

Genetic diversity in Perilla [*Perilla frutescens* (L.) Britton] land races of Nagaland

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ABSTRACT

Perilla is an underutilized crop which comes under the category of minor oil seed crop. A field experiment was conducted during the Kharif season (April-November) of the year 2016 at the experimental farm of Genetics and Plant Breeding under School of Agricultural Sciences and Rural Development (SASRD), Medziphema, Nagaland to study the nature and magnitude of genetic divergence in 15 *Perilla* genotypes and observations on 13 traits were recorded. Analysis of variance revealed significant differences among the different genotypes for all the traits under study. Based on relative magnitude of D^2 values 15 genotypes were grouped into six clusters. Cluster IV had highest landraces (4) followed by Cluster I (3) and the remaining clusters with two landraces each. Maximum genetic divergence was observed between Cluster V and Cluster VI and minimum genetic divergence was observed between Cluster I and Cluster II. Hence, the genotypes of cluster V and cluster VI could be utilized in hybridization program to achieve greater variability in the segregating generations. The analysis revealed maximum contribution of seed yield per plant followed by test weight, oil content and length of main inflorescence towards genetic divergence.

Key words: Cluster, D^2 values, genetic divergence, *Perilla*

INTRODUCTION

In India, *Perilla* (*Perilla frutescens* L.) is an underutilized crop which comes under the category of minor oil seed crop. It is cultivated majority in the northeastern hill region, Kumaon, Garhwal and Himachal Pradesh. *Perilla* is also reported to have medicinal values. Asian herbalists prescribe *perilla* for cough and lung afflictions, influenza prevention, restless fetus, seafood poisoning, incorrect energy balance, etc (Brenner, 1993). Along with the other Northeastern states, Nagaland state is endowed many landraces of its own; however, exploitation of germplasm has not been done so far. In any crop, germplasm is a valuable source of base population and provides the scope for wider variability. However, to understand the usable variability, grouping or classification of genetic stocks based on minimum divergence between them is quite imperative. The nature and magnitude of genetic divergence helps the plant breeder in choosing the right type of parents for higher amount of heterotic expression in F_1 and broad spectrum of variability in subsequent segregating generations (Maurya and Singh, 1977). Genetic diversity in *perilla* has been studied by Lee and Kim (2007), Pandey and Bhat (2008), Verma *et al.* (2009), Verma *et al.* (2010) and Hussain (20013). However,

information available on genetic diversity in *Perilla* (*Perilla frutescens* [(L.) Britton]) landraces of Nagaland is limited. Therefore, the present study was carried out to analyze the genetic diversity in *Perilla* (*Perilla frutescens* [(L.) Britton]) land races of Nagaland to select the potential parents for breeding program.

MATERIALS AND METHODS

The present investigation was undertaken during the kharif season of 2016 with 15 landraces from 10 districts of Nagaland. The experiment was laid out in randomized block design with three replication in the experimental farm of School of Agricultural Sciences and Rural Development, Medziphema campus, Nagaland University. The period of crop growth cycle was for seven months *i.e.* from May to November 2016. Seeds were sown on 8th May in line sowing with a depth of 1-1.5 cm. 120 kg FYM and Urea, SSP &MOP were applied in ratio of 2.2:6.3:0.8 kg. All the cultural practices were followed for raising a good crop. Data were recorded on five randomly sampled plants from each plot leaving all the border plants. The data collected were on the thirteen quantitative traits of the crop *viz.*, days to 50% flowering, plant height, number of leaves per plant, leaf length, leaf breadth, petiole length, number of primary

branches per plant, number of inflorescence per plant, length of main inflorescence, days to 80% maturity, test weight, oil content and seed yield per plant. Analysis of variance was done using standard statistical procedure. The genetic divergence among genotypes was computed by means of Mahalanobis D^2 technique (Mahalanobis, 1936) and the genotypes were grouped into different clusters following Tocher's method (Rao, 1952).

RESULTS AND DISCUSSION

Analysis of variance revealed significant variation among the 15 genotypes for all the characters. Several measures of distance have been proposed to suit various objectives of which Mahalanobis's generalized distance (Mahalanobis, 1930, 1936; Rao, 1952) had occupied a unique place in plant breeding. Using this technique, all the genotypes were grouped into 6 different clusters (Table 1).

Table 1: Clustering pattern of 15 landraces of *Perilla* on the basis of Genetic Divergence

Cluster No.	No. of land races	Land races
I	3	Pe-1(Akini), Pe-4 (Pintsu), Pe-8 (Mipeo)
II	2	Pe-6 (Nam), Pe-14 (Kuna)
III	2	Pe-5 (Azu), Pe-11 (Bhanjira)
IV	4	Pe-2 (Akini), Pe-3 (Pintsu), Pe-7 (Nam), Pe-10 (Namyu)
V	2	Pe-2 (Akini), Pe-3 (Pintsu), Pe-7 (Nam), Pe-10 (Namyu)
VI	2	Pe-9 (Namyu), Pe-15 (Bangdang)

- The local name of the landraces are denoted within the parenthesis

Cluster IV has the maximum number of landraces (4) followed by Cluster I (3) and the remaining clusters had two (2) landraces each. The estimates of intra and inter cluster distances have been presented in Table 2. The intra cluster distance (D^2) ranged from 51.309 (Cluster II) to 597.157 (Cluster IV). The divergence at inter cluster level was maximum between Cluster V and Cluster VI ($D^2= 852.785$) indicating wide genetic diversity between these

two clusters. Hence, the genotypes of cluster V and cluster VI could be utilized in hybridization program to achieve greater variability in the segregating generations. The divergence at inter cluster level was found to be minimum between Cluster I and Cluster II ($D^2 = 89.192$), followed by Cluster III and Cluster V ($D^2 = 136.726$) and Cluster II and Cluster VI ($D^2= 252.402$).

