Correlation and Path analysis in Cowpea [(Vigna unguiculata (L.) Walp.)]

Pushkar Singh Patel, Sanjay Kumar*, Rakesh Kumar Meena, Pradeep Kumar and Tribhuvan Rai

Department of Horticulture, Babasaheb Bhimrao Ambedkar University,
Vidya-Vihar, Rae Bareli Road, Lucknow-226025 (U.P.) India.

*Corresponding Author E-mail: sanjay123bhu@gmail.com
Received: 15.08.2018 | Revised: 22.09.2018 | Accepted: 29.09.2018

ABSTRACT
The present experiment was carried out entitled “Correlation and Path analysis in Cowpea [(Vigna unguiculata (L.) Walp.)]” during kharif season of the year 2014-2015 at Horticulture Research Farm, Department of Horticulture, Babasaheb Bhimrao Ambedkar University (A Central University), Vidya-Vihar, Rae Bareli Road, Lucknow-226025 (U.P.) India. The experiment was laid out in Randomized Block Design with three replications. The experimental materials consisting sixteen genotypes of cowpea i.e. Kashi Unnati, Kashi Shyamal, Kashi Gauri, Kashi Kanchan, Kashi Nidhi, IC-559393, IC-259063, IC-559405, IC-202786, IC-559386, IC-202776, IC-242598, EC-9736, EC-1738, EC-30590 and EC-15296. The maximum correlation coefficient at genotype level and phenotypic level was observed for average pod yield per plot. The results of path coefficient for parent are highest positive direct effect towards pod yield per plant was showed by plant height.

Key words: Correlation coefficient at genotype level, Phenotypic level and Path coefficient.

INTRODUCTION
The cowpea [(Vigna unguiculata (L) Walp.)] is native of Africa. It is one of the most popular and cosmopolitan vegetable crop grown in many parts of India and elsewhere in the world. It is a rich and inexpensive source of vegetable protein. It enriches soil fertility by fixing atmospheric nitrogen. Because of its quick growth habit it has become an essential component of sustainable agriculture in marginal lands of the tropics. Cowpea popularity with farmers can be attributed to its multiple uses and its adaptability to different environments. Cowpea farmers benefit through enhanced food security, cash income, crop diversification, fodder bank, in situ grazing after harvesting in periods of year when cowpeas grain prices peak and when good quality fodder is scarce. Farmers also benefit as they use cowpea products such as boiled beans, porridge and stock feed. Characterization of available germplasm is a necessary first step to facilitate breeding efforts; it especially benefits a plant breeder in choosing proper parental materials. To improve yield potentials in an existing crop, an understanding of the variability is necessary to formulate and accelerate breeding program13.
Corresponding heritability, genetic advance and genotypic and phenotypic coefficient of variation within a crop will facilitate in selection of superior genotypes which is proportional to the amount of genetic variability present and the extent to which the characters are inherited. Since, many economic traits are quantitative in nature and highly influenced by the environment, the progress of breeding is governed by the nature of genetic and non-genetic variations; it will be useful to partition the overall variability into its heritable and non-heritable components to know whether superiority of selection is inherited by the progenies. Effective selection of genotypes for desirable traits is determined by the estimates of heritability along with genetic advance. Therefore, the present investigation was undertaken to estimate the variability, heritability and genetic advance in 22 bush cowpea genotypes.

**MATERIAL AND METHODS**

The present investigation was done at Horticulture Research Farm, Department of Applied Plant Science (Horticulture), Babasaheb Bhimrao Ambedkar University, Vidya- Vihar, Rea Bareli Road, Lucknow during the year 2014-15. Lucknow is characterized by sub-tropical climate with hot, dry summer and cold winter. The soil of experimental farm was saline with soil pH 8.2, Electrical conductivity 4.0 and sodium exchangeable percentage 15.0. During the period of experiment, meteorological observations were recorded from Indian Institute of Sugarcane Research, Lucknow. The experiment was laid out in Randomized Block Design. In the present investigation sixteen diverse genotypes of cowpea were used as experimental materials. The 16 genotypes are collected from Indian Institute of Vegetable Research, Varanasi. Genotypes are Kashi Unnati, Kashi Shyamal, Kashi Gauri, Kashi Kanchan, Kashi Nidhi, IC-559393, IC-259063, IC-559405, IC-202786, IC-559386, IC-202776, IC-242598, EC-9736, EC-1738, EC-30590 and EC-15296 used. Observations were recorded like plant height (cm), number of primary branches/plant, number of branches per plant, days to first pod picking, pod length, pod diameter, number of pods per peduncle, pod weight per plant, pod yield per plot, peduncle length (cm), number of peduncle per plant, duration or reproductive phase, number of seeds per plant, number of seeds per pod, 100 seeds weight, vitamin A (IU) and vitamin C (mg/100g).were recorded. The heritable variation was further divided into additive and non additive components and the later function included dominance and interallelic interaction Fisher et al., Panse, and Lush. More attribution of the heritable component to the total variation of desirable characters becomes essential. Scientists have given more emphasis to improve the yield of a crop by studying the variability and heritability of yield and yield attributing components.

