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Meteroglyph Analysis of Cowpea (*Vigna unguiculata* L.Walp) Elite Genotypes

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ABSTRACT

The present experiment was carried out at Director Farm, CCSHAU, Hisar during *kharif* 2017 to evaluate the performance of 30 selected elite genotypes of cowpea. The variably was studied both within and between groups. The genotypes, KBC 9 and DC 7-15 were placed in the medium fodder-medium grain yield producing group and could be utilized for both, fodder as well as grain production. Moreover, the genotypes (UPC 12-007, KBC-6, KBC-8 and GC 901) were included in high fodder- medium grain yield, which had good potential of grain production as well as excellent potential of fodder production. Likewise, the genotypes (PL-3 Sel., CPD 240 and RC 101) were included in medium fodder-high grain yield, which had good potential of grain production as well as excellent potential of fodder production. It could be utilized for dual purpose after extensive testing over time and space. None of the genotypes was placed in high fodder-high grain yield. So, there is an urgent need to breed for high fodder-high grain so that the maximum fodder as well as grain yield could be obtained simultaneously. Therefore, the hybridization among the diverse genotypes viz., UCP 12-007 (high fodder yield) with PL-3 Sel. (high grain yield) may be suggested for developing dual purpose genotypes through the transgressive segregation.

Keywords**:** Cowpea, meteroglyph analysis, fodder yield, grain yield.

Introduction

Cowpea [*Vigna unguiculata* L.Walp] (2n=22) is a dicotyledonous crop in the order Fabaceae, subfamily Faboideae (Papillionoideae), tribe Phaseoleae, subtribe Phaseolinae, genus *Vigna*. The genus *Vigna* is pantropical and highly variable. In addition to cowpea, other members include mungbean (*V. radiata*), adzuki bean (*V. angularis*), blackgram (*V. mugo*), and the bambara groundnut (*V. subterranea*). Cowpea, *V. unguiculata* subspecies *unguiculata* includes four cultigroups: *unguiculata*, *biflora* (or *cylindrica*), *sesquipedalis*, and *textilis* (Ng and Maréchal, 1985). Moreover, *V. unguiculata* subspecies *dekindiana*, *stenophylla*, and *tenuis* are the immediate wild progenitors of cultivated cowpea. Based on the distribution of diverse wild cowpeas along the entire length of eastern Africa, east and southern Africa was proposed to be the primary region of diversity, and west and central Africa to be the secondary center of diversity (Singh et al., 1997; Timko and Singh, 2008; Lal and Vashisht, 2008; Rana, 2011). These authors also suggested Asia as a third center of diversity, specific for two cultigroups *cylindrical* (catjang bean) and *sesquipedalis* (yardlong bean).

Cowpea is one of the most important forage/pulse crops and generally grown in rainy as well as summer season. It can bear up drought as well as excessive rainfall up to some extent. Moreover, it responds well to irrigation and other management practices. Today, it is gaining importance due to its multi-purpose uses i.e. food, feed, vegetable, fodder and green manure. Its green tender plants and leaves are used for feeding domestic animals as green fodder. Being a leguminous crop, it is also used for improving the soil fertility. It's green tender pods are used as vegetable and mature dry seed used as whole grain pulse for human consumption. It is a nutritive crop and rich source of protein both for animals as well as human beings (Sanjeev et al., 2015; Vu et al., 2016). It is well known fact that the genetic diversity is the primary requirement for a flourishing breeding plan. Collection and evaluation of genotypes is a pre-requisite for crop improvement, which provides a better scope for exploiting genetic diversity. The assessment of available diversity in germplasm gives essential and effective information to the crop breeder for further genetic improvement of yield (Nagalakshmi et al., 2010; Vu et al., 2016).

A lot of morphological diversity is available in cowpea which has the genetic base. For assessing the genetic divergence among the different genotypes, there are many important biometrical/statistical techniques viz. many, D^2 statistics, principal component analysis (PCA) and meterolygraph analysis, etc. Out of these techniques, meterolygraph analysis is found simple and semi-graphic method to assess the morphological variability present in a large number of germplasm lines/genotypes taken at a time. Anderson (1957) developed this technique to investigate the pattern of morphological variations among the genotypes in crop plants. Keeping above points in view, the present experiment was carried to study the morphological diversity available in cowpea for further utilization.

