



Effect of bean common mosaic virus infection on yield potential and nodulation of cowpea genotypes

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Abstract

A study was conducted to assess the effect of *Bean common mosaic virus* (BCMV) disease incidence on yield potential and nodulation of cowpea genotypes. All the genotypes were artificially inoculated with virus inoculum collected from C-152 cowpea plants. The results showed BCMV could interfere with yield potential and rhizobium–cowpea symbiotic relationship. Based on extent of disease incidence, number of nodules plant⁻¹ varied among the genotypes. The resistance control, V-5 produced more of number nodules plant⁻¹ (22.8). The study indicated that genotype, IC 202782 was superior in terms of resistance, 100 seed weight (12.7 g), green fodder yield (17.8 t ha⁻¹) and fodder quality under virus pressure. The genotype, IC 8996 was also found resistant to BCMV infection and good grain yield (15.5 q ha⁻¹) with maximum height (68.3 cm). The statistical analysis showed disease incidence and yield attributes were negatively associated whereas, number of nodules and fodder quality parameters had positive association. The genotypes obtained with superior characteristics in terms of resistance, grain and quality fodder yields, are expected to be useful to growers and to breeding programmes seeking to control yield losses caused by viruses, particularly BCMV.

Keywords: Cowpea, Genotypes, Green fodder, Nodulation, Virus

Introduction

The total cultivated land is becoming scarce and cost of cultivation is increasing drastically because of rise in cost of inputs especially, fertilizer (Ayana *et al.*, 2013). But the increasing demand for food and animal feed resources must be met by raising the productivity of the crops under available cultivable land. Among the crops, legumes are the most important because these improve feed availability for livestock, house hold nutrition and decrease

the cost of cultivation by improving soil fertility (Alemayehu, 1997). In this context, Cowpea is an important legume crop in tropical and subtropical countries (Chinma *et al.*, 2008) because of its wide use as a grain, vegetable and fodder for animals.

Cowpea is considered as the 'hungry-season crop' because it is the first crop to be harvested before the cereal crops are ready. It is a crop that offers farmers great flexibility. They can choose to apply more inputs and pick more beans, or if cash and inputs are scarce - they can pick fewer beans and allow the plant to produce more foliage. This means more fodder for livestock, so that lower bean yields are balanced by more livestock feed, which in turn translates into more meat and milk. This flexibility in use makes cowpea an excellent crop under the challenging climatic conditions faced by farmers (Okike, 2000). The symbiotic association with rhizobium is most important character of cowpea which results in the fixation of the atmospheric nitrogen up to 240 kg/ha and leaves about 60 to 70 kg nitrogen for succeeding crops (Agyeman, 2015). Since nitrogen is a key element required for plant growth and the symptoms of its deficiency range from poor yield to crop failure (Lugtenberg, 1992).

Apart from this mutually beneficial relationship between crop plant and microorganisms, plant-microbe interaction could also result in harmful relationship, which may trigger crop failure (Oyatokun *et al.*, 2013). The interaction between virus and plants is one among them. Viruses are biological enigma and are strictly biotrophs. Out of 20 viruses of the cowpea *Bean common mosaic virus* (BCMV) is more prevalent in cowpea growing areas (Hughes and Shoyinka, 2003). The interaction between plants and microorganisms has been studied for both isolated and complex systems. Because of symbiotic association between cowpea and rhizobium there is a possibility of

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indirect interaction between BCMV and rhizobium. The detailed knowledge about this relationship or the interactive effects of plant microbes (beneficial or harmful) may attribute to improving the productivity and development of new biological methods for the plant protection or for increasing yields. Hence, the present study was undertaken to assess the yield potential and nodulation of different cowpea genotypes under BCMV pressure.

Materials and Methods

Experimental site: This study was conducted at the main research station (MRS), University of Agricultural Sciences, Bengaluru, India during 2013-14. The area is 899 m above mean sea level. The soil is red sandy loam (alfisols) of average fertility with pH of 6.1, moderate OC of 0.5%, available P_2O_5 of 22.5 kg/ha, available K_2O of 232.0 kg/ha. The annual rainfall occurs from April to November. The maximum temperature ranges from 26.2 °C in December to 34.2 °C in April. The mean minimum temperature ranges from 13.2 °C in January to 21.2 °C in May (Anonymous, 2013). During the cropping period, the weather conditions were normal except for variations in rainfall pattern.

