Studies of Skewness, Kurtosisi and Transgressive Segregants in $F_{2:3}$ Populations of Cowpea (*Vigna Unguiculata* L.)

ABSTRACT

The present investigation was carried out to study gene action and pattern of inheritance of different traits in cowpea. Two different F_3 segregating generation of crosses *viz.*, VBN-1 × RC-19 and KBC-9 × PGCP-6 were studied during *summer* 2021 using augmented random block design at College of Agriculture, Kalaburagi. Data were recorded on 10 different quantitative traits. Transgressive segregants with values exceeding the better parent were observed in both the $F_{2:3}$ populations for seed yield. In both the populations, negative skewness was observed for days to initiation of flowering, days to physiological maturity and number of pods/plant whereas test weight exhibited positive skewness suggesting a mild and intense selection would be sufficient to gain maximum genetic-gain in negatively and positively skewed traits, respectively. In both the $F_{2:3}$ populations, positive kurtosis was observed for number of branches/plant, test weight and dry matter content/plant indicating that these traits are governed by fewer numbers of genes.

Key words: Cowpea, Segregating generation, Quantitative traits, Transgressive segregants, Skewness and Kurtosis

INTRODUCTION

Cowpea (*Vigna unguiculata* L.) is a self pollinated crop with a chromosome number of 2n = 2x =22, belongs to the family Leguminosae genus *Vigna*, subfamily fabaceae and tribe phaseoleae. It is commonly known as Lobia. Its dry edible grains are rich in protein (20–32%) with high amounts of essential amino acids (lysine and tryptophan), minerals (zinc, iron, calcium), vitamins (thiamine, folic acid and riboflavin) and fibre (6%) with low fat (<1%) (Sebetha *et al.*, 2014; Boukar *et al.*, 2015). Cowpea is a multifunctional legume grown for food, fodder, vegetable and green manure (Timko and Singh, 2008; Gonçalves *et al*., 2016). It is photo insensitive in nature and can be cultivated throughout the year. Cowpea is grown in different cropping system as it has relatively drought tolerant nature (Vavilov, 1949). Cowpea can be grown in arid, semiarid and subtropical areas. It is resilient to high temperature and limited water stresses, and grows well on poor soil with a wide range of soil pH thus making it a good choice for resource-poor small-scale farmers for their sustenance (Carvalho *et al.*, 2017).

The skewness and kurtosis statistical analysis provides the information about nature of gene action (Fisher *et al.*, 1932) and number of genes controlling the trait (Robson, 1956). Generally, skewed distribution of the characters implies that the control of non additive type of gene effects and influenced by environmental variables. Positive skewness explained the complementary gene action whereas, negative skewness related to duplicate (additive × additive) gene effects (Kiran, 2012). Moreover, genes controlling characters with skewed distribution leads to be predominantly dominant irrespective of increasing or decreasing genes effect (Pooni *et al.*, 1977). Kurtosis characterizes the degree of peakedness of a distribution relative to normal distribution. Positive kurtosis of the character indicated that the presence of gene interactions while for negative sign of kurtosis or near to zero leads the absence of gene interactions (Kotch *et al.*, 1992). Positive kurtosis indicate leptokurtic distribution, caused by fewer number of genes controlling quantitative traits, while negative kurtosis indicates platykurtic distribution, caused by large number of genes controlling quantitative traits. Thus, kurtosis indicates the relative number of genes controlling the trait under investigation.

Transgressive segregant refers to pattern of inheritance where, progeny have a characteristic that falls outside the domain of either of the parent for that specific characteristic. Success in obtaining the desired transgressive segregants depends on obtaining genetic recombination between both linked and unlinked alleles (Briggs and Allard, 1953). In terms of fitness, the appearance of these transgressive (extreme) phenotypes can be either positive or negative. In segregating hybrid populations, these transgressive phenotypes have been speculated to contribute to niche divergence of hybrid lineages. Quantitative genetic studies of plant hybrids consistently designate the action of complimentary genes as the ultimate cause of transgressions, whilst over dominance and epistasis also contribute.

Keeping in view the importance of transgressive segregants in the present study an analysis was carried out to identify them. The segregants were identified by detecting those segregants that had a value exceeding the mean value of higher parent or straggling behind the mean value lower parent for ten characters. The number plants in harmony with this definition among both the segregating populations are presented in Table1 and Table 2 for $F_{2:3}$ population of VBN-1 × RC-19 and $F_{2:3}$ population of KBC-9 × PGCP-6, respectively. F_3 plants that surpassed the parental limits were observed in both the F_3 segregating population for seed yield/plant.

