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# Comparative evaluation of cowpea (Vigna unguiculata L.) genotypes for nutritional quality and antioxidant potential

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#### **Abstract**

Ten cowpea genotypes were evaluated for better fodder quality, antioxidant and yield potentials. The average content of crude protein, neutral detergent fibre, acid detergent fibre, crude fibre, ash and ether extract was 16.63, 48.15, 36.10, 28.44, 10.54 and 2.91%, respectively. The average sugar and starch content was observed 20.45 and 32.31 mg/g, respectively. The phenol, tannin and flavonoid content was positively correlated with 2, 2diphenyl-1-picryl hydrazyl free radical scavenging activity (P<0.05) and total reducing power (P<0.01). Saponin content was positively correlated with nitric oxide radical scavenging activity. Among all genotypes, UPC-628 genotype had low phenol and flavonoid content and C-88 had low tannin and saponin contents, respectively. The green fodder, dry matter and crude protein yields were found maximum in PFC-39, PFC-40 and PFC-12 genotypes, respectively. Nutritionally superior genotypes could be involved in breeding programme with high vielding genotypes PFC-39 and PFC-40 to develop nutritionally rich and high yielding genotypes.

**Keywords:** Antinutritional components, Antioxidant potential, Cowpea, Fodder quality, Fodder yield

## Introduction

India is an agricultural country and approximately 3/4<sup>th</sup> population dwell in little more than 6 lakh villages. The total area under cultivation is about 169.7 million hectares. India has nearly 4.9% of total cultivated area under forages. Cowpea (*Vigna unguiculata* L.) is an important *Kharif* legume crop, belongs to the *Fabaceae* family. It is widely cultivated in the tropical and subtropical regions. In India, area under cowpea cultivation is 3.9 million hectares (Singh *et al.*, 2012). Cowpea contains maximum protein content and also rich in carbohydrates, fats, important minerals, vitamins, phenolic compounds, unsaturated fatty acids and antioxidants (Liyanage *et al.*, 2014). Nutrient balance is reliant on the nutritional quality of feed stuff and its digestibility. The protein quality of

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forage cowpea is negatively affected by the presence of antinutritional factors such as protease inhibitors, phytic acid, saponins, flavonoids, tannins and phenols. These antinutritional factors impair the digestibility of carbohydrates, proteins and minerals thereby limiting their nutrient utilization and decreasing the food quality (Kaur *et al.*, 2014). Tannins reduce the palatability of the feed and lower protein digestibility. Several cases of livestock death have been associated with high tannin content of some foliage (Bharathidhasan *et al.*, 2013).

Free radicals generated in several biochemical reactions are mediators of many diseases and cause structural and functional damage to protein, lipid, nucleic acid and cellular molecules (Kumaran and Karunakaran, 2007). Antioxidant components scavenge free radicals and reactive oxygen species thus cause inhibition of degenerative diseases (Zia-UI-Haq et al., 2012). Different methods have been used to measure antioxidant potential of cowpea, including 2, 2-diphenyl-1-picryl hydrazyl (DPPH) radical scavenging activity, ferric reducing antioxidant power, total reducing power, nitric oxide and hydroxyl radical scavenging activity. The antioxidant capacity, antimutagenic activity and antiproliferative effects of legumes have been associated with the presence of phenolic compounds (Dong et al., 2007). There is need to evaluate and identify genotype with high fodder yield and low antinutritional content so as to involve in breeding programme to develop better genotypes. Genotypes with maximum nutritional composition and antioxidant potential are helpful in increasing milk yield and lowering the risk of diseases caused by free radicals. Keeping this in mind the present investigation was aimed to evaluate different cowpea genotypes with respect to nutritional, antinutritional, antioxidant and yield potentials.

## **Materials and Methods**

**Experimental design:** The present investigation was carried out on ten different cowpea genotypes. The CL-

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367 and CL-88 are the released varieties and PFC-12, PFC-39 and PFC-40 are cowpea genotypes of Punjab Agricultural University, Ludhiana. The BL-1 and BL-2 are recommended varieties of Indian Grassland and Fodder Research Institute, Jhansi. The Arka garima genotype was developed by Central Coastal Agriculture Research Institute, Goa. The Pusa sampada and UPC-628 was developed by Indian Agricultural Research Institute, New Delhi and Gobind Ballah Pant University of Agricultural Technology, Pantnagar, respectively. Cowpea crop was raised in the experimental area of Forage Research Farm, Department of Plant Breeding and Genetics, Punjab Agricultural University, Ludhiana in July, 2016. The crop was planted in plots with 3.5 m bed length in three replications using randomized block design (RBD). Each plot consisted of 4 rows with row to row spacing 30 cm.

