J. Soils and Crops 31 (2) 242-246, December 2021

ISSN 0971-2836 (Print)
ISSN 2582-2756 (Online)

ASSESSMENT OF RAJMA BEAN GERMPLASM GROWN UNDER LOWER ALTITUDE OF NAGALAND USING MULTIVARIATE ANALYSIS

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ABSTRACT

An experiment was conducted at ICAR Research Complex for NEH region, Nagaland centre during 2013-15 to study the genetic diversity of rajma bean (*Phaseolus vulgaris* L.) germplasm using descriptive statistics, principal component analysis (PCA) and cluster analysis. 32 germplasm collected from different parts of Nagaland were evaluated in randomized block design with three replications. Seventeen quantitative traits *viz.*, morphological, flowering, yield and yield attributing characters were studied. The results of descriptive statistics like mean, minimum, maximum, standard deviation and coefficient of variation showed significant variation in all the seventeen traits evaluated for the study. The analysis of PCA showed that totally five PCs was formed with cumulative variance of 72.59 %. High level of variation was observed for yield and yield attributing characters. The Neighbour-joining analysis showed that three clusters *viz.,* Cluster I (4 germplasm), Cluster II (13 germplasm) and Cluster III (15 germplasm) were formed based on the seventeen quantitative characters. The germplasm in Cluster I (RCN-5, RCN-11, RCN-12, RCN-20) were identified as high yielding germplasm. These germplasms can be used as genetic material for improvement programs.

(Key words: Rajma beans, principal component analysis, cluster analysis)

INTRODUCTION

Rajma bean (*Phaseolus vulgaris* L.), a native of Central and South America, is an important and one of the oldest food legumes in the world (Matthew *et al*., 2011). The seeds are rich in protein, fibre, starch, and minerals and rich in bioactive compounds like phenols, lectins, phytates, etc. (Broughton *et al.,* 2003; Kumar *et al.,* 2008). The dry seeds, pods, frozen grain, or canned grain are preferred by consumers and processing industries (Escribano *et al.,* 1997). It is one of the important *rabi* crops in India (Jagdale *et al*., 2005; Band *et al*., 2007). Northeast India is rich in horticultural diversity (Deka *et al.,* 2012) and rich in genetic resources of rajma beans. It is gaining importance in Nagaland due to its high nutritive content (Kumar *et al*., 2020) and is widely cultivated as a mixed crop in *Jhum fields*, backyards, and kitchen gardens. It is vernacularly called *Khollar, Ajokha, Ajoxa* and *Khetsuthi*. It is sown during February – March and harvested during May – July depending on the cultivars at high altitudes. It is grown during September – October (sowing) and December – January (harvesting) in lower altitudes (Thirugnanavel *et al*., 2019). It is used as a pulse (dried beans) and a fresh vegetable (green pods). It is consumed as either boiled or fried and served as one of the essential protein sources of plant origin.

The farmers grow several landraces which vary in size, shape, maturity, and quality. Rapid urbanization, depleting the soil nutrient status, introducing high-yielding and high-value vegetable crops, deforestation, and climate change poses a severe threat to the vast genetic resources of this region (Thirugnanavel *et al*., 2015, 2018). Genetic conservation and utilization of rajma germplasm is a significant challenge. Genetic diversity analysis is a prerequisite for its efficient utilization in the improvement program. Multivariate analysis like principal component analysis (PCA) and cluster analysis is widely used for genetic diversity analysis (Maji and Shaibu, 2012). The knowledge of the genetic diversity of rajma beans in Nagaland is limited. Therefore, the present study was aimed to assess the genetic diversity of the rajma germplasm of Nagaland based on PCA and cluster analysis. From this analysis, the germplasm could be classified into different groups, which would be helpful in rajma improvement programs.

