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MORPHOLOGICAL CHARACTERIZATION AND GENETIC VARIABILITY STUDY ON MAKOI (*SOLANUM NIGRUM* L.) GENOTYPES

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Abstract

A study was carried out during 2011-12 on morphological characterization and to ascertain the extent of genetic variability of Makoi genotypes. A total of twenty genotypes were characterized for several agro morphological characters based on IPGRI descriptors. Variations were observed in plant growth habit, stem color, leaf shape, fruit color *etc.*, Genetic divergence among genotypes was estimated using Mahalanobis's D^2 statistic. Genotypes were grouped into four clusters with maximum number of genotypes found in cluster I. The inter cluster distance was more between cluster I and cluster III (391.97). The cluster III with four genotypes recorded highest intra cluster distance (85.55).

Key words : Makoi, descriptors, characterization, variability, clustering.

Introduction

Makoi, commonly known as Black Nightshade belongs to the family *Solanaceae* and is a upcoming medicinal plant. Though, this species is distributed through out the world, they occur in greatest concentration in tropical and warm temperate regions with centres of diversity occurring in the Southern Hemisphere, Africa, Europe and Asia. In most part of the world, especially in Europe this species is consider to be a troublesome weed, but in many African and Asian countries they constitute a minor food crop with its leaves and fruits used as a nutritious vegetable. Besides, the leaves and immature green fruits are medicinally important and known to contain steroidal glycol alkaloids solamargine and solasodine (Anonymous, 2002). The total alkaloid content of the leaf and berry is 0.431 and 0.101%, respectively. The leaves are used to alleviate the pain in inflammation of the kidneys and bladder and are also used in the treatment of mouth ulcers, scrofulous dyscarasias and virulent gonorrhoea (Pereeze *et al*., 1998). Many commercial products from this plant *viz.,* Actilivforts, Geriforte, Herbolax, Manol, Liv – 52, Eve Care are also available.

By realizing the importance and need of medicinal plants which have great demand both in domestic and international market, the National Medicinal Plants Board (NMPB, New Delhi) is promoting development of 32 medicinal plants. Among them, Makoi (*S. nigrum* L.) has also been identified for conservation and cultivation (Anon, 2003).

In crop improvement programme efforts are being made to develop high yielding and stable cultivars or genotypes. Morphological descriptions of genotypes are required for their protection under plant variety protection (PVP) legislation, because varietal testing for distinctness, uniformity and stability (DUS) is the basis for grant of protection for new varieties. Therefore, the present study was undertaken to characterize morphological characters and to establish the distinctness of genotypes.

Also, the growing demand for this crop necessitates attempts to study the genetic variability existing in this crop. Considering the importance of the crop and the vast genetic diversity existing in this species, the genotypes from different ecological regions are evaluated on different parameters. Knowledge on genetic variability encompassed within the species will greatly aid direct exploitation of variability for different breeding programme.

Materials and Methods

The experimental material comprised of twenty genotypes collected from different eco geographical

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Table 1 : Geographical origin of Makoi genotypes.

Genotypes	Geographical origin	Genotypes	Geographical origin
Sn 01	Coimbatore, Tamil Nadu	*Sn* 11	Periya krishnapuram, Tamil Nadu
Sn 02	Namakkal, Tamil Nadu	*Sn* 12	Pachamalai, Tamil Nadu
Sn 03	Sirugamani, Tamil Nadu	*Sn* 13	Solan, Himachal Pradesh
Sn 04	Chinnakalvehalli, Tamil Nadu	*Sn* 14	KAU, Thrissur, Kerela
Sn 05	Ooty, Tamil Nadu	*Sn* 15	Pattikad, Kerela
Sn 06	Kolli hills, Tamil Nadu	*Sn* 16	Kottakkal, Kerela
Sn 07	Salem, Tamil Nadu	*Sn* 17	Nalhendra, Solan, Himachal Pradesh
Sn 08	Kallipalayam, Tamil Nadu	*Sn* 18	Arasanatham, Tamil Nadu
Sn 09	Namakkal, Tamil Nadu	*Sn* 19	Guddalore, Tamil Nadu
Sn 10	Coimbatore, Tamil Nadu	*Sn* 20	Kodaikanal, Tamil Nadu

regions (table 1) of the India and were evaluated in the experimental field at the Department of Medicinal and Aromatic Crops, Botanical Garden, Tamil Nadu Agricultural University, Coimbatore (Tamil Nadu), India in Randomized Block Design with three replications during 2011-12.

