. Among the rapeseed–mustard group *B. juncea* is grown on more than 75 per cent of the total cultivated area under rapeseed-mustard in the country as it suits perfectly in cropping system of rainfed areas. *Brassica napus* L. is second most important oilseed crop in the international oilseed market after soybean and important source of vegetable oil (Verma *et al.,* 2016). Much effort has been made to improve methods for recognizing varieties because of its economic value (Cooke, 1999). Genetic divergence is one of the suitable approaches for selecting and using parents effectively for hybridization in order to achieve high yield potential cultivars / hybrids. It is assumed that the introduction of more diverse parents into hybridization increases the likelihood of having stronger heterosis and provides a broad range of variation in segregating generations. Thus, the crop germplasm diversity is essential for crop enhancement (Jatoi *et al.,* 2012) and a good know how of these resources can help in gaining momentum in such crop enhancement breeding programmes (Zada *et al.,* 2013). Furthermore, in order to get hold of the ever-escalating requirements of the varietal enhancement and development programme, assembly, evaluation, preservation and characterisation of the entire current germplasm is necessary for more rewarding breeding efforts (Chatterjee *et al.,* 2007). Characterization of a variety is beneficial to identify and avoid duplication. As qualitative traits are more stable over generations, hence, are reliable for characterization of varieties (Raut, 2003).

To achieve higher produce, and thus shift the state's edible oilseed scenario, it is imperative to develop early maturing improved varieties of Gobhi Sarson with high yielding ability, high oil content, better oil quality. In view of the above fact the study was aimed to assess the genetic diversity and to characterize the genotypes on the basis of various morphological traits using the DUS Descriptor of PPVFRA, 2001.

Materials and Methods

The experiment was conducted with fifty genotypes of Gobhi Sarson (*Brassica napus* L) in the experimental farm of the Department of Genetics and Plant Breeding, Sher-e-Kashmir University of Agricultural Sciences and Technology, Jammu and Kashmir, India. The experiment was laid out in randomized complete block design (RCBD) with three replications. Five plants were selected randomly from each plot for collection of data for various yield contributing characters *viz.,* plant height, raceme length, siliqua per raceme, siliqua length, seeds per siliqua, 1000 seed weight, and yield/plot. Average of these five plants was worked out. The average values in all of the observations were used for statistical analysis whereas flowering, maturity and yield data was taken on plot basis. Recording of experimental data in quality traits was done at appropriate stages. Leaf hairiness was observed on lower side of the leaf on randomly selected 10 plants. Leaf colour was observed on the fully developed leaf between bud formations to flower initiation stage on randomly selected 10 plants. Absence or presence of lobes was observed on the fully developed leaf between bud formations to flower initiation stage on randomly selected 10 plants. Leaf dentation of margin was observed on upper one-third part of the leaf blade on randomly selected 10 plants. Flower petal colour was observed when 50% of the plants with at least one open flower were present. All observations on the siliqua were recorded in the mid part of the inflorescence of the main stem. Siliqua length (cm) between pedicel and beak was measured at lower one third portion of main shoot (10 randomly selected plants.) Morphological characterization of 50 genotypes was carried out using 24 DUS characters. Observations were recorded at appropriate growth stages as per descriptor of PPVFRA 2001. For the assessment of diversity Euclidian distance among genotypes was estimated from the standardized data matrix using Mahalanobis D^2 statistic method and clustering was done by Tocher method.