MATERIALS AND METHODS

Thirty-two genetically distinct rajma bean germplasm collected from major growing areas of Nagaland were used for the study (Table 1). The study was conducted at ICAR Research Complex for NEH Region, Nagaland

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Centre, Jharnapani, Nagaland during October-January in 2013-14 and 2014-15 and replicated thrice in randomized complete block design. The study site is situated at 25°45'24" N longitude and 93°50'26" E latitude with an altitude of 281m MSL. The germplasm was planted at 60 cm x 60 cm, and uniform cultural practices were followed. Ten plants were randomly selected in each germplasm in each replication for the observation. The observations were recorded on seventeen quantitative traits, *viz*., plant height (cm), inflorescence length (cm), no. of flowers inflorescence^{-1}, number of pods inflorescence^{-1}, pod length (cm), pod width (cm), pedicel length (cm), pod beak length (cm), seed length (cm), seed width (cm), test weight (g), locules pod^{-1}, no. of seeds pod^{-1}, seed weight (g), no. of pods plant^{-1}, no. of seeds plant^{-1}, and seed yield plant^{-1} (g). Descriptive statistics like mean, maximum, minimum, standard deviation (SD) and coefficient of variation (CV) were calculated using Web ICAR Central Coastal Agricultural Research Institute Agri Stat Package 2.0 (WASP 2.0). The principal component analysis (PCA) was calculated using 17 quantitative characters in SPSS 16.0. The cluster analysis between 32 rajma bean germplasm based on morphological characters was calculated by Neighbour joining method in Darwin 6.0.

Table 1. Details of the germplasm collected from different parts of Nagaland

Line	Village	District	Altitude	Latitude	Longitude
RCN1	Dzulhami	Phek	1814	25°49'35"	94°23'39"
RCN2	Dzulhami	Phek	1814	25°49'35"	94°23'39"
RCN3	Dzulhami	Phek	1814	25°49'35"	94°23'39"
RCN4	Dzulhami	Phek	1814	25°49'35"	94°23'39"
RCN5	Dzulhami	Phek	1814	25°49'35"	94°23'39"
RCN6	Aquba	Zunheboto	1055	26°0'37"	94°34'21"
RCN7	Aquba	Zunheboto	1055	26°0'37"	94°34'21"
RCN8	Aquba	Zunheboto	1055	26°0'37"	94°34'21"
RCN9	Aquba	Zunheboto	1055	26°0'37"	94°34'21"
RCN10	Aquba	Zunheboto	1055	26°0'37"	94°34'21"
RCN11	LizuNaghuto	Zunheboto	1367	26°2'36"	94°30'37"
RCN12	LizuNaghuto	Zunheboto	1367	26°2'36"	94°30'37"
RCN13	Sukhalu	Zunheboto	1835	25°58'18"	94°30'37"
RCN14	Sukhalu	Zunheboto	1835	25°58'18"	94°30'37"
RCN15	Sukhalu	Zunheboto	1835	25°58'18"	94°30'37"
RCN16	Sataka	Zunheboto	1623	25°55'12"	94°27'01"
RCN17	Sataka	Zunheboto	1623	25°55'12"	94°27'01"
RCN18	Sataka	Zunheboto	1623	25°55'12"	94°27'01"
RCN19	Sataka	Zunheboto	1623	25°55'12"	94°27'01"
RCN20	Kilo old	Zunheboto	972	25°54'15"	94°26'2"
RCN21	Kejok	Tuensang	1018	26°16'24"	94°50'11"
RCN22	Kejok	Tuensang	1018	26°16'24"	94°50'11"
RCN23	Chidema	Kohima	1398	23°39'54"	94°6'51"
RCN24	Chidema	Kohima	1398	23°39'54"	94°6'51"
RCN25	Wokha	Wokha	1123	26°5'51"	94°13'39"
RCN26	Wokha	Wokha	1123	26°5'51"	94°13'39"
RCN27	Wokha	Wokha	1123	26°5'51"	94°13'39"
RCN28	Wokha	Wokha	1123	26°5'51"	94°13'39"
RCN29	Wokha	Wokha	1123	26°5'51"	94°13'39"
RCN30	Wokha	Wokha	1123	26°5'51"	94°13'39"
RCN31	Longsachung	Wokha	1612	26°3'14"	94°15'41"
RCN32	Longsachung	Wokha	1612	26°3'14"	94°15'41"