Materials and Methods

For the present study, 30 diverse genotypes including check were selected from the material obtained for multi-location trials from the different research stations located in different parts of the country. The experiment was planned and carried out in RBD during *kharif* 2017, in Director Farm, CCS Haryana Agricultural University, Hisar (latitude 29°10′N, longitude 75°40′E and altitude 215.2m). The soil of Hisar is sandy loam. Each genotype was planted in paired rows, with 4 m row length, spaced 45 cm apart, with plant to plant distance of 15 cm. The sowing of genotypes was carried out by using dibbling method and all the recommended package of practices were adopted to raise the healthy and good crop stand. For data recording, five plants were randomly selected and tagged in each genotype. The observations were recorded on fodder yield/plant (g), grain yield/plant (g), number of branches/plant, number of pods/plant, number of seeds/plant and 1000-seed weight (g). The average value for the meteroglyph analysis was calculated as reported by Anderson (1957).

In meteroglyph representation, the X-axis depicts fodder yield/plant, while the Y-axis represents grain yield/plant. Each genotype is represented by a circle; the position of a circle on the graph is determined by the average fodder yield and grain yield/plant of the concerned genotype. The three rays emanating from each circle in left, middle and right side are presenting the three major grain yield contributing traits viz., number of pods/plant, number of seeds/plant and 1000-seed weight (g), respectively. The range of variation in trait is represented by the variation in length of the corresponding ray on all the circles. Therefore, the mean value of each trait was classified into three groups, viz., low (index score 1), medium (score 2) and high (score 3) (Kumar, 2015).

Results and Discussion

The data of cowpea were analyzed and two traits viz., grain yield (kg/ha) and fodder yield (kg/ha) exhibiting the highest variability were identified. Singh et al., (2010) also reported genetic variability in cowpea.

In the present study, grain yield (kg/ha) and fodder yield (kg/ha) were plotted on the X and Y-axis, respectively. For each genotype, the mean values of X and Y were used to determine its position in graph which is marked by a small circle. Thus, each genotype is represented by small circle on the graph (Fig.1). The other characters for different genotypes were represented as rays on the respective circles. The ray of all the three characters emanating from a definite position on circle i.e. number of pods/plant, number of seeds/pod and 1000-seed weight (g) on left, middle and right of the circle, respectively. The range of variation in these traits is represented by the variation in the lengths of the corresponding ray on all the circles. Therefore, the mean values of each trait were classified into these groups viz., low (index score 1), medium (index score 2) and high (index score 3). All the cowpea genotypes for number of pods/plant were classified into three groups i.e. low (30), medium (30-40) and high (>40). Likewise, for number of seeds/pod the genotypes were also classified as low (< 9), medium (9-11) and high (>11). Similarly, for 1000-seed weight (g) the genotypes were grouped as low (<9g), medium (9-11g) and high (>11g). As a result, the length of each ray on a circle is short (low mean value), medium (medium mean value) or long (high mean). A circle along with rays emanating from it is called a glyph (Fig. 2).

The X and Y-axis of the graph are also demarcated into low, medium and high mean values as shown in Fig 1. This divides the entire graph into nine quadrangles, each quadrangle representing one variability group. In cowpea, variability was also studied by various workers (Nagalakshmi et al., 2010; Singh et al., 2010; Kumar et al., 2015; Sanjeev et al., 2015). The sufficient variations were founded within a group as well as among the groups.

In general, the worth of an individual genotype was assessed from the sum of index scores for all the traits represented in the graph. Highest total index score (76) was obtained for 1000 seed weight. The genotype, PL-3 Sel. of cluster III had the highest total index score (13) which grouped into high score for seed yield/plant, number of pods/plant, number of seeds/pod and high score for number of seeds/plant. In cluster I, genotype DCS 47-1 had the lowest total index score (6) which distributed into low score for score for seed yield/plant, number of pods/plant, number of seeds/pod, dry fodder yield/plant and medium score for 1000-seed weight/plant.

In cluster IV genotypes GC 1110, KCB 9 and DC 7-15 grouped into medium score for seed yield per plant as well as for dry fodder yield per plant. In cluster III, PL-3 Sel., PGCP 28, TC 161 and CPD 29 showed high score for seed yield per plant and low score for dry fodder yield per plant. In cluster II, the highest number of genotypes (10) was observed which were distributed into medium dry matter yield per plant with low number of tillers per plant. Cluster I observed the lowest number of genotypes (2) which was distributed into low dry fodder yield/plant with low seed yield/plant (Table 3).

The genotypes, KBC 9 and DC 7-15 were placed in the medium fodder-medium grain yield producing group. These genotypes could be utilized for both, fodder as well as grain production. Moreover, the genotypes (UPC 12-007, KBC-6, KBC-8 and GC 901) were included in high fodder- medium grain yield, which had good potential of grain production as well as excellent potential of fodder production. It could be utilized for dual purpose after extensive testing over time and space. Likewise, the genotypes (PL-3 Sel., PCP-07-272, CPD 240 and RC 101) were included in medium fodder-high grain yield, which had good potential of grain production as well as excellent potential of fodder production. It could be utilized for dual purpose after extensive testing over time and space.