Sampling and laboratory analysis: For biochemical and quality analysis, five random plants from each plot were harvested at flowering stage and cut into small pieces. A 500 g sample was dried in a hot air oven at a temperature of 55°-65° C followed by processing in a grinding machine. Fodder samples were dried in hot air oven and then grinded for further analysis. The crude protein, crude fibre, ash content and ether extract were estimated as per AOAC (2005). Cell wall components (ADF and NDF) were estimated by Van soest et al. (1991). In-vitro dry matter digestibility content was estimated from protocol given by Tilley and Terry (1963). Total soluble sugars and starch content were estimated by Dubois et al. (1956). Standard curve was prepared by using glucose (10-100 µg) as a standard. Total phenols were estimated as per Swain and Hillis (1959). Tannins were estimated from protocol given by Sadasivam and Manickam (1992). Both phenol and tannin concentrations were expressed as tannic acid equivalents. Flavonoid was estimated as per Chang et al. (2002). The results were expressed as mg of rutin equivalents (RE/g). Saponins were estimated from the protocol given by Fenwick and Oakenfull (1983).

DPPH activity was determined by the method of Blois (1958). The percentage inhibition of reaction mixture was measured against reagent blank at 515 nm. Ferric reducing antioxidant power (FRAP) was determined by the method of Benzie and Strain (1996). The FRAP activity was calculated from standard curve of iron sulphate heptahydrate (5–30  $\mu$ g) run simultaneously. Total reducing power was determined by the method of Sreeramulu *et al.* (2009). The absorbance of reaction mixture was measured spectrophotometrically at 700 nm against reagent blank. Ascorbic acid (5–40  $\mu$ g) was used

as a standard. The hydroxyl ion radical scavenging activity was determined by the modified method of Li *et al.* (2008). Nitric oxide radical scavenging activity was estimated by the method of Marcocci *et al.* (1994). Free radical scavenging activity was calculated as follows:

Scavenging activity (%) = 
$$\frac{\text{Abs. (control) -Abs. (test)}}{\text{Abs. (control)}} \times 100$$

**Statistical analysis:** Statistical analysis was performed by using SAS package (Version 9.3). Mean and standard deviation were calculated and Tukey's test was used to identify the significant differences among the genotypes. Pearson correlation test was conducted to determine correlation among variables. Significant levels were defined using (P<0.05).

## **Results and Discussion**

Nutritional components: A significant (P<0.05) variation was observed between different cowpea genotypes with regard to quality traits (Table 1). Protein is an important trait in fodders as it is required for the growth, development and production of ruminant animals. The crude protein content (%) was ranged from 13.53 to 20.66 with an average value of 16.63. The results were in accordance with previous studies on cowpea fodder (Devasena et al., 2009; Sallam and Ibrahim, 2016). The protein content of other leguminous forages in Rabi season varied from 18.5 to 21.8% (Goyal et al., 2017). Generally high protein forages are more digestible and provide more energy. The in-vitro dry matter digestibility (IVDMD) was found positively correlated with crude protein (P<0.01, r=0.908\*\*) (Table 5) and found maximum in PFC-12 genotype. Acid detergent fibre and neutral detergent fibre are major indicators of digestibility and negatively affects feed quality (Eskandari et al., 2009). The ADF and NDF content was positively related with each other (P<0.01, r= 0.862\*\*). The ADF and NDF content (%) varied significantly from 27.10 to 41.83 and 38.3 to 52.4, respectively. The minimum ADF and NDF content was exhibited by Pusa sampada genotype. Our results were in accordance with previous studies on ADF content in cowpea (Devasena et al., 2009; Dahmardeh et al., 2009) and NDF content in cowpea (Prusty et al., 2013). The crude fibre (CF) content was found maximum in UPC-628 and negatively correlated with IVDMD content (P<0.05). The average content of ash and ether extract was found to be 10.54 and 2.91%, respectively. The ash content of ten different cowpea fodder genotypes varied from 9.97 to 12.20% (Mahala et al., 2014). The average sugar and starch content was observed 20.45 and 32.31 mg/g, respectively. Among all genotypes, Pusa sampada