RESULTS AND DISCUSSION

The descriptive statistics of quantitative traits like mean, minimum and maximum, standard deviation, and coefficient of variation were summarized in Table 2. All the characters showed considerable variation. The yield plant^{-1} showed a significantly increased level of coefficient of variation (66.61%), followed by the number of seeds plant^{-1} (52.53%),pods plant^{-1} (50.81%), and plant height (48.17%). The traits like the number of flowers inflorescence^{-1}, locules pod^{-1}, and pod width recorded a low level of coefficient of variation. The yield plant^{-1} ranged from 15.4-142.0 g with a mean of 38.99 g. The number of seeds plant^{-1} ranged from 36.8-250.6 with a mean of 97.9. The number of pods ranged from 8.8-40.95, with a mean of 17.36. The plant height ranged from 27.3 -253.1 cm, with a mean of 109.16 cm. These traits exhibited a high level of co-efficient of variation. The results revealed the genetic differences among germplasm and provided information on elite lines that the plant breeders could utilize. These results were supported by Raffi and Nath (2004), Ulukapi and Onus (2014), Laura *et al*. (2018), and Kalauni and Dhakal (2020). They reported the highest coefficient of variation for yield and yield attributing characters in common beans. The differences may be due to the influence of environmental conditions (photoperiod and temperature in particular) on the physiological traits (Meza *et al*., 2013).

The principal component analysis result explained the genetic diversity of rajma beans. This genetic diversity is used to identify the most significant variables in the data of rajma bean germplasm. The total number of principal components was seventeen, which is equal to the number of traits studied. The first five principal components with more than 1 eigenvalues explained 72.59 % of the cumulative variation for the seventeen quantitative traits (Table 3). The remaining PCA had less per cent of cumulative variation and was considered less important. Hence, the PCA was considered for the first five principal components (Table 4). The PC1 showed a high genetic variation for yield and yield attributing characters like individual seed weight, test weight, pod width, pod beak length, number of flowers inflorescence^{-1}, and yield. The no. of seeds plant^{-1}, no. of pods plant^{-1}, pedicle length, and yield showed a high genetic variation in the PC2. In the PC3, the pod length and seed length showed maximum variation. Inflorescence length showed a maximum variation in the PC4. Plant height and seed width showed a variation in the PC5. Legesse *et al*. (2013) and Hinkossa *et al*. (2013) also obtained similar results and they reported that yield attributing characters like seed weight, test weight, yield plant^{-1} were the major traits contributing to the genetic diversity of common beans.

Cluster analysis is predominantly used for evaluating the genetic diversity. Neighbour-joining hierarchical cluster analysis based on the seventeen quantitative characters showed significant genetic diversity in the evaluated germplasmand resulted in three main clusters (Fig. 1). The cluster I contained four germplasm (RCN-55,RCN-11, RCN-12, RCN-20), the cluster II contained 13 germplasm (RCN-2, RCN-7, RCN-14, RCN-15, RCN-23, RCN-24, RCN-25, RCN-26, RCN-27, RCN-28, RCN-29, RCN-31, RCN-32), and the cluster III contained 15 germplasm (RCN-1, RCN-3, RCN-4, RCN-6, RCN-8, RCN-9, RCN-10, RCN-13, RCN-16, RCN-17, RCN-18, RCN-19, RCN-21, RCN-22, RCN-30). These clusters were formed based on the yield and yield attributing characters, and cluster I was grouped under high-yielding germplasm. Equal manures and fertilizers are applied to all the germplasm, and hence this germplasm did not affect by the nutrients deficiency symptoms or stress symptoms during the growing period. The germplasm from cluster I could be potentially utilized for breeding programs. Confirming this study, Stoilova *et al.* (2005), Legesse *et al*. (2013) reported that the evaluation of phenotypic variability in common bean genotypes by cluster analysis led to the selection of superior germplasm for crop improvement.

The study concluded that there was rich genetic diversity observed for rajma bean germplasm in Nagaland. The PCA showed that the first five PCs showed a cumulative variation of over 70 %, and the PCs were formed mainly based on yield and yield attributing characters. The diversity analysis allowed us to classify the germplasm in Nagaland into three clusters. The rajma germplasm in cluster I have shown high yielding characters and could be recommended for farmers and could be used in further improvement programs.

