SHORT COMMUNICATION

STUDIES ON METEROGLYPH ANALYSIS IN COWPEA [*VIGNA UNGUICULATA* (L.) WALP]

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SUMMARY

The present experiment was carried out at Research Farm, CCSHAU, Hisar during **kharif** 2015 to evaluate the performance of newly developed 30 genotypes of cowpea under prevailing Haryana agro-climatic conditions. Both within between group variation was studied. The group low fodder-medium grain yield had maximum genotypes i. e. RC-101, GC-13-1, TC-142, TC-141, PGCP-11, KBC-5, GC-5, Pant lobia-3, while CP-05040, GPCP-28, PGCP-24 and GC-1105 having considerable value for grain yield. However, in low fodder-high grain yield group only one genotype i. e. PGCP-2-3 was placed. It had high value for grain production and could be utilized for cowpea grain production after testing over time and space. The medium fodder-low grain yield producing group included only six genotypes i. e. KBC-6, KBC-8, KBC-7, KBC-9, PTB-1 and DC-16 which could be utilized for further improvement of the fodder yield. However, only three genotypes, viz. KBC-5, Goa Cowpea-3 and GC-901 were included in the high fodder-low grain yield production and could be utilized for cowpea fodder production after testing over time and space. The genotype TPTC-29 was included in medium fodder-medium grain yield and one genotype (GC-1106) was included in medium fodder-high grain yield, which had excellent grain production as well as good potential for fodder production. It could be utilized for dual purpose after extensive testing over time and space.

Key words : Cowpea, meteroglyph analysis, fodder yield, grain yield

Cowpea [*Vigna unguiculata* (L.) Walp.] is considered as one of the most important forage/pulse crops and generally grown in rainy season. But, now-a-days, it is also cultivated in spring/summer season. It can withstand to drought up to some extent, but responds well to irrigation and other management practices. It is gaining importance due to its multi-purpose use. 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).

Genetic diversity is the primary requirement for a successful breeding programme. Collection and evaluation of genotypes is a pre-requisite for crop improvement, which provides a greater scope for exploiting genetic diversity. The assessment of diversity in germplasm gives essential and effective information to breeder for further genetic improvement of yield (Nagalakshmi *et al.*, 2010)

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 important biometrical techniques viz. many, D^2 statistics, principal component analysis (PCA) and meterolygraph analysis, etc. Out of these, meterolygraph analysis is simple and semi-graphic method to assess the variability present in a large number of germplasm lines taken at a time. Anderson (1957) developed this technique to investigate the pattern of morphological variations in crop plants.

The experimental material comprising 30 diverse genotypes including check were obtained from the different research stations located in different parts of India. The experiment was planned and carried out in augmented design during **kharif** 2015, in research area

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of Forage Section, Department of Genetics & Plant Breeding, CCS Haryana Agricultural University, Hisar (latitude 29°10′N, longitude 75°40′E and altitude 215.2 m). The soil of Hisar is sandy loam. Each genotype was sown in paired rows, with 4 m row length, spaced 45 cm apart, with plant to plant distance of 15 cm. The sowing of experiment was done by dibbling method on 25 July, 2015 and all the recommended package of practices were adopted to raise the good crop. 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 suggested 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).

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 cowea. 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 (≤17), medium (18-24) and high (≥25). Likewise, for number of seeds/pod the genotypes were also classified as low (≤7), medium (7-10) and high (≥11). Similarly, for 1000-seed weight (g) the genotypes were grouped as low (≤12 g), medium (12-15 g) and high (≥15 g). 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. 1). The worth of an individual genotype is assessed from the sum of index scores for all the traits represented in the graph. The genotypes TPTC-29, KBC-7 and DC-16 were having the maximum score 8 and PGCE-23, GC-3, GC-1106, CG-13-1, KBC-4, KBC-6, TC-141, Goa Cowpea-3, KBC-8 and PGCL-