32.31

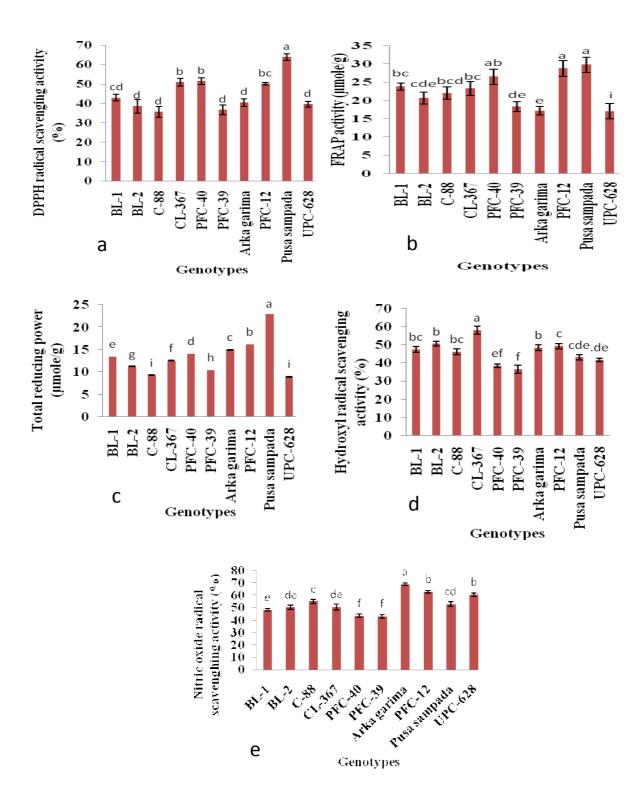
37.67±0.75ab 39.95±1.34ª 25.60±0.96cd 23.69±0.36d 29.24±1.58° 27.70±0.68° 34.01±1.47<sup>b</sup> 35.72±0.97<sup>t</sup> 35.66±1.24<sup>t</sup> 33.92±2.70<sup>t</sup> content (mg/g) sugars (mg/g) **Total soluble** 12.55±0.28<sup>de</sup> 14.20±0.27<sup>d</sup> 17.71±0.67° 13.10±0.30de 40.88±0.87<sup>b</sup> 16.67±0.35° 47.73±0.66ª 11.87±0.84e 20.45 13.37±1.06de 16.43±0.60° 3.01±0.03⁴ 3.59±0.15<sup>b</sup> 2.21±0.10<sup>f</sup> 2.76±0.10<sup>d</sup>  $4.15\pm0.06^{a}$ 2.43±0.09ef 3.03±0.05cd 1.87±0.099 3.32±0.11bc 2.74±0.18de extract (%) 10.69±0.14<sup>∞</sup> 11.01±0.29bc 9.91±0.23ef 11.39±0.17ab 10.13±0.17<sup>def</sup> 10.46±0.23 cde 10.59±0.20<sup>∞d</sup> 9.68±0.12f 9.76±0.21<sup>f</sup> 10.54  $11.79\pm0.20^{a}$ Ash (%) 32.60±0.76bc 33.62±0.36ab 27.32±0.93d 28.51±0.38cd 21.23±0.649 27.41±1.06d 23.53±1.05f 28.44 25.83±0.61e 29.66±1.66° 34.69±0.60ª fibre (%) Table 1. Study of nutritional composition of different fodder cowpea genotypes 50.92±0.85ab 48.15 50.15±0.54<sup>bc</sup> 50.72±0.42bc 46.73±0.26d 38.38±0.35f 52.43±0.34ª 47.06±0.49d 51.02±0.98ab 44.85±0.69e 49.21±0.58° detergent fibre (%) Neutral 36.10 40.61±0.20<sup>b</sup> 39.53±0.24° 37.70±0.34d 30.25±0.299 35.66±0.30e 37.66±0.26d 37.35±0.33d 27.10±0.22h 41.83±0.18ª  $33.29\pm0.72^{\dagger}$ detergent fibre (%) 73.41±0.49bc 70.44±0.59d 71.56±0.51d 74.13±0.83ab 75.82±0.92ª 59.81±0.929 69.29 72.10±0.83<sup>cd</sup> 67.21±0.60e 65.62±0.98e 62.79±0.40f (%) QWQAI Values are mean ± SD of triplicates 16.47±0.18cd 13.53±0.229 16.63 16.71±0.36cd 16.01±0.17° 7.52±0.36cd 15.54±0.36e 19.23±0.23b 20.66±0.28ª 16.10±0.18<sup>de</sup> 14.55±0.25f protein (%) Pusa sampada Arka garima Genotypes **UPC-628** PFC-12 PFC-39 PFC-40 CL-367 Mean C-88 BL-2