Results and Discussion

The Mahalanobis D^2 statistics (1936) estimated genetic divergence among fifty *B. napus* genotypes. Tocher's method defined by Rao (1952) based on D^2 statistics, divided the germplasms into a number of clusters. The pattern of clustering of all the genotypes is shown in Table-1. The 50 genotypes have all been divided into 8 clusters (Fig-1). Majority genotypes got positioned in Cluster II, which contained 18 genotypes followed by Cluster III (11 genotypes), Cluster I (9 genotypes), Cluster IV (6 genotype), Cluster V (2 genotype), Cluster VI (2 genotype), Cluster VII (1 genotype) and Cluster VIII (1 genotype). Similarly, Sood *et al.* (2019) in *B. campestris*

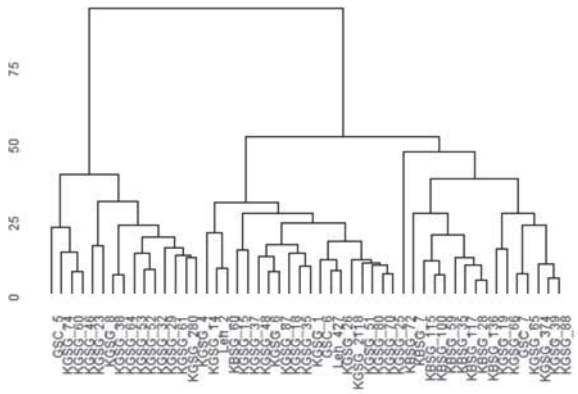


Fig. 1: Cluster analysis of yield and yield attributing traits in *Brassica napus* genotypes

Table-1: Classification of *Brassica napus* genotypes into different clusters using D^2 statistics

Cluster	No. of genotypes	Name of genotypes
I	9	KBSG-28, KBSG-136, KBSG-117, KBSG-35, KBSG-115, KBSG-100, KBSG-59, KBSG-7, KGSG-66
II	18	KGSG-39, KGSG-88, KGSG-374, KGSG-65, GSC-7, KGSG-70, KGSG-25, KGSG-51, KGSG-2118, KGSG-80, KGSG-26, HMMARI Leh-427, GSC-6, KGSG-6, KGSG-48, KGSG-87, KGSG-15, KGSG-37
III	11	KGSG-38, KGSG-64, KGSG-4, KGSG-32, KGSG-52, KGSG-53, KGSG-29, KGSG-61, KGSG-280, KGSG-46, KGSG-60
IV	6	HMMARI Leh-2, KBSG-60, KGSG-35, KGSG-1, KGSG-18, KGSG-14
V	2	KGSG-23, KGSG-8
VI	2	KGSG-74, GSC-5
VII	1	KGSG-19
VIII	1	KBSG-72

and Khan *et al.* (2013) in *B. rapa* obtained 6 clusters; Kumari *et al.* (2018) in *B. juncea* and Aktar *et al.* (2019) obtained 4 clusters.

The group constellation pattern proved considerable variation level to exist. The largest intra cluster distance was shown by Cluster VI (2 genotypes) followed by Cluster II (18 genotypes). Cluster I and V displayed max. inter cluster distance and minimum inter cluster distance was displayed by Cluster II and VII (Table-2).

Table 2: Cluster analysis along with inter and intra cluster distances using D^2 statistics in *Brassica napus* genotypes

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Cluster I	20.0	47.6	124.3	69.0	154.9	94.1	32.0	39.9
Cluster II		24.1	84.2	35.7	114.7	55.1	38.2	54.1
Cluster III			21.3	60.5	34.2	35.3	113.4	116.4
Cluster IV				17.8	89.8	33.4	60.8	61.6
Cluster V					15.6	63.8	143.9	145.1
Cluster VI						25.5	84.5	87.9
Cluster VII							0	52.1
Cluster VIII								0