MATERIALS AND METHODS

The experimental material for the present study was generated by selfing the F_2 population of the cross I (VBN-1 × RC-19) and cross II (KBC-9 × PGCP-6). The experimental material was generated in the Department of Genetics and Plant Breeding, College of Agriculture, Kalaburagi, University of Agricultural Sciences, Raichur. The F_3 families of crosses (100 family rows of cross I and 70 family rows of cross II) were grown during *Summer* 2021. The experiment material was evaluated using Augmented Block Design with five replications of checks (C-152, KBC-2, KBC-9, PGCP-6 and IT-803695-1) and parents. Each F_3 progeny family was sown in rows of 4 meter length with a spacing of 45 cm × 30 cm. The observation were recorded on ten traits *viz.*, days to initiation of flowering, days to physiological maturity, plant height, number of primary branches/plant, number of pods/plant, number of seeds/pod, pod length, test weight, dry matter/plant, seed yield/plant. The mean data of five randomly selected plants from each family row for all traits were recorded and utilized for statistical analysis *viz.*, skewness and kurtosis.

Measure of skewness (β and Υ coefficient of skewness): Karl pearson defined the following β and Υ coefficients of skewness, based upon the second and third central moments. It is used as measure of skewness. $\beta_1 = \frac{\mu_3^2}{\mu_2^3}$

For a symmetrical distribution, β_1 shall be zero. β_1 as a memories of skewness does not tell about the directions of skewness, *i. e.*, positive or negative. Because μ_3 being the sum of cubes of the deviations from mean may be positive or negative but μ_2^3 is always positive. Hence, β_1 would be always positive. This drawback is removed by Karl Pearsns's Gamma coefficient Υ_1 which is the square root of β_1. Then the sign of skewness would depend upon the value of μ_3; whether it is positive or negative. It is advice able to use Υ_1 as measure of skewness.

Measure of kurtosis (Karl Pearson's measure of kurtosis): For calculating the kurtosis, the second and fourth central movements of variable are used. For these following formulae given by Karl pearson (1929) is used.

$\beta_2 = \frac{\mu_4}{\mu_2^2}$ or $\Upsilon_2 = \beta_2\text{-}3$

Where,

μ_2 = second order central moment of distribution

μ_4 = Fourth order central moment of distribution

β_2 is often referred to as " Kurtosis excess " or " Fishers kurtosis".

Description: 1. If $\beta_2 = 3$ or $\Upsilon_2 = 0$, then curve is said to be mesokurtic

2. if $\beta_2 < 3$ or $\Upsilon_2 < 0$, the curve is said to be platykurtic

3. if $\beta_2 > 3$ or $\Upsilon_2 > 0$, then curve is said to be leptokurtic

RESULT AND DISCUSSION

Comment [Ma1]: Add implications

Transgressive segregants

In $F_{2:3}$ population of VBN-1 × RC-19, the F_3 plants surpassing the limits of highest parental value for seed yield/plant were considered for selecting the transgressive segregants. However, plants with values less than the parental values were also reported for this trait. A total of 7 superior segregants having value higher than either of the parents has been identified in this segregating population for seed yield/plant (Table 1). In $F_{2:3}$ population of KBC-9 × PGCP-6, a total of 8 transgressive segregants have been identified showing higher seed yield/plant than either of their parents (Table 2). Some plants have also shown lower values than either of their parents. Aryeetey and Laing (1973) identified transgressive segregation in the F_2 of cowpea for pod length and number of seeds/pod; Adeyanju *et al.* (2007) also observed transgressive segregation in the F_2 population of cowpea. Fernandes and Boiteux (2015) identified transgressive segregants in F_2 populations of cowpea for all minerals analyzed.

Skewness and kurtosis

As per skewness and kurtosis study, negative skewness was observe in days to initiation of flowering, days to physiological maturity and number of pods per plant whereas test weight exhibited positive skewness suggesting a mild and intense selection would be sufficient to gain maximum genetic gain in negatively and positively skewed traits, respectively (Table 3).

Negative skewness was observed for days to initiation of flowering, days to physiological maturity, number of branches/plant, number of pods/plant, pod length, number of seeds/pod, total dry matter content/plant and seed yield/plant in F_3 population of VBN-1 × RC-19; days to initiation of flowering, days to physiological maturity, plant height and number of pods/plant in F_3 population of KBC-9 × PGCP-6 suggesting a mild selection would be sufficient to gain maximum genetic gain.