Experimental materials and design: Field experiments were established using 25 cowpea genotypes including V-5 and IC 20451 as resistant and susceptible control to BCMV respectively (Manjunatha *et al.*, 2015). The phenotypic descriptors of cowpea genotypes are shown in Table 1. The experiments were planted in randomized block design (RBD) with three replications and the plot size was 10 m². The recommended packages of practices of University of Agricultural Sciences, Bengaluru, were followed for the growing of cowpea genotypes. Each experimental plot was surrounded by rows of susceptible cultivar C-152 to virus, which served as the source of the virus inoculum (*i.e.*, spreader plants). All spreader row plants were artificially inoculated with virus inoculum obtained from infected plants of C-152. Inoculation of spreader plants was repeated 10 days after the first inoculation to reduce the possibility of plants escaping infection.

Data collection and statistical analysis: At about 60 days after planting, leaf samples from spreader plants were taken randomly from different plants and presence of virus was confirmed by RT-PCR method using BCMV specific primers. The disease incidence (DI) of each genotype was recorded using following formula.

$$DI (\%) = \frac{\text{Number of plants infected}}{\text{Total number of plants}} \times 100$$

Insect control was carried at recommended rates only during the pod filling period to prevent damage by pod worms. From each genotype 10 plants were selected for green fodder yield estimation and nodules count. The crude protein and crude fibre contents were analyzed as per the procedure of AOAC (2000). Other parameters such as plant height, grain yield and 100-seed weight were recorded from 10 randomly selected plants from each genotype. The data was statistically analyzed using 'R' version 3.2.3 statistical software.

Results and Discussion

The comparative performance of 25 cowpea genotypes under BCMV infection is given in Table 2. Results showed that the values of studied parameters *viz.*, disease incidence, plant height, nodulation number, green fodder yield, 100-seed weight and grain yield varied among genotypes.

Plant height and nodulation: The disease incidence ranged from 0 to 55%. The genotypes, IC 8966, IC 202782 and V-5 (resistant check) were not infected by the virus. Highest disease incidence (55%) was recorded in susceptible genotype, IC 20451. The variation in the disease incidence might be due to genetic makeup of the genotypes (Oyatokum *et al.*, 2013). The plant height varied in different genotypes depending upon incidence of the disease. The genotype IC 8966 recorded highest (68.3 cm) plant height, followed by IC 39947 (67 cm). The susceptible genotypes (IC 20451 and IC 259024) showed reduced plant height. However, some genotypes (IC 52092 and KBC-2) were found taller than mean height (57.11 cm) at 20% diseases incidence. The observations were in agreement with several reports (Chant, 1960; Shoyinka, 1974; Tu and Ford, 1984). The reason for reduced growth could be due to virus mediated interference with physiological and metabolic process of plants.

The number of nodules varied with cowpea genotypes and level of virus infection. The genetic makeup of genotypes might account for the variation of number of nodules (Agyeman *et al.*, 2014). The obtained results showed that viruses had a detrimental effect on number of nodules plant⁻¹. The resistant genotypes namely, IC 8966, IC 202891, IC 39916, IC 202782 and resistant check V-5 produced more number of nodules. The lesser number of nodules plant⁻¹ were recorded in susceptible check, IC 20451 and IC 52092. O'Hair and Miller (1982)

Table 1. Phenotypic descriptors of 25 cowpea genotypes used for assessing fodder yield potential under virus pressure