In the present study, the inter-cluster distances were greater than the Intra-cluster distance in most cases indicating wider variability among distant group breeding lines. Similar results were also described by Akter *et al.* (2019) in *Brassica* genotypes, Pravin *et al.* (2019) *B. napus* in order to achieve much variability and high heterotic outcome, parents ought to be selected from those clusters or groups with wider inter-cluster distance. Wide range of variation was displayed for all the characters studied by the cluster mean values (Table 3). Cluster III exhibited highest mean value for days to 80 per cent maturity, while as cluster IV contained genotypes with highest mean value for main raceme length. Cluster V contained genotypes with highest value for number of seeds per siliqua. Cluster VI contained genotypes with highest value for days to 50 per cent flowering while Cluster VII also contained one genotype with highest mean value for plant height, siliqua number on main raceme length, siliqua length, seed weight, oil content and yield per plot. Cluster VIII contained one genotype with highest mean value for number of primary branches per plant. Such results indicated that there was no such cluster which contained genotypes having all of the looked-for traits that could be just picked and used directly. From the current study it has been revealed that the seed yield plot (g) contributed maximum (25.2%) towards divergence, followed by main raceme length (21.9%), no. of seeds silique^{-1} (18.3%), no. of pods plant^{-1} (13.4%), 1000 seed weight (8.5%), oil content (5.5%), days to 50 per cent flowering (4.2%) and days to 80 per cent maturity (2.9%) (Table 4). The hybridization between genotypes of different clusters showing good mean output is therefore important to establish desirable genotypes similar observations were also described by Sood *et al.* (2019) in *B. rapa*, Neeru *et al.* (2015) in *B. juncea* and Singh *et al.* (2014) in *B. juncea.*

Table 3: Cluster mean for various yield and yield attributing traits in *Brassica napus* genotypes

Clusters	D.F	P.H	NPBPP	MSL	SMRL	NSP	NSPS	SL	DM	SW	OC	YPP
Cluster I	189.7	165.5	20.1	75.7	49.1	273.1	6.9	4.1	235.9	3.6	40.7	0.75
Cluster II	183.2	140.2	19.9	74.4	38.7	216.0	5.3	3.9	226.7	3.5	39.6	0.67
Cluster III	198.7	167.7	20.7	70.5	46.0	226.7	5.9	4.6	239.7	3.5	39.3	0.77
Cluster IV	197.3	164.3	21.5	90.8	37.3	243.8	5.4	4.8	238.3	4.1	38.0	0.70
Cluster V	195.7	184.0	22.2	59.8	58.2	324.8	8.2	4.1	238.7	4.2	40.0	0.77
Cluster VI	199.3	179.0	21.4	86.3	55.0	333.9	7.8	4.8	239.3	4.1	38.7	0.77
Cluster VII	197.3	188.6	24.6	82.7	60.7	352.8	8.2	5.6	238.3	5.0	43.0	0.79
Cluster VIII	197.3	113.1	16.6	69.9	36.1	232.3	4.9	3.6	233.0	3.6	39.7	0.64

