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CHARACTERIZATION OF ELITE FORAGE COWPEA GENOTYPES FOR VARIOUS DUS TRAITS

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SUMMARY

Present investigation was carried out to characterize 20 forage cowpea genotypes on the basis of various morphological characters which were mentioned in cowpea germplasm catalogue of International Institute of Tropical Agriculture catalogue. The investigation was conducted in two environmental conditions. Results revealed that all the genotypes showed same expression in both the environments and found significant amount of variation among the genotypes for various morphological characters. All genotypes showed indeterminate type of main stem and raceme type of layer in canopy; whereas genotypes viz., KBC 2, IC 249141, HC 46, CO 4, EC 3941-1, EC 101980, Kohinoor and CO 5 showed unique state of expression among nine characters viz., incidence of cowpea mosaic virus, seed crowding in pod, texta structure, eye colour, pod shape, pod attachment to peduncle, terminal leaflet shape, twining tendency and flower pigmentation, respectively. While two genotypes HC 46 and EC 3941-1 had wrinkled texta structure with pigmented wings and tan (brown) eye colour with curved pod shape, respectively. Remaining genotypes showed various states of expression in a group of two or more genotypes together. This investigation reveals that classification of genotypes on the basis of DUS traits provided identification of key characteristics of various genotypes which can be used to distinguish them from others and also further investigation of these characters may help to crop improvement programme.

Key words : Cowpea, V*igna unguiculata*, characterization, morphological characters, DUS traits

Cowpea [*Vigna unguiculata* (L.) Walp.] is an important legume crop, which has the ability to do well even in the drought conditions. It has ability to fix atmospheric nitrogen, which allows it to grow effectively in poor soils. It provides nutritious grain and an inexpensive source of protein for both rural poor and urban consumers. Cowpea grain contains about 25% protein and 64% carbohydrate, therefore, has a tremendous potential to contribute to the alleviation of malnutrition among resource-poor farmers, meanwhile, it is more important as the source of green as well as dry fodder. Cowpea is only fodder crop which contains high protein content and rich in lysine and tryptophan amino acids as compared to other fodder crops, so it plays very important role in Indian conditions. Usually, cowpea haulm is used to feed the livestock, which later provides manure for soil (Tarawali *et al.*, 1997).

Like grain yield, fodder yield in cowpea is also a complex character. It depends on the expression of various independent characters. Therefore, selection on the basis of one or more characters may not necessarily lead to the improvement in forage yield. Moreover, improvement in forage crop has to be considered in terms of quality of forage, forage yield, palatability and animal performance which are to be taken into consideration simultaneously. It is, therefore, essential to know the association of various quantitative as well as qualitative characters in order to initiate an effective selection programme aiming at the improvement of yield and quality of the forage. Characterization, collection and evaluation of germplasm, quantification of the magnitude of variability existing for different characters and classification into groups help in identifying distinct genotypes which are having contrasting characters, can be used to operate effective selection for the improvement of crop yield potential. Keeping these aspects in view, the present study was initiated for evaluating the extent of genetic variability existing for different characters in cowpea germplasm collected from different environments.

MATERIALS AND METHODS

The experimental material consisted of 20 forage cowpea genotypes from various parts of India (Table 1). The trial was conducted during the kharif season of 2011 in Research Area, Forage Section, Department of Genetics & Plant Breeding, CCS Haryana Agricultural University, Hisar and KVK Rohtak.