Sl.No.	Genotypes	Plant habit	Leaf shape	Pod placement	Pod position	Seed coat colour	Seed shape	Seed size	Seed texture
1	IC 243501	P	SHb	AF	P	LB	S	M	S
2	V-5	SE	SHs	FL	P	LB	C	L	S
3	KBC-2	SP	SHm	FL	P	M	C	M	M
4	IC 206240	P	H	BF	P	LB	C	M	S
5	IC 202775	P	SHb	BF	P	LB	S	M	S
6	IC 202707	SP	SHs	FL	P	LB	C	V	M
7	IC 52092	SP	SHm	FL	P	W	N	M	R
8	IC 19778	P	SHm	FL	P	LB	S	V	R
9	IC 20504	P	H	FL	P	M	N	M	S
10	IC 22637	P	SHm	FL	P	M	N	M	M
11	IC 19775	SP	SHm	FL	P	M	S	V	M
12	IC 259043	P	SHm	BF	E	LB	C	M	S
13	IC 102826	P	SHm	BF	P	LB	S	S	M
14	IC 249594	P	SHs	AF	P	LB	C	M	S
15	IC 219594	P	H	FL	P	LB	N	M	S
16	IC 199702	P	SHm	FL	P	LB	S	M	S
17	IC 39947	SP	SHs	BF	I	W	S	M	M
18	IC 10810	P	SHs	AF	P	LB	C	S	S
19	IC 20523	P	SHb	FL	P	M	C	L	M
20	IC 8966	SE	SHs	FL	I	DB	C	M	S
21	IC 202891	P	SHm	FL	P	LB	C	M	S
22	IC 259024	P	H	BF	I	W	C	M	S
23	IC 39916	SP	SHm	FL	P	W	N	S	S
24	IC 202782	P	SHb	BF	P	M	N	M	M
25	IC 20451	P	SHb	BF	P	W	S	M	R

Descriptor coding: Plant habit: SE (semi erect), SP (semi prostrate), P(prostrate); Leaf shape :H (hastate), SHb (subhastate broader), SHm (Sub hastate medium), SHn (sub hastate smaller); Pod placement: AF(above foliage) FL (foliage level), BF (below foliage); Pod position: E (erect), I (intermediate), P (pendant); Seed coat color: B (brown), M (mixed), LB (light brown), DB (dark brown), W(white/ cream); Seed shape: C (crowder, seed flat on the both ends), S (semi-crowder, seed flat on one end and rounded on other), N (non-crowder, seed rounded on both ends); seed size: L (large), M (medium), S (Small), V (variable); Seed texture: R (rough), S (smooth), M (mixed)

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Table 2. Comparative performance of twenty five cowpea genotypes for different characters under virus disease pressure

Genotypes	Disease incidence (%)	Plant height (cm)	Nodules plant ⁻¹	Green fodder yield (t ha ⁻¹)	100 seed weight (g)	Grain yield (t ha ⁻¹)	Crude protein (%)	Crude fibre (%)
IC-243501	50	48	18.2	14.5	11.2	0.98	16.5	20.1
V-5	0	63.4	24.7	16.8	12.6	1.38	19.6	24.3
KBC-2	20	58.3	16.3	15.7	9.4	1.08	17.1	22.1
IC 206240	30	57.8	14.7	16.1	7.4	0.80	16.4	19.8
IC 202775	30	56.6	13.8	16.3	8.4	0.89	16.2	19.7
IC 202707	20	56	17.6	15.7	7.5	0.85	15.7	21.0
IC 52092	45	61	15.1	15.1	6.6	0.97	14.7	19.2
IC 19778	25	52.8	19.5	14.8	8.2	0.93	15.3	18.7
IC 20504	15	54.3	18.9	15.6	7.5	0.87	16.2	20.3
IC 22637	30	57	18.1	16.8	11.9	1.05	15.7	20.5
IC 19775	35	52.2	16.3	14.8	7.9	0.75	14.3	19.8
IC 259043	15	57.1	18.2	15.7	8.9	0.86	16.5	21.8
IC 102826	30	52	17.6	17.1	8.3	0.78	14.3	19.7
IC 249594	35	56.2	19.4	14.8	10	1.01	14.5	21.2
IC 219594	10	53.3	19.8	17.4	11.8	1.23	16.8	22.0
IC 199702	20	53.2	15.7	15.8	10	0.98	15.7	18.7
IC 39947	15	67	17.3	16.3	9.1	0.92	15.8	22.9
IC 10810	5	56	20.7	17.6	10.8	1.33	17.8	23.5
IC 20523	10	54.2	19.8	17.6	12.7	1.09	15.9	22.8
IC 8966	0	68.3	22.8	15.5	11.3	1.46	18.7	22.8
IC 202891	5	63.8	22.5	17.4	9.5	1.36	18.1	24.1
IC 259024	15	46.5	18.7	15.6	12.2	0.85	17.8	19.8
IC 39916	5	63.3	21.0	16.8	12.4	1.30	19.1	22.8
IC 202782	0	66.7	20.1	17.8	12.7	1.23	19.7	22.2
IC 20451	55	46.5	13.9	14.7	9.8	0.85	14.8	18.4
Mean		56.86	18.43	16.10	9.92	1.03	16.53	21.13
CV (%)		10.31	14.94	6.32	19.40	23.00	9.72	8.61