The land was brought to fine tilth by 3 times ploughing and the seedlings of each genotype were raised in portrays and 25 days old seedlings were transplanted to the field with the spacing of 60 × 45 cm. The recommended agronomic practices and plant protection measures were followed to ensure a normal healthy crop.

The diversity in terms of morphological variations among the genotypes was documented following IPGRI descriptors (Edmonds, 1972). The morphological characters such as growth habit, branching habit, leaf margin, leaf color, leaf pubescence, stem color, stem pubescence, stem shape, flower size and shape, fruit size and shape and biotic stress susceptibility were used for morphological characterization. The observations were recorded on ten plants in each replication at specified stage of crop growth period, when the character under study was full expressed. The growth habit, leaf, stems and flower characters were observed at 50% flowering. While, the fruit shape and fruit color was observed at horticultural maturity.

For studying genetic variability among the genotypes, the observations were recorded on all the morpho agronomic characters *viz*., plant height, plant spread, number of primary branches per plant, days to maturity, fresh and dry leaf yield per plant and fresh and dry fruit yield per plant. For this study, the crop was harvested 3 months after planting at matured green fruit stage. The statistical parameters like mean, standard error and critical difference for all characters were worked out by adopting the standard methods of the analysis as suggested by Panse and Sukhatme (1978). The analysis of genetic divergence was done using D^2 statistics (Mahalanobsis, 1936). The genotypes were grouped into clusters by the Tocher's method (Rao, 1952).

Results and Discussion

Considerable variations were observed among the twenty Makoi genotypes, for all the important attributes. The characterization of makoi genotypes is presented in table 2. In the present study, all the genotypes were erect in growth habit except genotypes *Sn* 8, *Sn* 10, *Sn* 11, *Sn* 18 and *Sn* 19 which were spreading in habit and *Sn* 17 was distinct from all the genotypes as it was prostrate in its growth habit. Genotypes were also classified based on branching habit also. In the germplasm collection, maximum genotypes have sparse branching habit, while intermediate branching was seen in *Sn* 09, *Sn* 06, *Sn* 08, *Sn* 13, *Sn* 17 and *Sn* 20, but dense branching was seen in *Sn* 05, *Sn* 10 and *Sn* 19. Since, the leaves are the main economic part, the dense branching genotypes with erect growth are highly preferred. When, there are more number of branches, number of leaves will also increase, followed by increased leaf yield. Erect growing genotypes are ideal than spreading and prostrate types since it allows maximum and uniform exposure of sunlight and would result in an increase in dry matter production and subsequently increase in yield (Hanson, 2005). Moreover, there is less chance of leaves drenching the ground (or) soil.

In case of stem shape, flattened stem was seen in all accessions except in *Sn* 04, *Sn* 06, *Sn* 09, *Sn* 10, *Sn* 11, *Sn* 13, *Sn* 17 and *Sn* 19 which have ridged stem. Stem pubescence was sparse in some genotypes (*Sn* 04, *Sn* 05, *Sn* 09, *Sn* 13 and *Sn* 20) where else, dense in four genotypes (*Sn* 10, *Sn* 11, *Sn* 17 and *Sn* 19) and pubescence was totally absent in rest of eleven genotypes. Genotypes having pubescence may have some resistance to pests and disease compared with rest of the genotypes. Green

Table 2 : Morphological characterization of Makoi genotypes.