Values with different letters in the same column are significantly different (P<0.05)

genotype exhibited maximum sugar content followed by Arka garima genotype. Starch content was found maximum in BL-2 which was statistically at par with BL-1 genotype.

Antinutritional components/factors: A significant (P<0.05) difference was reported among fodder genotypes for antinutritional factors (Table 2). Total phenols (mg/g) ranged from 1.55 to 3.73 with an average value of 2.29. The maximum phenol content was observed in Pusa sampada genotype which was statistically at par with Arka garima genotype. Genotypes with low phenolic content are preferred for nutritional purpose, as they are known to decrease the digestibility of proteins, minerals and carbohydrates (Sahoo et al., 2016) and also lower the activity of digestive enzymes (Othman et al., 2007). The genotypes with high phenols are beneficial to crops against insect/pest resistance and also as a source of bioactive compounds (Xu and Chang, 2008). Tannin content (mg/g) among different forage genotypes was varied from 1.04 to 2.37 with mean value of 1.59. The concentration of condensed tannins above 4 per cent is toxic for ruminants as they are harmful to a variety of rumen microbes (Waghorn et al., 1994). In our study, total tannin content of cowpea genotypes was much lesser than 4% so may be considered nutritionally good for livestock consumption. Total flavonoid content (mg/g) revealed significant variation from 2.91 to 6.68 with mean value of 4.18. The maximum flavonoid content was found in Pusa sampada and minimum in UPC-628. The accumulation of flavonoids in external cells acts as UV-screen and protects the plant from harmful radiations (Agati et al., 2012). Flavonoids combat oxidative stress in plants by quenching and inhibiting the generation of reactive oxygen species. They also act as protectants of plants from insect and pest infestations by influencing their behavior, growth and development (Harbourne, 1993). The phenol, tannin and flavonoid content was found to be positively correlated with DPPH free radical scavenging activity (P<0.05) and total reducing power (P<0.01) (Table 6). Saponin content (mg/g) was ranged from 8.52 to 11.84 and found maximum in PFC-40 genotype which was at par with BL-1 genotype. Saponins also have lytic action on erythrocyte membrane when consumed in larger amounts. Despite of this, they lower harmful LDL-cholesterol level and stimulate immune response (Segal et al., 2003).

Antioxidant potential: 2, 2-Diphenyl-1-picryl hydrazyl (DPPH) scavenging assay is extensively used to test the ability of compounds to act as free radical scavenger of



**Fig 1.** Evaluation of (a) DPPH free radical scavenging activity, (b) total reducing power, (c) FRAP activity, (d) hydroxyl radical scavenging activity and (e) nitric oxide radical scavenging activity in fodder cowpea genotypes. Vertical bars show mean ± SD of triplicates. Values with different letters are significantly different (P<0.05)

hydrogen donors present in fodder extract. In cowpea fodder, DPPH scavenging activity (%) revealed significant variation from 35.54 to 63.81 with an average value of 44.97 (Fig 1). The maximum DPPH scavenging activity was observed in *Pusa sampada* genotype. FRAP activity (mg/g) among different cowpea genotypes varied from

17.03 to 29.74 with an average value of 22.69. The maximum FRAP activity was found in *Pusa sampada* genotype which was at par with PFC-12 and PFC-40 genotypes. Legumes manifest remarkable antioxidant activity (Sinha *et al.*, 2013) and serve as an excellent dietary source of natural antioxidants for prevention of