reported that cowpea strains of TMV reduced nodules weight and their numbers. This depression was probably due to virus replication causing physiological changes of reduced photosynthesis or increased respiration (Tu and Ford, 1984), imbalanced auxins and enzyme levels which directly or indirectly affected the rhizobium cowpea symbiotic relationship (Oyatokum *et al.*, 2013).

Green fodder yield and seed weight: The green fodder yield of the genotypes did not vary with severity of disease incidence. However, lowest green fodder yield (14.5 t ha⁻¹) was recorded in IC 243501 genotype at 50% disease incidence. Green fodder yield in majority of genotypes was more or less identical to the mean yield, which

indicated that virus disease incidence was not related to green fodder yield. The genotypes without virus infection had more grain yield than the mean yield of genotypes, including the virus resistant control V-5 (Table 2). The variation in the yield of genotypes was due to both biotic and abiotic factors. The latter included abiotic conditions during critical stages of crop (Goenaga *et al.*, 2011) and the disease incidence at early stage of the crop (Ayana *et al.*, 2013). The results were also in agreement with the work of Agyeman *et al.* (2014), who reported that magnitude of variation in biomass of cowpea related to genetic constitution of varieties. The genotypes like KBC-2, IC 22637 and IC 219594 yielded more even at 10% disease incidence. Thus, the results confirmed the