TABLE 1
Cowpea genotypes used in the present study

| S. No.	Genotypes	Source
1.	RC-101	Rajasthan
2.	GC-3	Gujarat
3.	Phule CP-05040	-
4.	GC-901	Gujarat
5.	KBC-4	UAS, Bangalore
6.	PCP-0306	-
7.	TPTC-29	-
8.	GC-13-1	Gujarat
9.	TC-142	-
10.	KBC-6	UAS, Bangalore
11.	CPD-172	-
12.	GC-1106	Gujarat
13.	PGCP-24	-
14.	PGCP-23	-
15.	GC-1105	Gujarat
16.	PGCP-11	-
17.	KBC-9	UAS, Bangalore
18.	PGCP-27	-
19.	TC-141	-
20.	GC-1110	Gujarat
21.	CPB-165	-
22.	KBC-7	UAS, Bangalore
23.	Goa Cowpea-3	Goa
24.	KBC-8	UAS, Bangalore
25.	PGCP-12	-
26.	KBC-5	UAS, Bangalore
27.	PTB-1	Pattambi
28.	Pant Lobia-3	Pantnagar
29.	DC-16	-
30.	PGCP-28	-
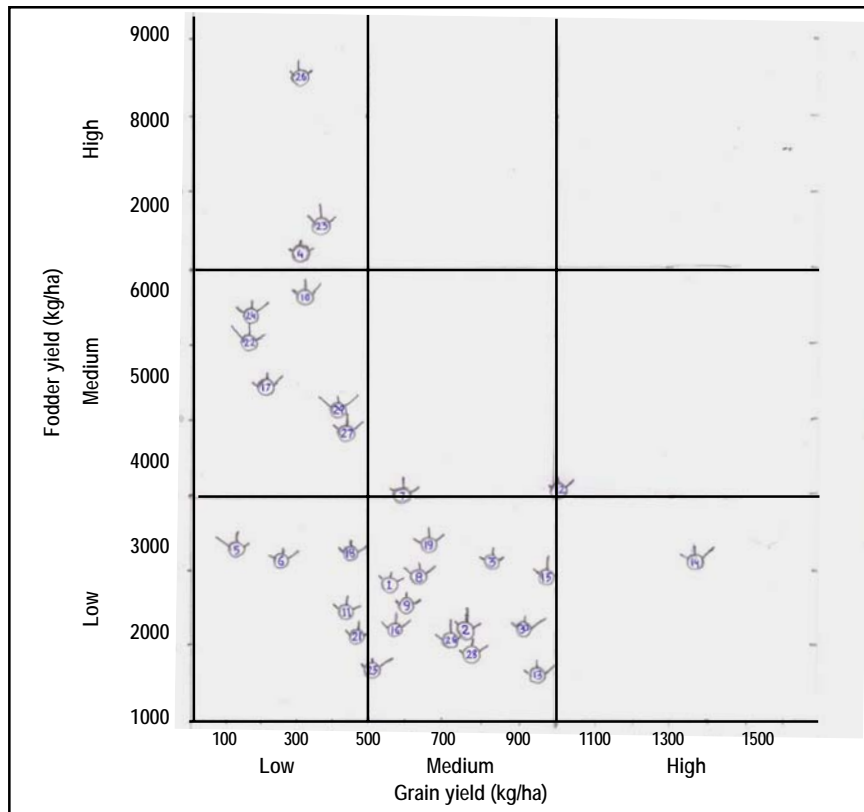
Fig. 1. Meteroglyph analysis in cowpea. Grain yield (kg/ha) is used as the X-axis, while the other trait fodder yield (kg/ha) is plotted on the Y-axis. For each genotype, the mean values of X and Y were used to determine its position, which is marked by a small circle. Thus, each genotype is represented by small circle on the graph.

28 exhibited the score-7. Keeping the importance of grain yield contributing traits in consideration, these genotypes may be used in further yield improvement programme.

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 variation was studied within a group as well as among the groups. The low fodder-low grain yield group had five genotypes viz., KBC-4, PCP-0306, CPD-172, PGCP-27 and CPB-165 having low value for fodder as well as grain yield. The present study revealed that the group low fodder-medium grain yield had maximum genotypes i. e. RC-101, GC-13-1, TC-142, TC-141, PGCP-11, KBC-5, GC-5, Pant lobia-3, while, CP-05040, GPCP-28, PGCP-24 and GC-1105 having considerable value for grain yield. However, in low fodder-high grain

yield group only one genotype i. e. PGCP-2-3 was placed. It had high value for grain production and could be utilized for cowpea grain production after testing over time and space.

The medium fodder-low grain yield producing group included only six genotypes i. e. KBC-6, KBC-8, KBC-7, KBC-9, PTB-1 and DC-16, which had substantial value for fodder yield production and could be utilized for further improvement for fodder yield. However, only three genotypes viz., KBC-5, Goa Cowpea-3 and GC-901 were included in the high fodder-low grain yield production and could be utilized for cowpea fodder production after testing over time and space.

Only one genotype TPTC-29 was placed in the medium fodder-medium grain yield producing group. This genotype could be utilized for both, fodder as well as grain production. Likewise, the only genotype (GC-1106) was included in medium fodder-high grain yield, which had excellent potential of grain production as well

as good 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 group high fodder-medium grain yield and 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 photosynthic components. So, there is an urgent need to breed for high fodder-high grain-medium fodder-high grain or high fodder and medium grain yield so that the maximum fodder as well as grain yield could be obtained simultaneously. Therefore, the hybridization among the diverse genotypes viz., GC-901 (high fodder yield) with GC-1106 (high grain yield) may be suggested for developing dual purpose genotypes through the transgressive segregation.

CONCLUSIONS

It was concluded from the present study that the genotype GC-901 was high in the fodder and GC-1106 was the highest in grain yield production and could be used for commercial cultivation after testing over time and space. Moreover, genotype (GC-1106) was included in medium fodder-high grain yield, which had excellent potential of grain production as well as good potential of fodder production. It could be utilized for dual purpose after extensive testing over time and space.

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