Positive skewness was observed for plant height and test weight in F_3 population of VBN-1 × RC-19; number of branches/plant, pod length, number of seeds/pod, test weight, total dry matter content/plant and seed yield/plant in F_3 population of KBC-9 × PGCP-6 suggesting a intense selection would be sufficient to gain maximum genetic gain.

Negative kurtosis was observed for plant height, number of pods/plant, pod length and number of seeds/pod in F_3 population of VBN-1 × RC-19; days to initiation of flowering and days to physiological maturity in F_3 population of KBC-9 × PGCP-6 indicating the absence of gene action.

Positive kurtosis was observed for days to initiation of flowering, days to physiological maturity, number of branches/plant, test weight, total dry matter content/plant and seed yield/plant in F_3 population of VBN-1 × RC-19; plant height, number of branches/plant, number of pods/plant, pod length, number of seeds/pod, test weight, total dry matter content/plant and seed yield/plant in F_3 population of KBC-9 × PGCP-6

Similarly, skewness was observed negative by Dinesh *et al.* (2018) for plant height, number of pods/plant; Oliveira *et al.* (2020) and Misra *et al.* (2008) for number of seeds/pod. However contradict findings were obtained by Dinesh *et al.* (2018) for number of branches/plant, seed yield; Irtwange (2009) and Oliveira *et al.* (2020) for pod length; Misra *et al*. (2008) for plant height, number of pods/plant, seed yield/plant.

CONCLUSION:

Transgressive segregants with values exceeding the better parent were observed in both the $F_{2:3}$ populations for seed yield. In both the populations, negative skewness was observed for days to initiation of flowering, days to physiological maturity and number of pods/plant whereas test weight exhibited positive skewness suggesting a mild and intense selection would be sufficient to gain maximum genetic gain in negatively and positively skewed traits, respectively. In both the $F_{2:3}$ populations, positive kurtosis was observed for number of branches/plant, test weight and dry matter content/plant indicating that these traits are governed by fewer numbers of genes

REFERENCE:

Comment [Ma2]: Eliminate the very old reference and change with the recent.

Adeyanju, A. O., Ishiyaku, M. F. and Omoigui, L. O., 2007, Inheritance of time to first flower in photo-insensitive cowpea (*Vigna unguiculata* L. Walp.). *Asian J. Pl. Sci.*, 6(2): 435-437.

Aryeetey, A. N. and Laing, E., 1973, Inheritance of yield components and their correlation with yield in cowpea (*Vigna unguiculata* L. Walp.). *Euphytica.*, 22: 386-392.

Boukar, O., Fatokun, C. A., Roberts, P. A., Abberton, M., Huynh, B. L., Close, T. J. and Ehlers, J. D., 2015, Cowpea, In: De Ron AM (ed) Grain legumes, Hand Book of Plant Breeding. *Springer*, *New York*, pp. 219–250.

Briggs, F. N., and Allard, R. W., 1953, The current status of the backcross method of plant breeding. *Agron*. *J*., 45: 131-138.

Carvalho, M., Lino Neto, T., Rosa, E. and Carnide, V., 2017, Cowpea: a legume crop for a challenging environment. *J. Sci. Food. Agric.*, 97: 4273–4284.

Dinesh, H. B., Viswanatha, K. P., Lohithaswa, H. C., Pavan, R. and Poonam S., 2018, Genetic association estimates using third and fourth degree statistics in early segregating generations of cowpea. *Int. J. Curr. Microbiol. App. Sci.*, 7(1): 867-873.

Fernandes S. C. A, and Boiteux, L. S., 2015, Genetic control and transgressive segregation of zinc, iron, potassium, phosphorus, calcium, and sodium accumulation in cowpea (*Vigna unguiculata*) seeds. *Genet. Mol. Res.*, 14(1): 259-68.

Fisher, R. A., Immer, F. R. and Tedin, O., 1932, The genetical interpretation of statistics of the third degree in the study of quantitative inheritance. *Genetics*, 17: 107-124.

Gonçalves, A., Goufo, P., Barros, A., Domínguez-Perles, R., Trindade, H., Rosa, E. A. and Rodrigues, M., 2016, Cowpea (*Vigna unguiculata* L. Walp.), a renewed multipurpose crop for a more sustainable agri food system: nutritional advantages and constraints. *J. Sci. Food Agric.*, 96: 2941-2951.

Irtwange, S. V., 2009, Design, fabrication and performance of a motorized cowpea thresher for Nigerian small-scale farmers. *African J. Agril. Res.*, 4(12): 1383-1391.