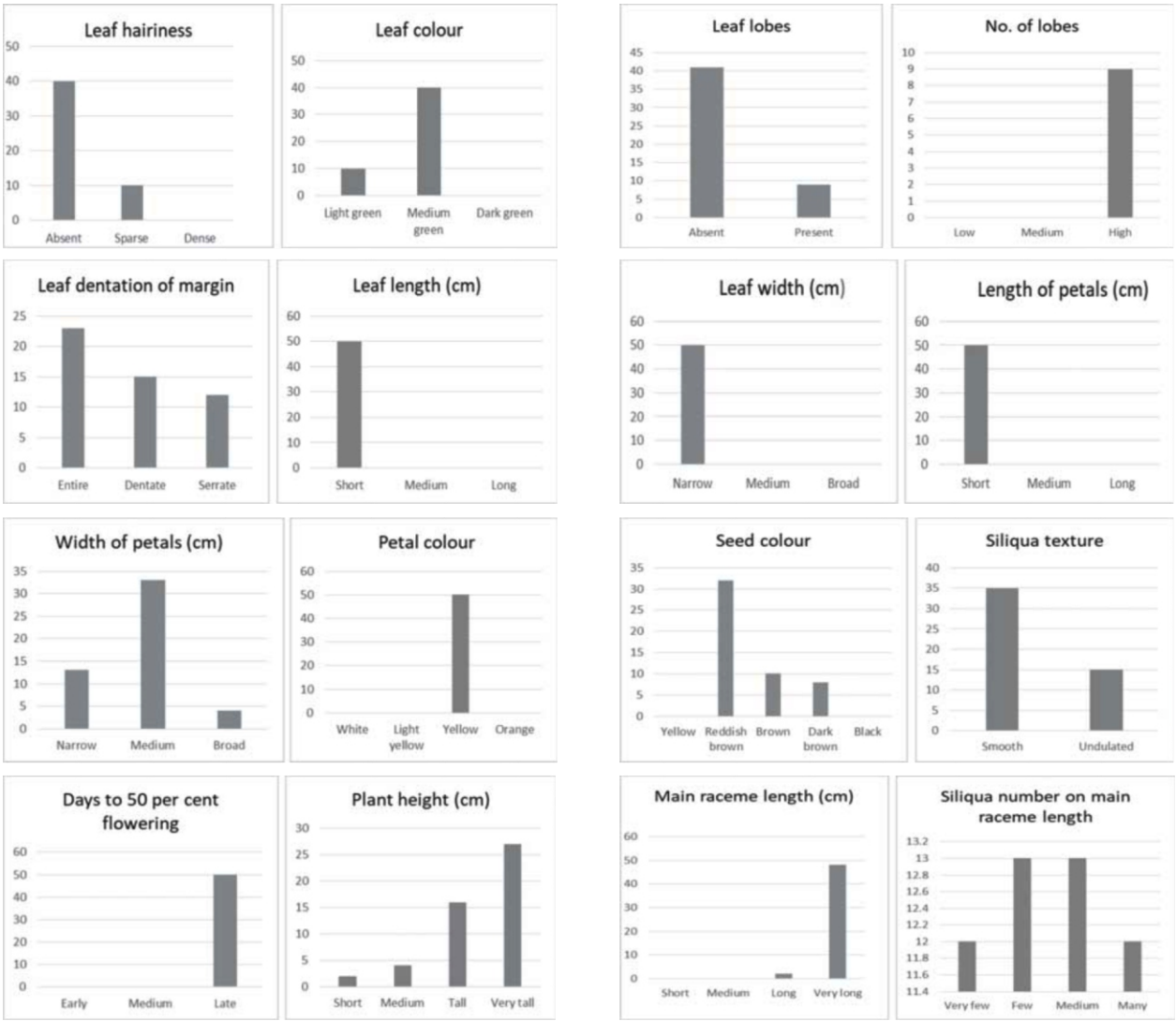
Where; DF = days to 50% flowering, PH = plant height (cm), NPBPP = Number of primary branches per plant, MRL = main raceme length (cm), SMRL = siliqua number on main raceme length, NSPP = number of siliqua per plant, NSPS = number of seeds per siliqua, SL = siliqua length (cm), DM = days to 80% maturity, SW = seed weight (g), OC = oil content (%), YP = yield per plot (kg)

Table 4: Per cent contribution of characters towards divergence in *Brassica napus* genotypes

Characters	Per cent contribution
Seed yield plot^{-1} (kg)	25.2
Main raceme length (cm)	21.9
Number of seeds siliqua^{-1}	18.3
Number of pods plant^{-1}	13.4
1000 seed weight (g)	8.5
Oil content (%)	5.5
Days to 50% flowering	4.2
Days to 80% maturity	2.9

It was observed that seed yield plot (g) contributed maximum towards divergence, followed by raceme length, seeds/ silique, siliqua per plant, thousand seed weight, oil content, 50% flowering period and 80% maturity period. Similarly, Solanki *et al.* (2019) indicated maximum contribution towards genetic divergence by days to maturity. Sood *et al.* (2019) in *B. rapa* also reported major contribution from seeds per siliqua, siliqua per plant and seed yield per plot.