Table 2. Study of antinutritional factors of different fodder cowpea genotypes

Genotypes	Total phenols (mg/g)	Tannins(mg/g)	Flavonoid(mg/g)	Saponin(mg/g)
BL-1	2.33±0.10 <sup>bcd</sup>	1.54±0.13 <sup>b</sup>	4.11±0.22 <sup>cd</sup>	11.24±0.13 <sup>ab</sup>
BL-2	1.61±0.13e	1.20±0.08°	3.28±0.03 <sup>de</sup>	8.59±0.54 <sup>f</sup>
C-88	1.58±0.28e	1.04±0.12°	3.00±0.42 <sup>e</sup>	8.52±0.15 <sup>f</sup>
CL-367	2.44±0.27bc	1.66±0.14 <sup>b</sup>	4.03±0.14 <sup>cd</sup>	$9.03\pm0.32^{f}$
PFC-40	2.49±0.30 <sup>b</sup>	1.78±0.10 <sup>b</sup>	4.22±0.04°	11.84±0.16°
PFC-39	1.88±0.14 <sup>de</sup>	1.52±0.12 <sup>b</sup>	3.78±0.26 <sup>cde</sup>	10.88±0.15bc
Arka garima	$3.38\pm0.30^{a}$	2.20±0.13 <sup>a</sup>	5.77±0.14 <sup>b</sup>	10.05±0.20 <sup>de</sup>
PFC-12	1.92±0.22 <sup>cde</sup>	1.53±0.15 <sup>b</sup>	$4.07\pm0.25^{cd}$	10.52±0.34 <sup>cd</sup>
Pusa sampada	3.73±0.14 <sup>a</sup>	2.37±0.12 <sup>a</sup>	6.68±0.40 <sup>a</sup>	9.81±0.09e
UPC-628	1.55±0.07e	1.10±0.05°	2.91±0.03e	10.10±0.18 <sup>de</sup>
Mean	2.29	1.59	4.18	10.06

Values are mean ± SD of triplicates; Values with different letters in the same column are significantly different (P<0.05)

Table 3. Study of yield parameters of different fodder cowpea genotypes

Genotypes	Plant height (cm)	Vine length (cm)	Number of	Leaf/stem ratio	Dry matter (%)
			leaves per plant		
BL-1	54.3±2.08 <sup>cd</sup>	124.3±6.02 <sup>abc</sup>	69.3±4.04 <sup>ef</sup>	0.88±0.01 <sup>b</sup>	13.0±0.23 <sup>f</sup>
BL-2	61.3±1.15°	124.6±17.89abc	85.6±5.50 <sup>cde</sup>	1.11±0.01a	14.4±0.15 <sup>e</sup>
C-88	73.0±1.00a	136.6±5.77a	43.3±7.63 <sup>g</sup>	$0.36 \pm 0.02^{h}$	14.1±0.30e
CL-367	59.3±1.15°	140.0±8.18ª	93.3±9.45 <sup>cd</sup>	0.72±0.02°	15.5±0.10 <sup>d</sup>
PFC-40	71.3±1.15 <sup>b</sup>	146.3±10.69 <sup>a</sup>	66.3±9.07 <sup>ef</sup>	0.43±0.01g	16.0±0.20°
PFC-39	61.0±1.00°	100.6±9.01cd	75.6±11.01 <sup>def</sup>	0.61±0.02d	14.6±0.26e
Arka garima	71.3±1.52 <sup>b</sup>	103.0±8.18 <sup>cd</sup>	116.7±6.50 <sup>b</sup>	0.71±0.02°	16.1±0.10°
PFC-12	77.0±1.00 <sup>a</sup>	106.6±12.58bcd	218.3±7.63 <sup>a</sup>	0.52±0.01e	16.6±0.15 <sup>b</sup>
Pusa sampada	72.3±2.51 <sup>b</sup>	79.3±3.78d	103.6±5.50bc	0.49±0.02 <sup>f</sup>	17.2±0.15 <sup>a</sup>
UPC-628	71.3±1.15 <sup>b</sup>	133.3±11.5 <sup>ab</sup>	61.0±6.55 <sup>fg</sup>	0.40±0.01 <sup>g</sup>	15.2±0.10 <sup>d</sup>
Mean	67.2	119.5	93.3	0.62	15.2