Kiran, K. K., 2012, Genetic variability for grain yield, its components and inheritance of resistance to BPH in two F_2 population of rice (*Oryza sativa* L.). *M. Sc. Thesis*., Univ. Agric. Sci., Bangalore.

Kotch, G. P., Ortiz, R. and Ross W. M., 1992, Genetic analysis by use of potato haploid populations. *Genome*., 35: 103-8.

Misra, R. C., Sahu, P. K., Jali, C. R., Mishra, H. P. and Misra, L. D., 2008, Studies on skewness, kurtosis and transgressive variation in M2 populations of rice bean (*Vigna umbelata*) varieties. *Legume Res*., 31(2): 94-99.

Oliveira, A. L. G., Zate, Z. Z., Olasanmi, B., Boukar, O., Gedil, M., and Fatokun, C., 2020, Genetic dissection of yield associated traits in a cross between cowpea and yard-long bean (*Vigna unguiculata* L. Walp.) based on DArT markers. *J. Genet.*, 99: 57.

Pearson, K., 1929, Inequalities for moments of frequency functions and for various statistical constants. *Biometrika*, 21(1-4): 361-375.

Pooni, H. S., Jinks, J. L. and Cornish, M. A., 1977, The causes and consequences of non normality in predicting the properties of recombinant inbred lines. *Heredity*, 38: 329-38.

Robson, D. S., 1956, Applications of K_4 statistics to genetic variance component analysis. *Biometrics*, 12(4): 433-444.

Sebetha, E. T., Modi. A. T. and Owoeye, L. G., 2014, Cowpea crude protein as affected by cropping system, site and nitrogen fertilization. *J. Agric. Sci.*, 7: 224.

Timko, M. P. and Singh, B. B., 2008. Cowpea, a multifunctional legume. *Genomics of Tropical Crop Plants*, *Springer*, New York, pp. 227-258.

Vavilov, N. J., 1949, The origin, variation, immunity and breeding cultivated plants. *Chron. Bot.* Vol. 10. The Ronald Press Co.; Newyork., pp. 364.

Verdcourt, B., 1970, Studies in the Leguminosae-Papilionoideae for the flora of tropical East Africa. *IV Kew Bulletin*., 24: 507–569.

Table 1: Transgressive segregants for seed yield per plant in $F_{2:3}$ population of VBN-1 × RC-19

Sl. No.	Parents		F_3 Generation		No. of transgressive segregants	
	Higher value (g)	Lower value (g)	Higher plant value (g)	Lowest plant value (g)	Higher than the highest parent	Lower than the lowest parent
1.	28.15	10.32	35.21	8.82	7.00	5.00

Table 2: Transgressive segregants for seed yield in $F_{2:3}$ population of KBC-9 x PGCP-6

Sl. No.	Parents		F_3 Generation		No. of transgressive segregants	
	Higher value (g)	Lower value (g)	Higher plant value (g)	Lowest plant value (g)	Higher than the highest parent	Lower than the lowest parent
1.	23.42	9.50	34.90	7.21	8.00	4.00

Table 3: Estimation of skewness and kurtosis in F_3 segregating generations of cowpea

Sl. No.	Character	$F_{2:3}$ population	Skewness	Kurtosis
1	Days to initiation of flowering	VBN-1 × RC-19	-0.8425	0.0109
		KBC-9 × PGCP-6	-0.7114	-0.3920
2	Days to physiological maturity	VBN-1 × RC-19	-0.4051	0.2987
		KBC-9 × PGCP-6	-0.2181	-0.4293
3	Plant height (cm)	VBN-1 × RC-19	0.3206	-0.4896
		KBC-9 × PGCP-6	-0.0377	0.4411
4	Number of branches per plant	VBN-1 × RC-19	-0.0392	0.8223
		KBC-9 × PGCP-6	0.2209	0.9719
5	Number of pods per plant	VBN-1 × RC-19	-0.3758	-0.5892
		KBC-9 × PGCP-6	-0.7397	0.1372
6	Pod length (cm)	VBN-1 × RC-19	-0.9538	-0.1701
		KBC-9 × PGCP-6	1.5147	1.0841
7	Number of seeds per pod	VBN-1 × RC-19	-1.0174	-0.1782
		KBC-9 × PGCP-6	0.8047	0.8483
8	Test weight (g)	VBN-1 × RC-19	1.9159	1.5315
		KBC-9 × PGCP-6	2.3356	0.4071
9	Total dry matter content per plant (g)	VBN-1 × RC-19	-0.4711	0.2258
		KBC-9 × PGCP-6	1.2031	1.0915
10	Seed yield per plant (g)	VBN-1 × RC-19	-0.6935	0.1800
		KBC-9 × PGCP-6	1.7203	1.2279