Table 2: Average Intra (bold) and Inter Cluster distance

Cluster No.	I	II	III	IV	V	VI
I	140.541 (11.855)	89.192 (9.44)	290.177 (17.035)	644.724 (25.391)	444.155 (21.075)	305.499 (17.479)
II		51.309 (7.163)	396.340 (19.908)	758.683 (27.544)	583.226 (24.150)	252.402 (15.887)
III			65.154 (8.072)	449.620 (21.204)	136.726 (11.693)	686.978 (26.210)
IV				597.157 (24.437)	475.116 (21.797)	736.368 (27.136)
V					208.868 (14.452)	852.785 (29.202)
VI						264.266 (16.256)

- *D* values are in parenthesis

The cluster means of all the six clusters are presented in Table 3. Cluster I showed highest mean value for days to 80% maturity

(200.889). Cluster II showed highest mean value for days to 50% flowering (162.167) and oil content (36.750). Cluster III showed highest

Table 3: Cluster wise mean values of 13 characters in *Perilla frutescens*

Clusters	Characters												
	Days to 50% flowering	Plant height (cm)	No. of leaves/ plant	Leaf length (cm)	Leaf breadth (cm)	Petiole length (cm)	Primary branches/ plant	Infloresce nce/ plant	Length of main inflorescence (cm)	Days to 80% maturity	Test Weight (g)	Oil Content (%)	Seed yield/ Plant (g)
I.	159.33	150.00	214.56	13.01	11.46	6.39	14.67	137.78	9.69	200.89	1.38	36.55	5.19
II.	162.17	131.50	242.67	12.73	10.48	5.78	13.33	136.67	7.48	192.17	1.28	36.75	4.30
III.	147.67	165.33	141.50	13.35	10.85	6.57	22.00	146.67	10.23	195.17	1.23	35.65	9.63
IV.	148.25	151.58	203.08	14.68	12.15	7.08	16.42	160.00	11.78	194.33	1.63	35.16	16.33
V.	149.83	161.83	187.17	13.77	13.62	7.42	19.17	196.67	12.52	181.67	1.07	30.75	12.21
VI.	157.17	139.17	318.83	14.90	12.73	7.48	18.17	168.33	8.95	193.17	2.13	30.05	9.98

mean value for plant height (165.333) and number of primary branches (22.000). Cluster IV showed highest mean value for seed yield per plant (16.334). Cluster V showed highest mean value for no. of inflorescence per plant (196.667) and length of main inflorescence (12.517). Cluster VI showed highest mean value for no. of leaves per plant (318.833), leaf length (14.900), leaf breadth (12.733), petiole length (7.483) and test weight (2.133). Cluster II showed the maximum number of lowest mean value for

It was observed that the landraces of Cluster IV possessed the highest seed yield (Pe-2), oil content (Pe-3), leaf length (Pe-7), length of main inflorescence (Pe-7) and earliest 50% flowering (Pe-10). Cluster V possessed highest leaf breadth (Pe-12) and earliest 80% maturity

characters plant height (131.500), leaf length (12.733), leaf breadth (10.483), petiole length (5.783), no. of primary branches (13.333), no. of inflorescence per plant (136.667), length of main inflorescence (7.483), days to 80% maturity (192.167) and oil content (36.750). Cluster III showed lowest mean values for days to 50% flowering (147.667) and no. of leaves per plant (141.500). Cluster V lowest mean value for test weight (1.067). Cluster VI showed lowest mean value for oil content (30.050).

(Pe-13) landraces. Cluster VI possessed landraces with highest petiole length (Pe-9), no. of leaves per plant (Pe-15) and highest test weight (Pe-15). Cluster III possessed landraces with highest plant height (Pe-5) and number of primary branches per plant (Pe-11).

Table 4: Contribution of each character to divergence

Character	No. of first rank	Contribution (%)
Days to 50% flowering	0	0.00
Plant height	0	0.00
Leaves / plant	3	2.86
Leaf length	0	0.00
Leaf breadth	0	0.00
Petiole length	0	0.00
Primary branches/ plant	1	0.95
Inflorescence/plant	1	0.95
Length of main inflorescence	6	5.71
Days to 80% maturity	1	0.95
Test weight	8	7.62
Oil content	8	7.62
Seed yield/plant	77	73.33

The contribution of each character to the D^2 values or divergence is presented in Table 4. It reveals that seed yield per plant contributed maximum (73.33%) towards divergence, followed by test weight (7.619%), oil content (7.619%) and length of main inflorescence (5.71%). This was in agreement with the findings of Rupanga *et al.* (2017) for yield, Hussain *et al.*

(2013) and Soniasabnam *et al.* (2018) for test weight. The present study suggests that the genotypes of cluster V (Pe-2 (Akini), Pe-3 (Pintsu), Pe-7 (Nam), Pe-10 (Namyu) and cluster VI (Pe-9 (Namyu), Pe-15 (Bangdang) could be utilized in hybridization program to achieve greater variability in the segregating generations.

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