Values are represented as mean ± standard deviation of triplicates; Values with different letters in the same column are significantly different (P<0.05)

Table 4. Yield data of different fodder cowpea genotypes

Genotypes	Green fodder yield (q/ha)	Dry matter yield (q/ha)	Crude protein yield (q/ha)
BL-1	281.7±17.24 <sup>ab</sup>	36.7±2.24 <sup>ab</sup>	5.9±0.36 <sup>bc</sup>
BL-2	253.9±47.42ab	36.7±6.85 <sup>ab</sup>	6.1±1.14 <sup>abc</sup>
C-88	257.9±24.41ab	36.3±3.44 <sup>ab</sup>	6.2±0.60 <sup>abc</sup>
CL-367	269.8±7.23ab	41.8±1.21 <sup>a</sup>	6.9±0.18 <sup>ab</sup>
PFC-40	285.7±5.50 <sup>ab</sup>	45.8±0.88°	7.1±0.14 <sup>ab</sup>
PFC-39	309.5±13.01°	45.1±1.89 <sup>a</sup>	6.6±0.28 <sup>ab</sup>
Arka garima	47.6±12.05d	7.6±1.93°	1.5±0.33 <sup>d</sup>
PFC-12	230.2±24.97 <sup>bc</sup>	38.2±4.15 <sup>ab</sup>	7.9±0.77ª
Pusa sampada	166.7±24°	28.7±4.14 <sup>b</sup>	4.7±0.68°
UPC-628	265.8±17.89ab	40.4±2.72°	5.5±0.36bc
Mean	236.88	35.7	5.8

Values are represented as mean ± standard deviation of triplicates; Values with different letters in the same column are significantly different (P<0.05)

Table 5. Correlation coefficient between nutritional components and yield of fodder cowpea

	Crude	Crude	Ether	Ash	Nitrogen	Nitrogen Neutral	Acid	In vitro	Soluble Starch Green	Starch	Green
	protein	fibre	Extract		free	detergent	detergent	detergent detergent dry matter	sugars		fodder
					extract	fibre	fibre	digestibility			yield
Crude fibre	**677.0-										
Ether Extract	-0.263	0.156									
Ash Content	0.451	0.022	0.039								
Nitrogen free extract	0.412	0.412 -0.869**	-0.254	-0.439							
Neutral detergent fibre	-0.176	-0.019	-0.545	-0.527	0.335						
Acid detergent fibre	-0.369	0.273	-0.234	-0.519	0.008	0.862**					
In vitro dry matter digestibility 0.908**	**806.0	-0.653*	-0.205	0.559	0.297	-0.036	-0.234				
Soluble sugars	0.268	-0.220	0.278	0.269	-0.007	-0.806**	-0.899**	0.071			
Starch	0.044	0.355	0.216	0.662*	-0.623	-0.370	-0.259	0.193	0.016		
Green fodder yield	-0.432	0.423	-0.017	-0.197	-0.237	0.421	*679.0	-0.349	-0.828**	0.230	
Dry matter yield	-0.396	0.356	-0.037	-0.248	-0.179	0.401	0.655*	-0.393	-0.757*	0.186	0.966**
*Significant at 5% level, **Significant at 1% level	at 1% level										

various diseases and health promotion. Total reducing power of different cowpea fodder genotypes varied significantly from 8.95 to 22.95 µmole/g. The maximum total reducing power was found in Pusa sampada and minimum in UPC-628 genotype. The hydroxyl radical scavenging rate (%) among cowpea genotypes revealed significant variation from 36.47 to 57.95 with an average value 45.91. The maximum hydroxyl radical scavenging capacity was observed in CL-367 and minimum in PFC-40 genotype. Hydroxyl radical scavenging capacity of a plant extract is directly related to its antioxidant activity (Babu et al., 2001). Hydroxyl radical reacts with lipid, polypeptides, proteins and DNA (Manian et al., 2008). The nitric oxide radical scavenging rate (%) among different cowpea fodder genotypes varied significantly from 42.98 to 69.02 with an average value of 53.60. The maximum nitric oxide radical scavenging activity was found in Arka garima genotype and minimum in PFC-39 genotype. In a previous study, 72.48 % and 70.43% DPPH and nitric oxide radical scavenging activity was observed in leaves extract of Leonotis leonurus (L.), respectively.