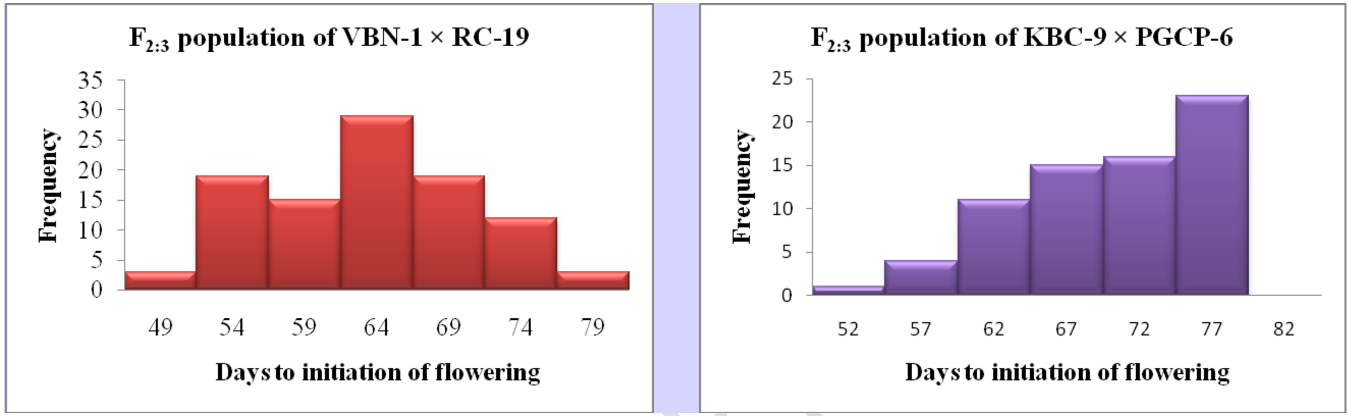

Fig. 1: F_3 frequency distribution in the form of histogram of F_3 segregating generations for days to initiation of flowering.

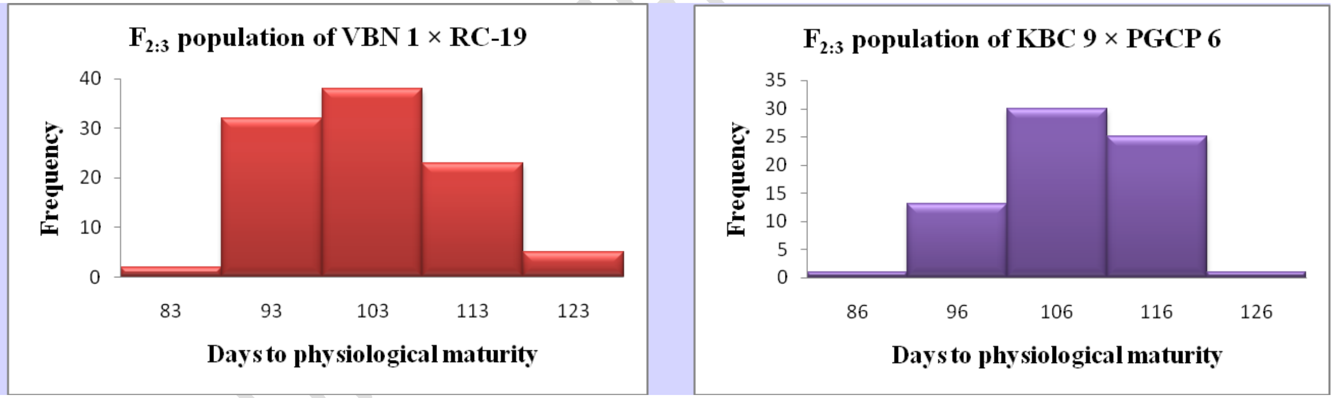

Fig. 2: F_3 frequency distribution in the form of histogram of F_3 segregating generations for days to physiological maturity.