None of the genotypes was placed in high fodder-high grain yield. This may be due to low photosynthetic/physiological efficiency of cowpea genotypes as well as improper translocation and petitioning of photosynthetic components (Vu et al., 2017). So, there is an urgent need to breed for high fodder-high grain so that the maximum fodder as well as grain yield could be obtained simultaneously. Therefore, the hybridization among the diverse genotypes viz., UCP 12-007 (high fodder yield) with PL-3 Sel. (high grain yield) may be suggested for developing dual purpose genotypes through the transgressive segregation.

This finding indicated the non-linear relationship of seed yield/plant with dry fodder yield, however, it exhibited positive linear relationship with other contributing traits. Keeping the importance of seed yield contributing traits in consideration, these genotypes may be used in further yield improvement. These results support our contention that groupings made on the basis of metroglyph of diagnostic features contribute towards preliminary identification of diversity grouping of breeding entries which have undergone random mating for several generations and also for their worth in the breeding programme.

Conclusions

It was concluded from the present study that the cowpea genotype, UCP 12-007 was high in the fodder and PL-3 Sel. was the highest in seed yield production and could be used for commercial cultivation after testing over time and space. Moreover, genotype (CPD 240) was included in medium fodder-high seed yield, which had excellent potential of seed production as well as good potential of dry fodder production. It could be utilized for dual purpose after extensive testing over time and space.

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Table 1. List of genotypes utilized during experiment

Sr. No.	Genotype	Sources	Sr. No.	Genotype	Sources
1.	PL-3 Sel.	Pant Nagar	16.	KBC-8	UAS, Bangalore
2.	GC 1203	Gujarat	17.	Goa Cowpea-3	Goa
3.	PGCP 28	Pant Nagar	18.	Pant Lobia-3	Pant Nagar
4.	TC 161	Tamil Nadu	19.	DCS 47-1	Dharward
5.	RC 101	Rajastan	20.	KBC-6	UAS, Bangalore
6.	CPD 240	NAU, Navsari	21.	GC 1207	Gujarat
7.	KBC 10	UAS, Bangalore	22.	TPTC-29	Andha Pradesh
8.	CPD 29	NAU, Navsari	23.	PCP-07-272	Rahori
9.	UCP 12-007	Uttar Pradesh	24.	TC 150	Tamil Nadu
10.	GC 1304	Gujarat	25.	KBC 9	UAS, Bangalore
11.	VCP 09-019	-	26.	PGCP-54	Pant Nagar
12.	DC 7-15	Dharward	27.	GC 901	Gujarat
13.	Chirodi	-	28.	PGCP-23	Pant Nagar
14.	CS 88	HAU, Hisar	29.	GC1110	Gujarat
15.	PTB-1	Pattampi	30.	GC-3	Gujarat

Source: Department of Agricultural Meteorology, CCS Haryana Agriculture University, Hisar.

Figure 1. Agro-meteorological data recorded during the period of experimentation from May to October, 2017. (Source: Department of Agricultural Meteorology, CCS Haryana Agriculture University, Hisar.)