TABLE 1
List of genotypes evaluated along with their sources

S. No.	Genotypes	Source
1.	COFC8	TNAU, Coimbature
2.	EC101980	NBPGR, Delhi
3.	IC249141	NBPGR, Delhi
4.	KOHINOOR	NBPGR, Delhi
5.	CO4	TNAU, Coimbature
6.	CO5	TNAU, Coimbature
7.	TVu 92-2	KAU, Vellanikkara
8.	NDFC-15	NDUA & T, Faizabad
9.	GFC-1	AAU, Gujrat
10.	GFC-2	AAU, Gujarat
11.	GFC-3	AAU, Gujarat
12.	EC 4216	NBPGR, Delhi
13.	EC3941-1	NBPGR, Delhi
14.	HC46	HAU, Hisar
15.	BL2	IGFRI, Jhansi
16.	CO(CP)-7	TNAU, Coimbature
17.	KBC-2	UAS, Bangalore
18.	CS88	HAU, Hisar
19.	GFC-4	AAU, Gujarat
20.	IC528491	NBPGR, Delhi

The data were collected based on the instructions given in cowpea germplasm catalogue by International Institute of Tropical Agriculture, Ibadan, Nigeria. The experiment was conducted in randomized block design (RBD) with three replications. Each genotype was sown in single row of 2 m length with a row to row distance of 60 cm and plant to plant spacing of 10 cm at both the locations. Observations were recorded on 32 morphological characters at seedling, panicle emergence, flowering, physiological and matured seed stages. In case of visually assessed characters for determining (colour of various characters was differentiated by using Royal Horticultural Society Colour Chart) distinctness, differences between two lines were considered clear if the expression of one or more characteristics fell into two different states in the test guidelines.

RESULTS AND DISCUSSION

Characterization and evaluation of variability in germplasm is very vital for any varietal identification and crop improvement programme. Increase in the number of commercially available varieties has created problem in identification of different varieties in field and seed levels. Varietal descriptions provided by the concerned breeders are generally inadequate to characterize a variety or varietal mixture. Therefore, there is a great need to develop keys to identify varietal purity.

The study revealed that on the basis of plant pigmentation the genotypes were divided into two groups viz., moderate on base and tip of petioles (nine genotypes) and extensive (11 genotypes). In case of flower colour, genotype HC 46 had wing pigmentation which was distinct from other genotypes, whereas on the basis of pod colour, three genotypes had pigmentation in tip and all other 17 genotypes had green pods. Similar type of experiment was conducted for the classification on the basis of plant pigmentation, pod and flower colours were previously done by Nkouannessi (2005) in cowpea; Ashok *et al.* (2008) in french bean; Muthaiah (2006) in greengram and Tarasatyvathi *et al.* (2004) in soybean. Great diversity in pigmentation of cowpea was observed. This may be due to the cumulative effect of 1-5 pairs of genes which were involved in the inheritance of plant pigmentation in cowpea (Venugopal, 1998). While genotypes were characterized on the basis of plant growth habit at six weeks after planting and grouped into four categories (acute, erect, semi-erect and semi-prostrate) for plant growth habit. Variation in the growth habit of the genotypes was due to genetic characteristics of the genotypes. Similar results and growth habit were reported by Nkouannessi (2005), Sarutayophat *et al.* (2007) in cowpea and Jain and Khare (2002) in greengram.

Determinant type of main stem is very common in pulses which may lead to decrease in yield. Results in this experiment showed that all genotypes had indeterminate type of growth habit of main stem which could improve the performance of cowpea, but sometimes semi-determinate type of growth also existed which was mainly influenced by environment (Jain and Khare, 2002). Whereas all genotypes had all layers of canopy type of raceme position. On the basis of twining tendency, genotypes were divided in three groups in which CO 5 showed pronounced type of twining

remaining five and 14 genotypes had no and moderate twining, respectively.

Cowpea genotypes were classified into different groups based on pod colour, pod shape, pod attachment to peduncle, leaflet shape and raceme position, expression of these characters are shown in Table 2. These are most important characters in case of cowpea because they are directly contributing to yield of the crop. Performance of a particular genotype depends on their direct/indirect associations of characters which were contributing in growth and development and buffering capacity of the genotype under consideration. Similar types of variation were observed by Stoilva and Berova (2009) and Lingaraj (2009) in cowpea; Gnyandev

TABLE 2
Characterization of 20 elite cowpea genotypes based on characteristics given in guidelines