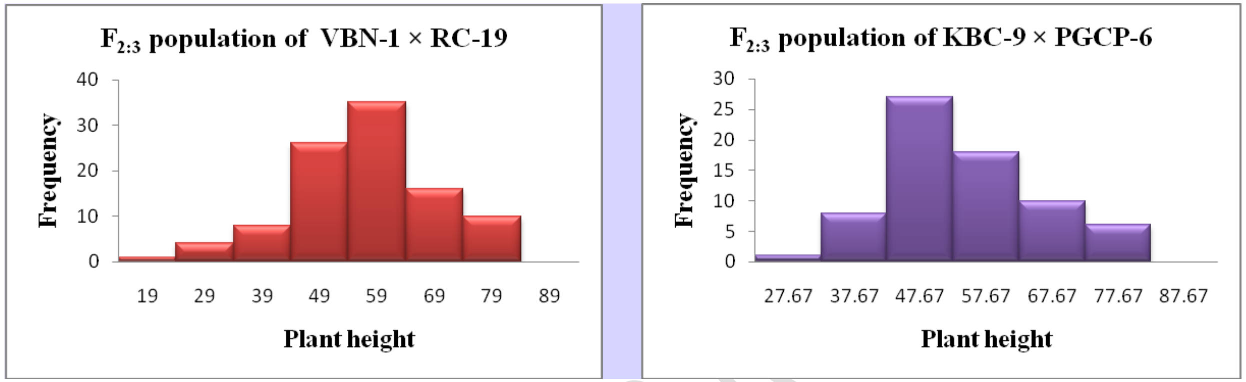

Fig. 3: F_3 frequency distribution in the form of histogram of F_3 segregating generations for plant height.

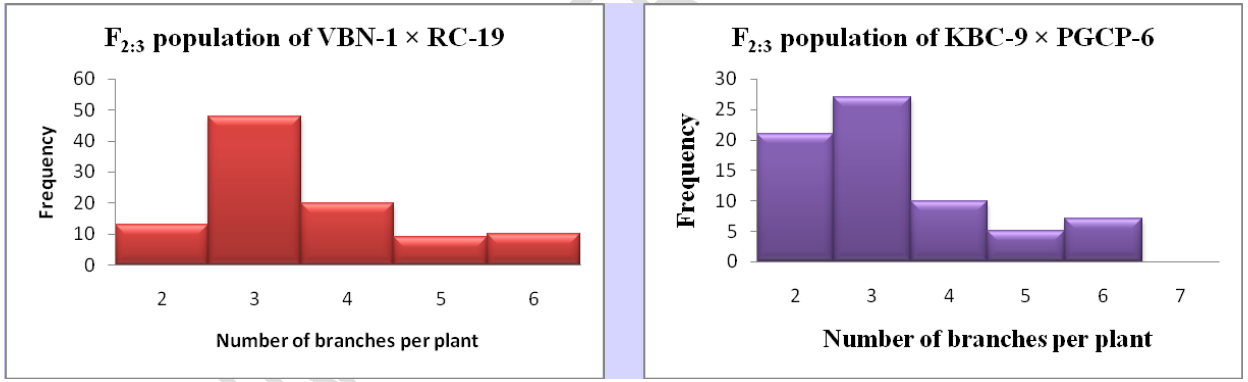

Fig. 4: F_3 frequency distribution in the form of histogram of F_3 segregating generations for number of branches per plant.

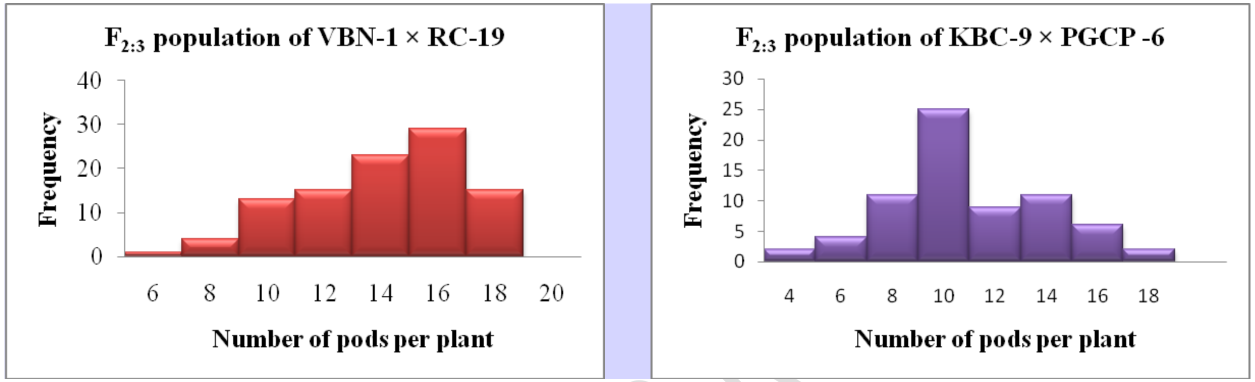

Fig. 5: F_3 frequency distribution in the form of histogram of F_3 segregating generations for number of pods per plant.

