

GENETIC VARIABILITY IN GENEPOOL OF BUTTERFLY PEA (*Clitoria ternatea*) FOR FORAGE ATTRIBUTES

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Ninety two genotypes of Butterfly pea (*Clitoria ternatea*) collected from different parts of the country were evaluated. A wide range of variation in various characteristics for different genotypes in germplasm collections were observed. The maximum variation (CV 35%) was recorded in green fodder yield per plant followed by number of leaves per plant (CV 31%) and leaf stem ratio (CV 27%). Genotype ILCT 281 from Uttar Pradesh and ILCT 276 from Rajasthan had the lowest total index score value after the meteroglyph analysis. Genotypes ILCT 261, ILCT 213 and ILCT 221 were found to have the maximum total index score value and thus the aggressive growth habit. Results indicated that materials from the different regions were randomly represented in all TIV grades of plant growth types.

Key words: *Clitoria ternatea*, genetic variability, forage attributes

Availability of nutritious fodder from arable areas is vital to increase animal productivity in the country. The major source of cattle feed is through pasture crops and native grasslands besides other sources. The native grasslands are in a highly degraded state providing low biomass of poor nutritional quality, and are dominated by different grass species namely *Sehima nervosum*, *Dichanthium annulatum*, *Cenchrus* spp., *Heteropogon contortus*, *Phragmites* spp., *Saccharum* spp., *Themeda* spp., and *Iseilema* spp. etc. (Dabhadgaon and Shankarnarayan, 1973). The cheapest way to improve forage quality world over has through increasing the occurrence of productive forage legumes in the native grasslands. Grass-legume pastures are known to improve forage quality and soil status in terms of organic carbon, available nitrogen and phosphorus.

Among the indigenous legumes, *Clitoria ternatea* commonly known as Butterfly pea or aparajita is a productive forage legume that has

shown wide range of adaptability and persistence in arid to warm humid areas of the country (Singh and Singh, 1988; Singh and Gupta, 1991). *Clitoria* is endowed with excellent forage productivity and quality, as its crude protein content varies from 13-25 per cent on dry matter basis and has more than 70 per cent digestibility (Upadhyay and Pachauri, 1983). Wide genetic diversity in different regional accessions of *Clitoria* has been observed in Indian material (Singh and Singh, 1988). Keeping in view the immense importance of germplasm collections and its proper evaluation and categorization, the present investigation was framed to study the genetic diversity and also to classify the material and identify the desirable types among a sizeable collection of *Clitoria ternatea* genotypes made from different parts of the country.

MATERIALS AND METHODS

Ninety-two genotypes of butterfly pea were collected from different agroclimatic situations of

tropical and warm humid regions of India. The material was grown at Central Research Farm of National Research Centre for Agro-Forestry, Jhansi. The research farm is situated at 25°-27' North, 78°-35' East, 271 m above the sea level and falls in semi arid plateau of Bundelkhand having mean annual rainfall 890 mm. The soil is neutral in reaction, poor in nitrogen and organic content but rich in potassium. The experiment was laid out in randomized block design in sandy loam soils. The seeds of all the germplasm lines were sown in 3m long row spaced at 50 cm and 10-15 cm distance between plant to plant respectively. Each plot had three lines and was replicated thrice. The experiment was maintained under rainfed conditions for three consecutive years.

The observations on various morphological, growth and fodder yielding attributes were recorded at 50% flowering stage on three randomly selected plants from each plot. These were cut at 10 cm above the ground level for recording data on fodder yielding attributes. For the classification and cataloguing of germplasm, score index method was followed as proposed by Anderson (1957). Each parameter was divided into three scoring groups: 1. Low II. Medium III. High. These groups were denoted by numerical values 0, 1 and 2 respectively. For score index, various characters viz., days to flowering, plant height (cm), branch number, secondary branch number, branch length (cm), number of leaves per plant green fodder yield per plant (g), dry matter yield per plant (g), leaf stem ratio (dry matter) and crude protein content were considered. Score for each character ranged from 0-2 and accordingly maximum score by any genotype could be 20. The entire germplasm was thus grouped and classified.

RESULTS AND DISCUSSION

A wide range of variation observed in characters in germplasm collection (Table 1).

Among all the characters studied, maximum variation (CV 35%) was observed in green fodder yield per plant followed by number of leaves per plant (CV 31%), leaf stem ratio (CV 27%) and minimum in branch number per plant (CV 14.0%) and days to flowering (CV 15%) (Table 1).