Genotypes	Plant height	Branc-hing habit	Stem shape	Stem pubes-cence	Stem color	Leaf shape	Leaf pubesc-ence	Leaf margin	Leaf color	Flower diameter	Corolla arrang-ement	Corolla color	Fruit size	Fruit color	Biotic stress susceptibility
Sn 01	1	3	4	1	1	2	1	1	3	1	1	1	1	1	2
Sn 02	1	3	4	1	1	2	1	1	3	1	1	1	1	1	2
Sn 03	1	3	4	1	1	2	1	1	3	1	1	1	1	1	2
Sn 04	1	5	3	2	1	2	2	2	3	1	2	1	1	1	2
Sn 05	1	7	4	2	2	2	3	1	4	3	1	1	3	1	1
Sn 06	1	5	3	1	1	2	1	2	3	1	1	1	1	1	2
Sn 07	1	3	4	1	1	2	1	1	3	1	1	1	1	1	2
Sn 08	2	5	4	1	1	2	1	1	3	1	1	1	1	1	2
Sn 09	1	3	3	2	1	2	2	2	4	1	2	1	1	2	2
Sn 10	2	7	3	3	2	4	3	2	4	2	2	1	2	2	1
Sn 11	2	7	3	3	2	4	3	2	3	2	1	1	2	1	1
Sn 12	1	3	4	1	1	2	1	1	3	1	1	1	1	1	2
Sn 13	1	5	3	2	1	2	2	2	3	1	1	1	1	1	2
Sn 14	1	3	4	1	1	2	1	1	3	1	1	1	1	1	2
Sn 15	1	3	4	1	1	2	1	1	3	1	1	1	1	1	2
Sn 16	1	3	4	1	1	2	1	1	3	1	1	1	1	1	1
Sn 17	3	5	3	3	2	2	3	2	3	3	2	1	3	3	2
Sn 18	2	3	4	1	1	3	1	1	3	1	1	1	1	1	2
Sn 19	2	7	3	3	2	2	3	2	4	2	1	2	3	3	1
Sn 20	1	5	4	2	1	2	2	2	3	1	1	1	1	1	2
Status of characterisation according to IPGRI descriptors	t cere-1 gni daerps-2 etart sorp-3	esar ps-3 etai de mret ni-5 esned-7	deg dr-3 dend alf-4	t nes ba-1 esr aps-2 es ned-3	neer g-1 el pr up-2	et avo-2 et al oecnal-3 1 ad ob mohr-4	t nes ba-1 esr aps-2 es ned-3	erit ne-1 dt ares-2	neer g-3 neer g kr ad-4	mc 8 0-7 0-1 mc 9 0-8 0-2 mc 0 1-9 0-3	et aned-1 erit ne-2	eti h w-1 hti wetih w-2 sepirts el pr up	mc 6 0-5 0-1 mc 7 0-6 0-2 mc 8 1-7 0-3	kcal b hsil pr up-1 der-2 egnar o-3	wol-1 etai de mret ni-2 hg h-3 hg h yrev-4

Table 3 : Quantitative variations in Makoi genotypes.