In the present investigation, width of petals, seed colour, leaf dentation of margin, plant height, siliqua no. on main raceme length and 1000-seed weight recorded highest variation among genotypes (Fig. 2). After that, leaf hairiness, leaf colour, leaf lobes, siliqua texture, main raceme length, siliqua length and oil content percentage observed low variation in different genotypes. All the 50 germplasm lines exhibited 100% short leaf length, narrow leaf width, short petal length, yellow flower petal colour, days to 50 per cent flowering, no. of seeds per siliqua and days to 80 per cent maturity and marked no differences among genotypes for these traits. Thus, germplasm characterization establishes distinctiveness



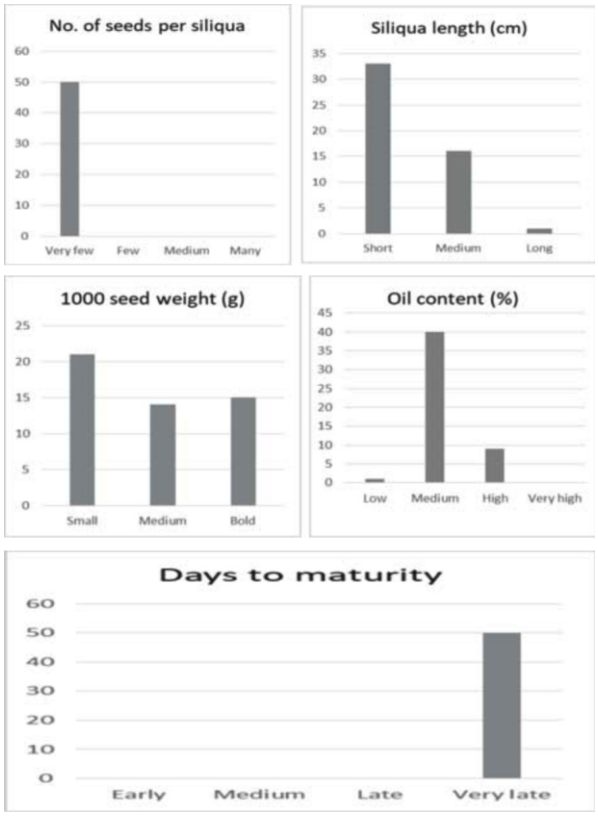


Fig. 2: Frequency distribution of *Brassica napus* genotypes for various DUS traits

among *B. napus* genotypes. It is essential for exploiting the suitable trait-based donors in breeding programmes, as well as necessary in the existing era for safeguarding the genotypes. Similar study was undertaken by Singh *et al.* (2018), Neeru *et al.* 2017 and Tiwari *et al.* (2017) for characterizing Indian mustard genotypes on the basis of their qualitative and quantitative morphological characters.

Conclusion

Genetic diversity is a requirement because it not just provides a selection basis but also provides some useful knowledge about the selection of different parents for use in the hybridization system. Mahalanobis D2 Clustering process divided the genotypes into eight clusters. Cluster II consisted of eighteen genotypes which constituted the largest cluster. Bearing in mind the significance of genetic distance and the relative contribution of traits to total divergence, the present investigation suggested that the selected genotypes from Cluster VII (KGSG-19) for plant height, primary branches per plant, siliqua on the raceme length, siliqua length, thousand seed weight, oil content and yield per plot, Cluster VI (KGSG-74 and GSC-5) for no. of siliqua per plant and number of siliqua per plant, Cluster IV for main raceme length (HMMARI Leh-2, KBSG-60, KGSG-35, KGSG-1, KGSG-18, KGSG-14), Cluster V (KGSG-23 and KGSG-8) for no. of seeds per siliqua and Cluster III (KGSG-38, KGSG-64, KGSG-4, KGSG-32, KGSG-52, KGSG-53, KGSG-29, KGSG-61, KGSG-280, KGSG-46, KGSG-60) for days to 80% maturity. Therefore, the genotypes from these clusters can be used to produce high genetic variability through hybridization and in that way the progenies are likely to inculcate both quantitative traits and qualitative traits in a positive direction and further selection will be successful. In the present investigation, Gobhi Sarson genotypes were characterised for different quantitative and quality traits. These characteristics can be regarded as markers in the characterization of Gobhi Sarson germplasm genotypes, which would not only aid in the use of suitable trait-based donors in the breeding system, but then again would also be important for the safety of the varieties in the present era.

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