Table 2. Descriptive statistics among 32 rajma bean germplasm (Pooled data of two years)

Variables	Mean	Minimum	Maximum	Standard deviation	Coefficient of variation
Plant height	109.16	27.3	253.1	52.58	48.17
Inflorescence length	6.22	4.1	7.8	0.93	14.95
No. of flowers inflorescence^{-1}	3.82	3.0	4.8	0.46	12.04
No. of pods inflorescence $^{-1}$	2.29	1.0	3.7	0.53	23.14
Pod length	12.33	7.0	17.1	2.23	18.09
Pod width	1.2	0.9	1.6	0.17	14.17
Pedicle length	0.79	0.4	1.1	0.18	22.78
Pod beak length	1.01	0.4	1.9	0.33	32.67
Seed length	1.34	0.9	2.0	0.26	19.40
Seed width	0.82	0.6	1.2	0.15	18.29
Test weight	38.95	18.9	61.7	10.43	26.78
Locules pod^{-1}	6.31	4.5	7.7	0.87	13.79
No. of seeds pod^{-1}	5.66	3.9	7.1	0.82	14.49
Individual seed weight	0.39	0.2	0.6	0.1	25.64
No. of pods plant^{-1}	17.36	8.8	40.9	8.82	50.81
No. of seeds plant^{-1}	97.95	36.8	250.6	51.45	52.53
Yield plant^{-1}	38.99	15.4	142.0	25.97	66.61

Table 3. Eigenvalue and proportion of total variability among rajma bean germplasm

PC	Eigen value	Variance (%)	Cumulative (%)
1	4.694	27.61	27.61
2	3.144	18.49	46.10
3	2.132	12.53	58.64
4	1.592	9.36	68.01
5	1.238	7.28	75.29

Table 4. Correlation between original variables and first five principal components

Variables	PC1	PC2	PC3	PC4	PC5
Plant height	-.175	-.074	-.520	.144	.630
Inflorescence length	.425	-.040	-.386	.605	.163
No. of flowers inflorescence^{-1}	.462	.413	-.303	.449	.243
No. of pods inflorescence $^{-1}$	.559	-.141	.137	-.433	-.003
Pod length	.062	.170	.570	.064	.391
Pod width	.683	-.319	-.060	.207	.105
Pedicle length	.398	-.538	-.072	-.168	-.164
Pod beak length	.661	-.197	.052	.244	-.366
Seed length	.465	-.121	.627	-.129	.329
Seed width	.409	.003	.325	-.304	.507
Test weight	.842	.075	.262	.227	-.189
Locules pod^{-1}	-.418	.656	.486	.236	-.041
No.of seeds pod^{-1}	-.408	.680	.395	.356	-.116
Individual seed weight	.849	-.013	.223	.216	-.063
No. of pods plant^{-1}	.441	.658	-.379	-.431	.011
No. of seeds plant^{-1}	.308	.824	-.321	-.286	-.027
Yield plant^{-1}	.668	.680	-.101	-.157	-.101

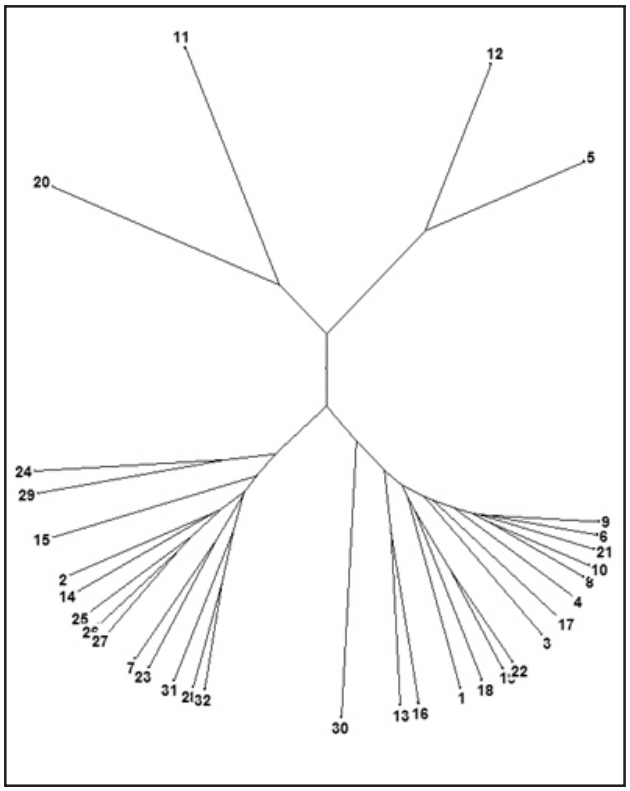

Fig. 1. Neighbour-joining tree based on 17 quantitative characters

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Rec. on 15.05.2021 & Acc. on 19.05.2021