Table 1. Mean, range and coefficient of variation, values of different morphological and fodder yielding attributes in 92 genotypes of *C. ternatea*

Characters	Range	Mean	CV%
1. Days to flowers	39.5-49.6	44.55±1.18	15.05
2. Plant height (cm)	53.2-94.9	73.88±3.15	20.72
3. Branch numbers	8.0-17.9	12.86±0.93	14.00
4. Number of secondary branches	10.0-24.8	17.40±1.30	18.00
5. Branch length	54.1-95.1	73.68±3.45	20.86
6. Leaf numbers	90.4-183.5	136.80±5.36	31.00
7. Green fodder yield	39.3-97.7	68.00±2.16	35.00
8. Dry matter yield (g)	11.01-26.66	17.96±1.35	24.06
9. Leaf-stem ratio (dry matter)	0.64-1.24	0.93±0.92	27.04
10. Crude protein content %	20.13-26.99	23.56±0.56	17.54

The genetic diversity is the basic input required for any crop improvement programme. It offers scope for direct selection of elite material as a new cultivar or helps in identifying specific traits for use in breeding programme. On the basis of index score method (Anderson, 1957), the entire genepool was classified into 15 groups. The values of total index score in the different group ranged between 1-15 (Table 2). The materials from different regions were distributed in different groups with specific index score values (Table 3). The values of total index score of respective groups were further classified into four major groups and their index score values are : group I : 0-4, group II : 5-8, group III : 9-12, and group IV : 13-15. Depending upon the

magnitude of the expression of all the traits the respective group indicate; (I) low vigour expression (II) medium vigour expression, (III) medium high vigour expression and (IV) very high vigour expression.

Among all the genotypes ILCT 281 from Uttar Pradesh and ILCT 276 from Rajasthan had the lowest total index score value [TIV (Table 2)]. The medium vigour expression group had the maximum number of accessions (45). Medium high vigour expression group comprising

Table 2. Grouping of *C. ternatea* genepool in respected of their score values and name of accessions

Groups	Score value	Name of accessions
I	01	ILCT.281
II	02	ILCT.276
III	03	ILCT.218, 259 and 266
IV	04	ILCT.256, 263, 274, 280 and 291
V	05	ILCT.230, 240, 267, 275, 287, 293 and 294
VI	06	ILCT. 210, 226, 233, 237, 242, 253, 255, 282, 284 and 285
VII	07	ILCT.209, 211, 217, 225, 229, 231, 232, 234, 238, 250, 252, 257, 268, 286
VIII	08	ILCT.223, 245, 251, 258, 260, 264, 270, 273, 279, 283, 288, 296, 297 and 300
IX	09	ILCT.220, 235, 236, 265, 277 and 290
X	10	ILCT.227, 241, 246, 254, 262, 271 and 292
XI	11	ILCT.214, 216, 224, 239, 244 and 299
XII	12	ILCT.212, 219 and 243
XIII	13	ILCT.215, 222, 228, 247, 248, 278, 289, 295 and 298
XIV	14	ILCT.249, 269 and 272
XV	15	ILCT.213, 221 and 261

22 genotypes was characterised by medium expression of most and high expression of some of the characters. The accessions of very high vigour expression group were most productive

forage yielders as most of the characters showed maximum expression. Out of 15 genotypes in the group, accessions ILCT 261, ILCT 213 and ILCT 221 were the most aggressive plant growth types. Results also indicated that materials from different regions were randomly represented in all TIV grades of plant growth types (Tables 2 and 3).

Table 3. Grouping of *C. ternatea* genepool in respect of their score value, number of accession and source of origin

Groups	Score value	No. of accessions	Source and number of accessions
I	1	1	UP (I)*
II	2	1	Raj (1)
III	3	3	UP (1), Raj (1) and Dlh (1)
IV	4	5	UP (2), Raj (2) and Guj (1)
V	5	7	UP (1), Raj (3), MST (1), NT (1); Guj (1)
VI	6	10	Raj (3), MP (4), Dlh (1), Guj (1), VM (1)
VII	7	14	Raj (6), NT (3), Dlh (3), Guj (1), WB (1)
VIII	8	14	UP (5), Raj (5), NV (1), MS (2), Bhr (1)
IX	9	6	UP (3), Dlh (1); Guj (2)
X	10	7	UP (2), Raj (4); Guj (1)
XI	11	6	UP (3), Dlh (2); TN (1)
XII	12	3	UP (1); Dlh (2)
XIII	13	9	UP (2), Raj (3), Dlh (2), MS (1); Bhr (1)
XIV	14	3	Raj (2); Dlh (1)
XV	15	3	Dlh (2); TN (1)

Number of accession, given in parenthesis

UP: Uttar Pradesh; Raj: Rajasthan; Dlh : Delhi State; MP: Madhya Pradesh; MS: Maharashtra; Guj: Gujarat; WB: West Bengal; TN: Tamil Nadu; Bhr: Bihar

Studies also emphasized the existence of considerable genetic diversity within the major geographical areas of *Clitoria ternatea* distribution. Presence of diverse growth forms in the material from same region may as well indicate the different plant types may have differential adaptation to

varying range of soil, climatic conditions prevailing within the broad expanse of *Clitoria* distribution. Trend, which has emerged in the present study, may potentially be utilised for selecting the desirable types among the collections as per need.

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