Genotypes	Plant height (cm)	No. of primary branches	Plant spread		Days to harvestable maturity	Leaf yield per plant		Fruit yield per plant	
			N-S	E-W		Fresh	Dry	Fresh	Dry
SN 01	108.23	7.08	49.24	49.02	61.52	50.46	7.12	16.45	4.46
SN 02	109.42	7.52	49.45	49.47	61.73	50.92	7.23	16.56	4.35
SN 03	109.02	7.48	49.62	49.60	61.91	50.86	7.20	16.49	4.41
SN 04	125.24	9.46	52.42	52.33	58.14	54.02	9.57	19.92	6.12
SN 05	135.46	12.22	53.96	53.88	50.12	70.06	12.92	22.02	6.57
SN 06	124.52	9.64	52.23	52.28	58.16	54.10	9.60	19.97	6.23
SN 07	109.59	7.97	49.68	49.73	61.80	50.52	7.32	16.47	4.40
SN 08	112.42	9.02	50.42	50.48	61.75	60.15	10.46	18.09	5.52
SN 09	126.44	9.48	53.85	53.86	58.19	54.19	9.69	19.94	6.19
SN 10	140.22	14.24	56.14	56.34	49.12	60.52	11.05	17.62	7.43
SN 11	139.76	13.92	55.92	55.87	49.20	60.23	10.98	17.59	7.35
SN 12	108.42	7.24	49.38	49.23	61.54	50.49	7.14	16.49	4.48
SN 13	126.65	9.46	52.49	52.52	58.21	54.21	9.59	19.96	6.19
SN 14	109.04	7.52	49.35	48.38	61.34	50.96	7.25	16.58	4.48
SN 15	109.26	7.58	49.37	49.30	61.86	50.82	7.22	16.54	4.42
SN 16	108.42	7.10	49.25	49.32	61.43	50.36	7.10	16.40	4.36
SN 17	60.46	12.24	57.52	57.46	49.32	60.21	11.01	17.60	7.31
SN 18	108.59	7.02	49.20	49.27	61.76	50.51	7.18	16.53	4.29
SN 19	138.92	14.02	56.09	56.03	49.24	60.31	11.02	17.54	7.34
SN 20	124.56	9.65	52.23	52.34	58.21	54.12	9.62	19.89	6.20
Mean	116.70	9.47	51.90	51.84	57.73	54.90	9.02	17.93	5.61
S.ED.	1.53	1.39	1.16	1.25	0.06	1.53	1.81	0.76	0.23
C.D. (0.5%)	3.11	2.82	2.53	2.53	0.12	3.11	3.66	1.54	0.49

Table 4 : Distribution of Makoi genotypes into different clusters by Tocher's method.

Cluster	Total no. of genotypes	Genotypes
I	10	*Sn* 01, *Sn* 02, *Sn* 03, *Sn* 07, *Sn* 09, *Sn* 12, *Sn* 14, *Sn* 15, *Sn* 16 and *Sn 18*
II	5	*Sn* 04, *Sn* 06, *Sn* 09, *Sn* 13 and *Sn* 20
III	4	*Sn* 05, *Sn* 10, *Sn* 11 and *Sn* 19
IV	17	*Sn* 17

colored stems are common among the genotypes, but few have purple pigmentation in stem (*Sn* 05, *Sn* 10, *Sn* 11, *Sn* 17 and *Sn* 19).

Three types of leaf shape were noticed in germplasm collection. Among the genotypes, seventeen genotypes have ovate leaves and two genotypes *Sn* 10 and *Sn* 11 have rhomboidal leaf shape. *Sn* 18 was distinct with lanceolate type of leaf shape. The leaf margin was entire in all genotypes except few, which have serrated leaves (*Sn* 04, *Sn* 06, *Sn* 09, *Sn* 10, *Sn* 11, *Sn* 13, *Sn* 17, *Sn* 19 and *Sn* 20). Leaf pubescence was dense in *Sn* 05, *Sn* 10, *Sn* 11, *Sn* 17 and *Sn* 19 and was sprays in *Sn* 04, *Sn* 09, *Sn* 13 and *Sn* 20 where else, it was absent in rest of the eleven genotypes. In genotypes *Sn* 05, *Sn* 09, *Sn* 13 and *Sn* 19 the leaf color was dark green while others are normal.

In case of floral characters, variations were noted in flower diameter, corolla arrangement and corolla color. Flower diameter was maximum in *Sn* 05 and *Sn* 17 (0.9 -1.0 cm) followed by *Sn* 10, *Sn* 11 and *Sn* 18 (0.8 – 0.9 cm). The corolla arrangement was dentate in all genotypes except *Sn* 04, *Sn* 09, *Sn* 10 and *Sn* 17 which have entire corolla. Corolla was white in all genotypes, except *Sn* 19 which have white flower with purple stripes.

Three distinct fruit color was noticed in germplasm collection. Most of them have purplish black fruits (sixteen

Table 5 : Cluster mean for quantitative characters of Makoi genotypes.