**RESULTS AND DISCUSSION**

The correlation coefficient at genotypic level are presented in (Table-1) that pod yield per plant had positive and significant genotypic correlation coefficient with pod yield per plant (1.000) followed by number of peduncle per plant (0.0269). However, negative and significant correlations were recorded for pod yield per plant with days to first pod picking (-1.4504). Days to first pod picking (0.9483) showed positive and significant correlation followed by number of seeds per pod (-0.1115) and negative and significant correlations were recorded for plant height (-0.4931). Number of primary branches per plant (0.5380) showed positive and significant correlation followed
by days to first pod picking (0.0365) and negative and significant correlations were recorded for primary branches per plant (-0.9256). Positive and significant genotypic correlation coefficient with vitamin-C (0.2426) followed by number of seeds per plant (0.05380). However, negative and significant correlations were recorded for number of peduncle per plant (-0.8543). Number of peduncle per plant (0.4851) followed by days to first pod picking (0.0043) showed positive and significant correlation and negative and significant correlations were recorded for number of branches per plant t (-0.5223), peduncle length (cm) (0.4751) followed by plant height (0.02997) showed positive and significant correlation and negative and significant correlations were recorded for number of branches per plant (-0.4498), and positive and significant genotypic correlation coefficient with number of seeds per plant (0.3597) followed by 100 seed weight (0.0835). However, negative and significant correlations were recorded for number of peduncle per plant (-0.6540).

At the phenotypic level are presented in (Table-2) that pod yield per plant had positive and significant genotypic correlation coefficient (1.000) followed by number of seeds per pod (0.0731). However, negative and significant correlations were recorded for vitamin-C (-0.0182). Vitamin-A had positive and significant correlation with pods per peduncle (0.0461) except negative and significant correlation with number of branches per plant (-0.0114), number of primary branches per plant (0.5696) showed positive and significant correlation followed by vitamin-C (0.0103) and negative and significant correlations were recorded for pod diameter (-0.4396). Vitamin –C (0.5363) followed by peduncle length (0.0216) showed positive and significant correlation and negative and significant correlations were recorded for number of peduncle per plant (-0.2555), days to first open flower (0.5155) followed by number of pods per plant (0.01919) showed positive and significant correlation and negative and significant correlations were recorded for number of branches per plant (-0.0166), and positive and significant genotypic correlation coefficient with 100 seeds weight (0.5092) followed by number of seeds per pod (0.0348). However, negative and significant correlations were recorded for number of peduncle per plant (-0.0828).

The path coefficient analysis was obtained for clear, understanding of association of the genotypic correlation coefficient of yield with contributing components. The genotypic correlation coefficient was partitioned into direct and indirect effects through path coefficient analysis of parents. The results of path coefficient for parent are presented in Table-3. At genotypic level, highest positive direct effect towards pod yield per plant was showed by plant height (2.0266) followed by number of seeds per plant (2.0180), pod length (cm) (1.3435), days to first pod picking (1.3398), number of pods per peduncle (1.2163), vitamin-A (1.2087), number of primary branches per plant (1.0063), pod diameter (cm) (0.8480) and days to first open flower (0.3174). Highest negative effect towards pod yield per plant was showed by number of peduncle per plant (-3.8261) followed by vitamin-C (-2.5669), number of seeds per plant (-1.8234), pod weight per plant (-1.8234), number of pod per plant (-1.2892), number of branches per plant (-0.4917) and number of seeds per pod (-0.4038).
Table 1: Genotypic Correlation coefficient for different pairs of characters in 16 parents of cowpea 2014-15

Table 2: Phonotypical Correlation coefficient for different pairs of characters in 16 parents of cowpea 2014-15

Table 3: Genotypic path coefficient analysis (direct and indirect effect) of yield contributing characters of Cowpea 2014-15
REFERENCES