Characters/genotypes	COFC 8	EC 101980	IC 249141	KOHINOOR	CO 4
Plant pigmentation	Moderate	Extensive	Moderate	Extensive	Moderate
Flower pigmentation	Completely pigmented	Completely pigmented	Completely pigmented	Completely pigmented	Completely pigmented
Pod pigmentation	Tips	None	Tips	None	None
Plant growth habit	Erect	Erect	Semi-erect	Semi-erect	Semi-erect
Twining tendency	Moderate	Moderate	Moderate	Moderate	Moderate
Determinacy	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate
Raceme position	All layers of canopy	All layers of canopy	All layers of canopy	All layers of canopy	All layers of canopy
Terminal leaflet shape	Sub-hastate	Sub-hastate	Sub-hastate	Globose	Sub-hastate
Pod attachment to peduncle	Angle of 30 to 90	Pendant	Angle of 30 to 90	Angle of 30 to 90	Angle of 30 to 90
Pod shape	Straight	Straight	Straight	Straight	Straight
Eye shape	Kubba	Narrow	Kubba	Small	Kubba
Eye colour	Black & blue	Red	Black & blue	Red	Speckling
Texta structure	Smooth	Smooth	Smooth	Smooth	Smooth
Seed length	Intermediate	Short	Short	V. short	V. short
Seed thickness	V. flat	V. flat	V. flat	Thick	V. flat
Extent of seed crowing in pod	Non-crowder	Crowder	Semi-crowder	Extreme crowder	Non-crowder
Incidence of leaf mosaic virus	None	None	None	Yellow mosaic	None
	GFC-3	EC 4216	EC 3941-1	HC 46	BL 2
Plant Pigmentation	Moderate	Extensive	Extensive	Moderate	Extensive
Flower pigmentation	Completely pigmented	Completely pigmented	Completely pigmented	Wing pigmented	Completely pigmented
Pod pigmentation	None	None	None	None	None
Plant growth habit	Erect	Acute	Semi-erect	Erect	Acute
Twining tendency	Moderate	Moderate	Moderate	Moderate	None
Determinancy	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate
Raceme position	All layers of canopy	All layers of canopy	All layers of canopy	All layers of canopy	All layers of canopy
Terminal leaflet shape	Sub-globose	Sub-globose	Sub-hastate	Sub-globose	Sub-hastate
Pod attachment to peduncle	Angle of 30 to 90	Angle of 30 to 90	Angle of 30 to 90	Erect to 90	Angle of 30 to 90
Pod shape	Straight	Straight	Curved	Straight	Straight
Eye shape	Narrow	Small	Holstein	Holstein	Watson
Eye colour	Black & blue	Brown splash	Tan & brown	Brown splash	Brown splash
Texta structure	Smooth	Smooth	Smooth	Wrinkled	Smooth
Seed length	Short	Short	Intermediate	Intermediate	Short
Seed thickness	Flat	V. flat	V. flat	V. flat	V. flat
Extent of seed crowding in pod	Crowder	Non-crowder	Crowder	Non-crowder	Non-crowder
Incidence of cowpea mosaic virus	None	None	None	None	None

contd.

Table 2 contd.