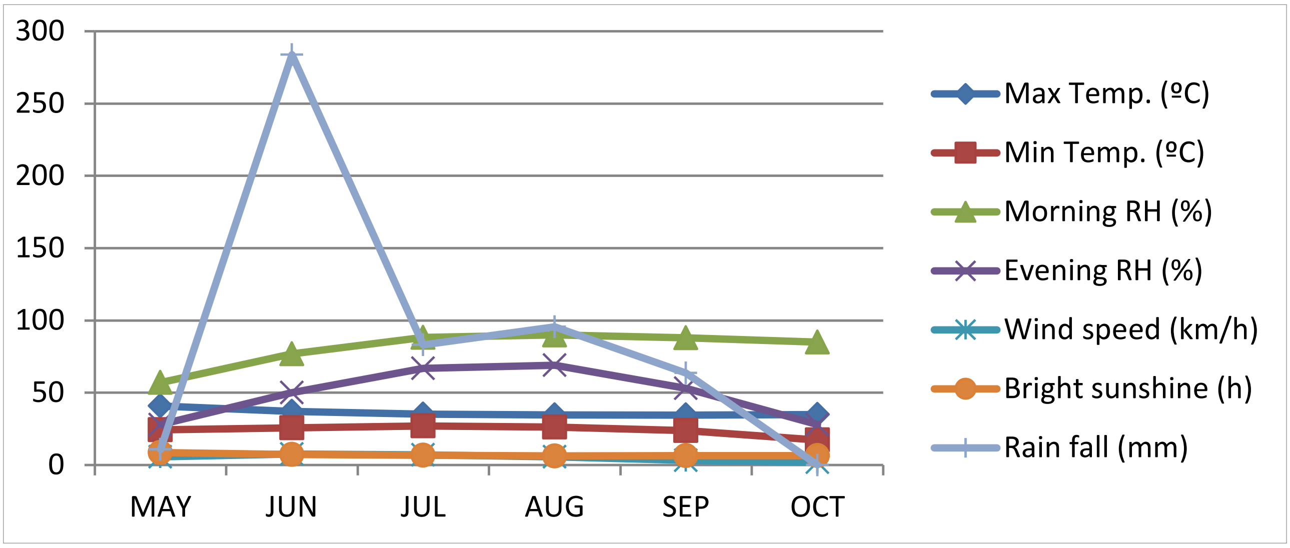

Figure 2. Meteroglyph analysis in cowpea. Grain yield (kg/ha) is used as the X-axis, while the other trait fodder yield (kg/ha) is plotted on the Y-axis. For each genotype, the mean values of X and Y were used to determine its position, which is marked by a small circle. Thus, each genotype is represented by small circle on the graph

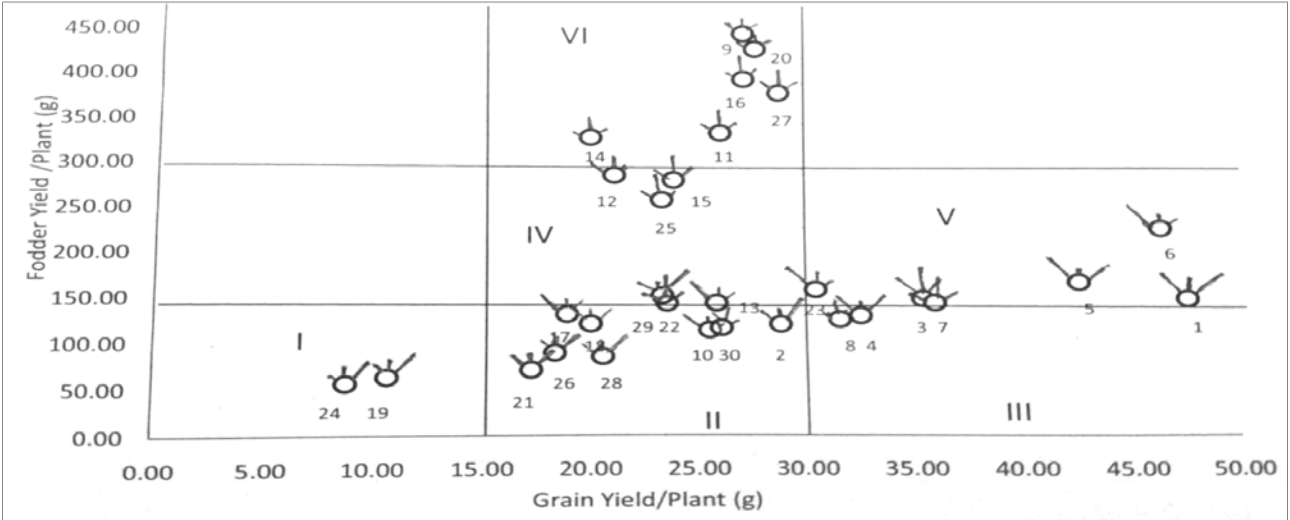

Table 2. Distribution of thirty accessions of cowpea into different clusters

Cluster	Number of accessions	Composition of cluster	Distribution
I	2	DCS 47-1, TC 150	Low dry fodder yield/plant with low seed yield/plant
II	10	GC 1203, GC 1304, Chirodi, Goa Cowpea-3, Pant Lobia-3, GC 1207, TPTC-29, PGCP-54, PGCP-23, GC-3	Low dry fodder yield/plant with medium seed yield/plant
III	3	TC 161, CPD 29, KBC 10	Low dry fodder yield/plant with high seed yield/plant
IV	4	DC 7-15, PTB-1, KBC 9, GC1110	Medium dry fodder yield/plant with medium seed yield/plant
V	5	PL-3 Sel., RC 101, PGCP 28, CPD 240	Medium dry fodder yield/plant with high seed yield/plant
VI	6	UCP 12-007, VCP 09-019, CS 88, KBC-8, KBC-6, GC 901	High dry fodder yield/plant with medium seed yield/plant

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