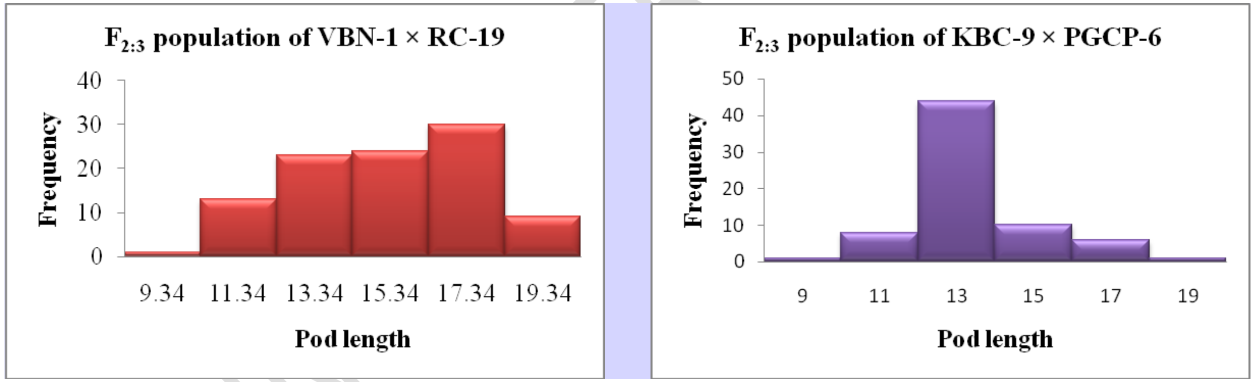

Fig. 6: F_3 frequency distribution in the form of histogram of F_3 segregating generations for pod length.

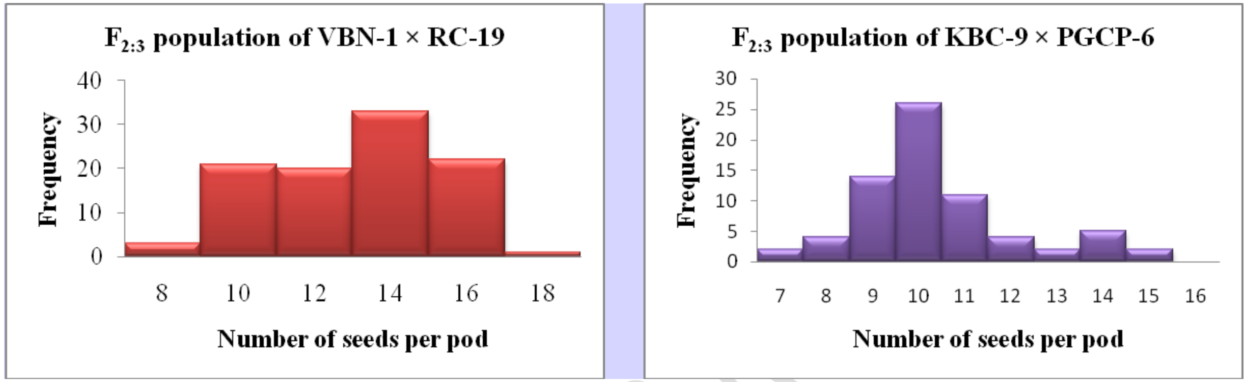

Fig. 7: F_3 frequency distribution in the form of histogram of F_3 segregating generations for number of seeds per pod.

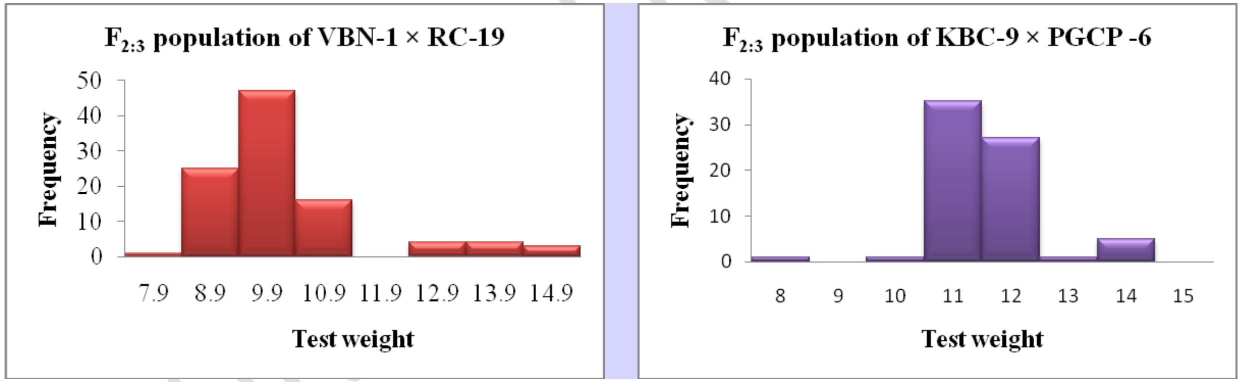

Fig. 8: F_3 frequency distribution in the form of histogram of F_3 segregating generations for test weight.