Characters/genotypes	CO 5	TVu 92-2	NDFC-15	GFC-1	GFC-2
Plant pigmentation	Moderate	Moderate	Moderate	Moderate	Extensive
Flower pigmentation	Completely pigmented	Completely pigmented	Completely pigmented	Completely pigmented	Completely pigmented
Pod pigmentation	Tips	None	None	None	None
Plant growth habit	Erect	Erect	Erect	Semi-prostate	Semi-prostate
Twining tendency	Pronounced	None	Moderate	Moderate	Moderate
Determinacy	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate
Raceme position	All layers of canopy	All layers of canopy	All layers of canopy	All layers of canopy	All layers of canopy
Terminal leaflet shape	Sub-globose	Sub-hastate	Sub-hastate	Sub-hastate	Sub-globose
Pod attachment to peduncle	Angle of 30 to 90	Angle of 30 to 90	Angle of 30 to 90	Angle of 30 to 90	Angle of 30 to 90
Pod shape	Straight	Straight	Straight	Straight	Straight
Eye shape	Small	Watson	Holstein	Watson	Watson
Eye colour	Brown splash	Brown splash	Brown splash	Brown splash	Brown splash
Texta structure	Smooth	Smooth	Smooth	Smooth	Smooth
Seed length	Intermediate	Short	Short	Short	Short
Seed thickness	V. flat	V. flat	V. flat	V. flat	V. flat
Extent of seed crowing in pod	Non-crowder	Extreme crowder	Non-crowder	Non-crowder	Non-crowder
Incidence of leaf mosaic virus	Yellow mosaic	None	None	None	None

Characters/genotypes	CO(CP)-7	KBC-2	CS 88	GFC-4	IC 528491
Plant pigmentation	Extensive	Extensive	Extensive	Extensive	Extensive
Flower pigmentation	Completely pigmented	Completely pigmented	Completely pigmented	Completely pigmented	Completely pigmented
Pod pigmentation	None	None	None	None	None
Plant growth habit	Erect	Erect	Semi-prostate	Semi-prostate	Semi-prostate
Twining tendency	None	None	Moderate	Moderate	None
Determinancy	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate
Raceme position	All layers of canopy	All layers of canopy	All layers of canopy	All layers of canopy	All layers of canopy
Terminal leaflet shape	Sub-hastate	Sub-hastate	Sub-hastate	Sub-hastate	Sub-hastate
Pod attachment to peduncle	Erect to 90	Angle of 30 to 90	Angle of 30 to 90	Angle of 30 to 90	Angle of 30 to 90
Pod shape	Straight	Straight	Straight	Straight	Straight
Eye shape	Watson	Small	Narrow	Watson	Watson
Eye colour	Brown splash	Brown splash	Brown splash	Black & blue	Brown splash
Texta structure	Smooth	Smooth	Smooth	Smooth	Smooth
Seed length	Short	Short	V. short	Short	Short
Seed thickness	Flat	V. flat	Thick	V. flat	Flat
Extent of seed crowding in pod	Crowder	Non-crowder	Extreme crowder	Non-crowder	Non-crowder
Incidence of cowpea mosaic virus	None	Green mottle	None	None	None

(2009) in chickpea and Suhasini (2006) in sesame. Based on eye pattern, genotypes were classified into five categories (Watson, holstein, small eye group, narrow eye and kabba group). On the basis of eye colour, genotypes were divided into five groups (black and blue, speckling, tan and brown, red, white and creamy gray). However, on the basis of seed length and seed thickness, genotypes were divided into three groups. In case of extent of seed crowding, all genotypes were divided into four groups but texta texture had two classes. The variation among the genotypes for various seed characteristics may be due to inherent genotypic differences that had existed during the crop growth, seed development and maturation and capacity to utilize reserve food material. The results of the present findings are similar to those of Negri *et al.* (2000), Iqbal *et al.*

(2003) and Muhammad *et al*. (2010). The main constraint of cowpea is incidence of yellow mosaic virus which causes tremendous loss in crop production. In this investigation, 17 genotypes showed none incidence of this disease, but genotype KBC-2 had green mottle leaves and remaining two genotypes viz., Kohinoor and CO 5 had incidence of yellow mosaic in their leaves. None incidence of yellow mosaic virus in these 17 genotypes may be due to their genetic potential to resist this disease, which could be used in crop improvement programme to increase the production potential of forage cowpea as well as vegetable cowpea by introgression of resistance gene in the elite genotypes. Finally, characterization of various forage cowpea genotypes leads to identification of elite genotypes with unique characteristics. Utilization of these genotypes with their unique characteristics in breeding programmes may boost the yield as well as resistance to biotic and abiotic stresses of forage cowpea.

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