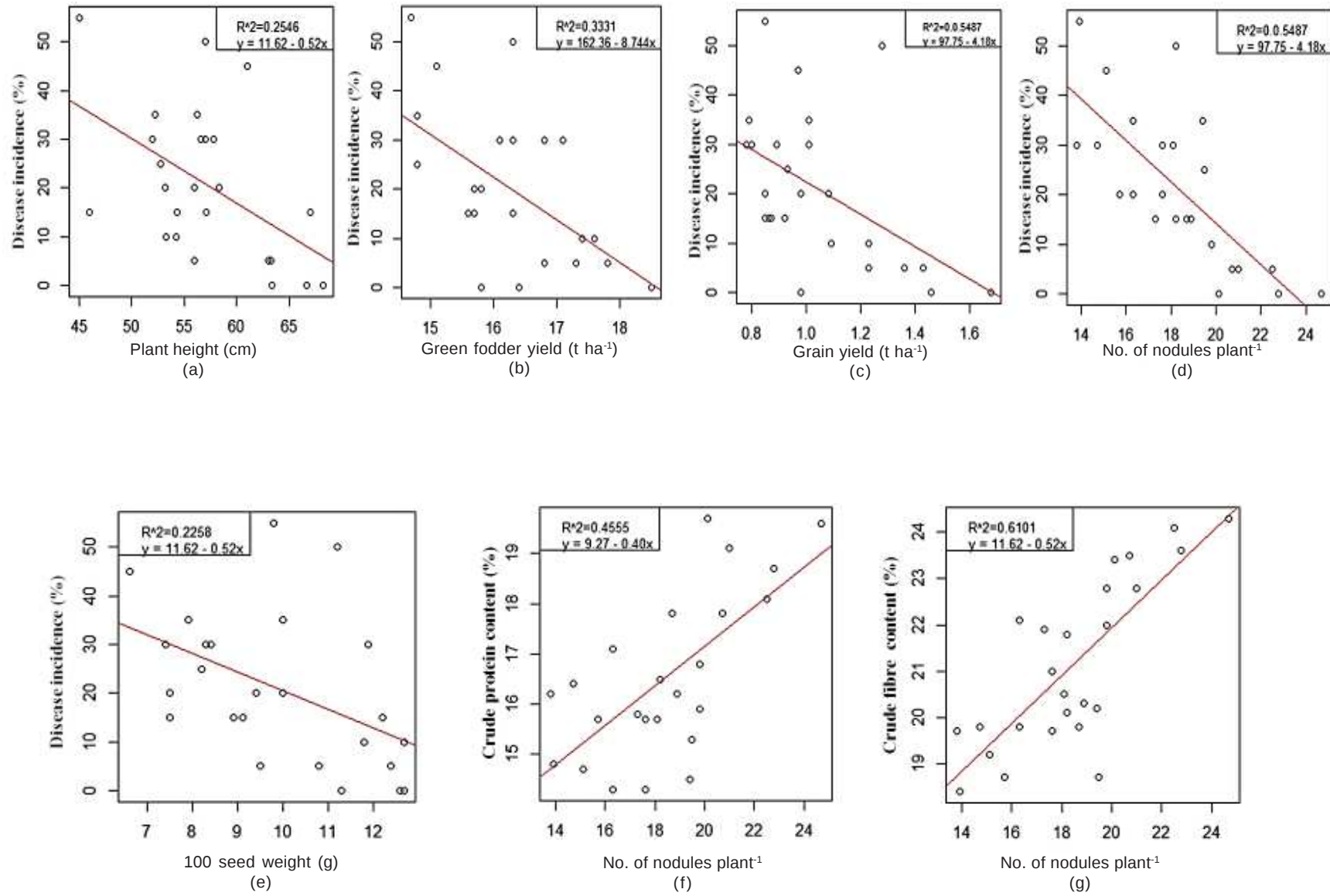


Fig 1. Relationship of virus disease incidence with yield attributes of cowpea genotypes and influence of number of nodules on fodder quality parameters

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previous studies which showed that some cowpea genotypes were excellent yielder even when plants were infected with BCMV or CMV (Goenaga *et al.*, 2011).

Seed weight did not vary significantly among genotypes with the severity of the disease incidence. The genotype IC 202782 recorded the highest 100-seed weight (12.7 g) and IC 206240 had the lowest weight (7.4 g). Our results were contradictory to the reports Goenaga *et al.* (2008) who showed that the seed weight of CMV and BCMV infected plants of cowpea genotypes varied significantly.

Association of disease incidence with yield attributes and fodder quality parameters :

The green fodder quality parameters such as crude protein (CP) and crude fibre (CF) varied among the cowpea genotypes (Table 2). The highest CP (19.7%) was obtained from genotype, IC 202782 followed by resistant check V-5 (19.6 %) and maximum CF was obtained in resistant check, V-5 (24.3%), followed by IC 202891 (24.1%). Our findings were in agreement with Mohammad *et al.* (1993), who observed variability of cowpea genotypes in green fodder yield and fodder quality under stress conditions.

The influence of virus disease incidence on yield attributes and influence of numbers nodules on fodder quality were analyzed by plotting scattered diagram (Fig.1a to g). A positive gradient was observed in the scatter plots 1(f) and 1(g). Thus, these two plots indicated increase in the response variable (number of nodules/plant) as the explanatory variable (CP) increases. In contrast, plots 1(a), 1(b), 1(c), 1(d) and 1(e) showed a negative gradient *i.e.* decrease in percent disease incidence when the yield parameters and number of nodules per plant increase.

In all the scatted plots more or less a linear association was observed from the R^2 values. A strong positive correlation between crude fibre content and number of nodules plant⁻¹ was evident in plot 1(g). Plots 1(b), 1(c), 1(d) and 1(f) showed moderate correlation and plot 1(a) ($R^2=0.25$) and 1(e) ($R^2 = 0.22$) showed a weak correlation between the variables. This could be due to outliers or influential points such genetic constitution of the genotypes, edaphic and environmental factors. Mohammad *et al.* (1993) also reported positive and significant association of green fodder yield and crude

protein under various cropping system and abiotic stress conditions.

Conclusion

Based on the present study, it was concluded that viruses had negative influences on cowpea growth, nodulation, biomass production, grain yields and fodder quality. The superior genotypes identified in this study interms of resistance and yield will be useful to growers and breeding programmes. Significant correlation was not observed for some parameters, because many factors such as environmental, time of infection, virus and rhizobium strains involved, genetic constitution of the genotypes, etc. have impact on performance of the genotypes.

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