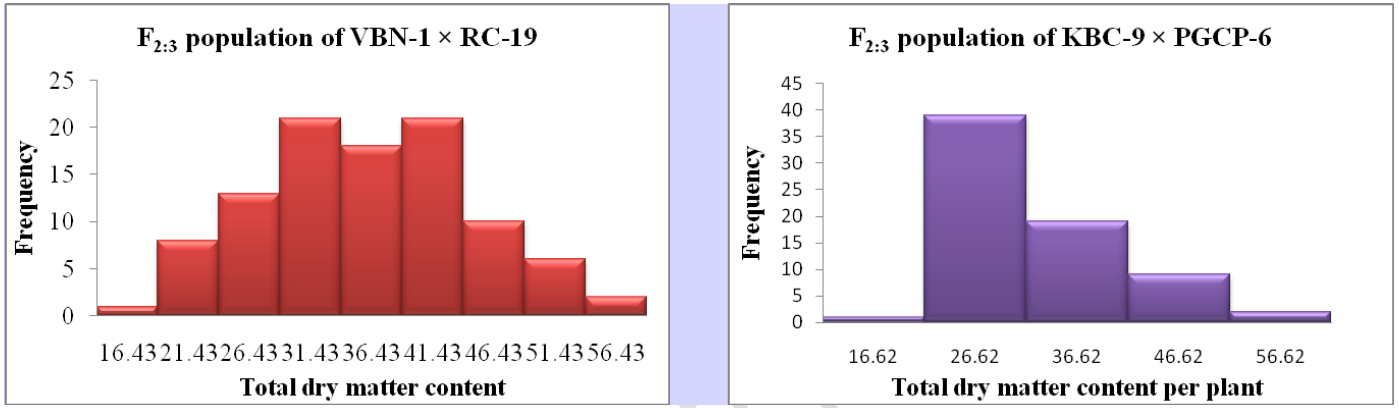

Fig. 9: F_3 frequency distribution in the form of histogram of F_3 segregating generations for total dry matter content per plant.

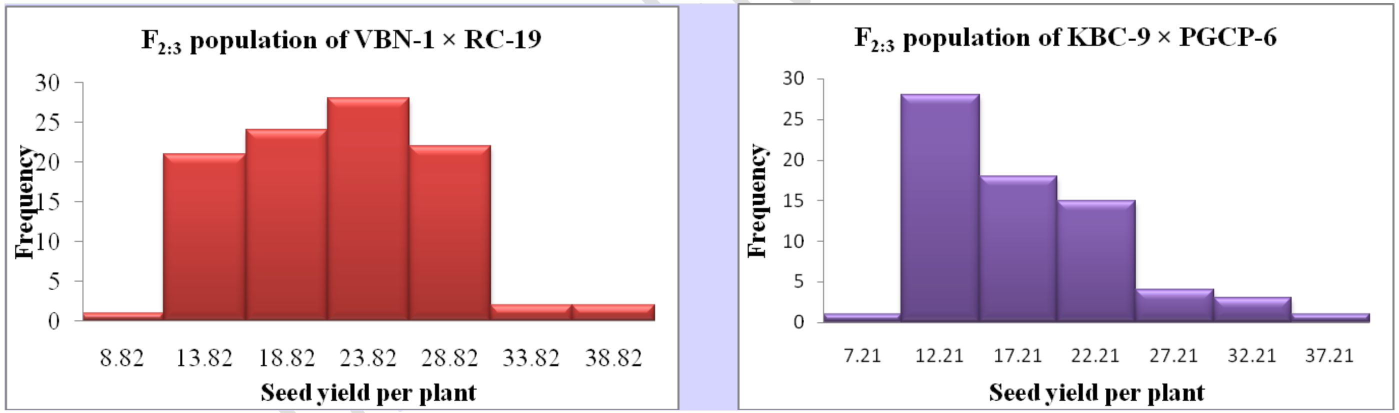

Fig. 10: F_3 frequency distribution in the form of histogram of F_3 segregating generations for seed yield per plant.

Comment [Ma3]: Kindly undergo grammarly check. There are statements with wrong grammar.