Nitric oxide is widespread signaling molecule and participates in some cellular functions of the body. It also acts as a neurotransmitter and an important mediator of the immune response (Fang et al., 2002). Nitric oxide radical scavenging activity showed positive correlation with saponin (P<0.05) (Table 6).

Yield parameters: The increase in the yield was mainly due to increasing plant height, stem diameter, number of leaves, leaf area per plant and number of branching per plant (Hasan et al., 2010). Plant height and vine length of cowpea genotypes varied from 54.3 to 77.0 cm and 79.3 to 146.3 cm, respectively (Table 3). Our results on plant height were in agreement with that reported previously for cowpea (Hassan et al., 2010; Kumar and Pandita, 2016). Number of leaves varied significantly and ranged between 43.3-218.3. The variation in performance of the studied cultivars depends on the genetic and environmental factors (Nwosu et al., 2013). Leaf/stem ratio is an important component of determining forage quality. Young plants have high leaf/stem ratio as compared to mature plants. It was varied significantly from 0.36 to 1.11. Our results showed good agreement with previous studies on cowpea leaf/stem ratio (Dhonde et al., 2016; Shekara et al., 2012). Dry matter contnt varied significantly from 13.0 to 17.2%. Dry matter percentage was observed maximum in Pusa sampada genotype and minimum in BL-1 genotype. The results were in accordance with the findings of Devasena et al. (2009).

Table 6. Correlation coefficients between antinutritional factors and antioxidant potential of fodder cowpea

	Phenol	Tannin	Flavonoid	Saponin	DPPH	FRAP	TRP	HRSA
Tannin	0.974**							
Flavonoid	0.974**	0.973**						
Saponin	0.189	0.301	0.185					
DPPH	0.674*	0.691*	0.690*	0.195				
FRAP	0.342	0.372	0.402	0.190	0.823**			
TRP	0.831**	0.847**	0.901**	0.191	0.873**	0.727*		
HRSA	0.034	-0.029	-0.014	-0.579	0.08	0.09	0.02	
NORSA	0.172	0.124	0.204	0.764*	-0.077	-0.192	0.125	0.326

<sup>\*</sup>Significant at 5% level; \*\*Significant at 1% level; TRP: Total reducing power; HRSA: Hydroxyl radical scavenging activity; NORSA: Nitric oxide radical scavenging activity

**Yield:** The green fodder yield (q/ha) of cowpea genotypes revealed significant variation, ranging from 47.6 to 309.5 with an average value of 236.88 (Table 4). The maximum yield was observed in PFC-39 and minimum was in *Arka garima* genotype. Our results were in accordance with previous studies on cowpea green fodder yield (Pal *et al.*, 2014; Sharma *et al.*, 2008; Surve *et al.*, 2012). The dry fodder yield (q/ha) was varied from 28.77 to 45.88 with an average value of 35.77. The maximum dry fodder yield was observed in PFC-40. The maximum crude protein yield was observed in PFC-12 and minimum in *Arka garima*. The DMY and CPY was reported to vary from 30.65-43.40 q/ha and 4.40-6.41q/ha, respectively in cowpea genotypes (Shekara *et al.*, 2012).

## Conclusion

The PFC-12 was considered nutritionally important as it possessed maximum crude protein, *in-vitro* dry matter digestibility, crude protein yield, plant height, leafiness and medium antinutritional factors. The green fodder and dry matter yield was found maximum in PFC-39 and PFC-40 genotypes, respectively. The genotype *Pusa sampada* had possessed maximum DPPH scavenging activity, FRAP activity and total reducing power. High antioxidant activity contributes significantly to the prevention of degenerative diseases associated with free radical damage. The cowpea genotypes with high nutritional value (PFC-12) and high antioxidant potential (*Pusa sampada*) could be involved in breeding programme with high yielding genotypes (PFC-39, PFC-40) for the production of superior genotypes.

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