Cluster	Plant height	No. of primary branches	Plant spread (N-S)	Plant spread (E-W)	DHM	FLY/ plant	DLY/ plant	FFY/ plant	DFY/ plant
I	108.88	7.39	49.62	49.42	61.70	50.69	7.16	16.55	4.39
II	125.85	9.48	53.45	52.52	58.18	54.12	9.58	17.90	6.42
III	138.59	13.32	56.20	56.08	49.56	62.15	11.20	18.92	7.20
IV	60.42	12.20	57.57	57.45	49.30	50.49	7.17	17.02	4.26

Table 6 : Inter and intra cluster distances.

Cluster	I	II	III	IV
I	38.12	272.84	391.97	226.71
II		65.75	362.83	212.15
III			85.55	136.61
IV				0

genotypes), two genotypes have red colored fruit (*Sn* 09 and *Sn* 10) and two genotypes have orange colored fruits (*Sn* 17 and *Sn* 19). Fruit size was maximum in genotypes *Sn* 05 (0.7 -1.8 cm) followed by *Sn* 10 and *Sn* 11 (0.6-.07 cm).

In any crop improvement programme, genetic diversity and genetic relationship between available germplasm plays an important role. It is essential while initiating hybridization or crop improvement programme as the choice of the potential and diverse parents are pre requisite to determine the success of the breeding programme and will score purpose of combining desirable genes to obtain superior combinations. The germplasm exhibited wide range of variability for all nine quantitative characters assessed. The variations among genotypes were highly significant for all characters. The data presented in table 3 clearly indicate that maximum plant height was noticed in *Sn* 10 and *Sn* 11 (140.22 and 139.76 cm, respectively) followed by *Sn* 19 (138.92 cm). Number of branches was maximum in *Sn* 10 and *Sn* 32 (14.24 and 13.92, respectively). *Sn* 17 have maximum plant spread (57.52 cm and 57.46 cm) followed by *Sn* 19 (56.09 cm and 56.03 cm). Fresh and dry leaf yield per plant were high in *Sn* 05 (70.06g and 12.92 g per plant) followed by *Sn* 10 (60.52 g and 11.05 g per plant). Fresh and dry berry yield per plant was high in *Sn* 05 (22.02 g and 6.57 g per plant) followed by *Sn* 06 (19.97 and 6.23 g per plant). Total alkaloid content in leaves and fruits was maximum in *Sn* 05 (0.41% and 0.158%, respectively) followed by *Sn* 11 (0.40% and 0.157%).

Grouping of genotypes into different clusters was carried out using Tocher's method and presented in table 4. All the genotypes were distributed into four clusters. Cluster I was the largest, consisting of ten genotypes from different districts of Tamil Nadu and Kerala. Cluster II consists of five genotypes, of which two are from temperate regions of Tamil Nadu, one from Solan, Himachal Pradesh and two from tropical region of Tamil Nadu. Cluster III consists of totally four genotypes from Tamil Nadu, among them three are from tropical parts and one from temperate region.

The cluster mean of nine quantitative characters have been presented in table 5. Highest cluster mean for plant height (138.59), number of primary branches (13.32), fresh leaf yield per plant (61.56), dry leaf yield per plant (11.20), fresh fruit yield per plant (18.92) and dry leaf yield per plant (7.20) was recorded in cluster III. While, cluster IV recorded highest mean for plant spread (57.57 (N-S) and 57.45 (E-W)). Highest cluster mean for days to harvestable maturity was noticed in cluster I (61.70).The clustering pattern of genotypes showed that geographic diversity was not related with genetic diversity. The frequent movement of seed material and subsequent adaptation to agro climatic condition may be responsible for such variations. Therefore, selection of genotypes should be based on genetic diversity rather than geographical diversity. The inter cluster distance (table 6) was more between cluster I and cluster III (391.97) followed by cluster II and cluster III (362.83), indicating that two clusters are highly divergent and hybridization would produce heterotic hybrids and a great spectrum of variability in the segregating generations. The cluster III with four genotypes recorded highest intra cluster distance (85.55) indicating the wide divergence between the genotypes.

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