International Journal of Genetics
ISSN: 0975-2862 & E-ISSN: 0975-9158, Volume 11, Issue 2, 2019, pp.-564-568.
Available online at https://www.bioinfopublication.org/jouarchive.php?opt=&jouid=BPJ0000226

Research Article

STUDIES IN THREE F_2 POPULATIONS OF GREENGRAM (*Vigna radiata* L. Wilzeck)

I. MARIYAMMAL[1], M. PANDIYAN[2], C. VANNIARAJAN[1], J.S. KENNEDY[4] AND N. SENTHIL[3]

[1]Department of Plant Breeding and Genetics, Agricultural College and Research Institute, Madurai, 625104, Tamil Nadu Agricultural University, Coimbatore, 641003, Tamil Nadu, India.

[2]Agricultural College and Research Institute, Eachangkottai, 613006, Tamil Nadu Agricultural University, Coimbatore, 641003, Tamil Nadu, India

[3]Department of Plant Molecular Biology and Bioinformatics, Center for Plant Molecular Biology and Biotechnology, Tamil Nadu Agricultural University, Coimbatore, 641003, Tamil Nadu, India

[4]Horticulture Research Station, Yercaud, Salem, 636601, Tamil Nadu Agricultural University, Coimbatore, 641003, Tamil Nadu, India

*Corresponding Author: Email - mari.tnau@gmail.com

Received: February 01, 2019; Revised: February 11, 2019; Accepted: February 12, 2019; Published: February 28, 2019

Abstract: Present experiment was conducted to study the frequency distribution in F_2 populations of three crosses in greengram *viz*., VBN 2 x RIL 165, VBN 2 x RIL 169 and VRM (Gg)1 x RIL 165. In this study, observation of eight traits, the range of yield and its attributes were exposed to descriptive statics analysis to find out the distribution. The traits namely, days to first flowering, plant height, number of clusters per plant and number of pods per cluster showed positive skewed and platykurtic. It showed the presence of complimentary gene action and duplicate gene interaction. Hence, these populations must be handled with stringent selection process to achieve quick genetic gain since they are governed by large number of genes with complimentary gene action. Negative skewness and platykurtic was recorded by number of seeds per pod which is influenced by large number of genes with duplicate epistasis interaction and mild selection is adequate to get rapid genetic gain.

Keywords: *Greengram, Range, Skewness, Kurtosis, Frequency*

Citation: I. Mariyammal, *et al*., (2019) Studies in Three F_2 Populations of Greengram (*Vigna radiata* L. Wilzeck). International Journal of Genetics, ISSN: 0975-2862 & E-ISSN: 0975-9158, Volume 11, Issue 2, pp.- 564-568.

Academic Editor / Reviewer: Anil Kumar Kushwaha, Dr Shahid Ahamad

Introduction

Pulses belonging to the sub family, Fabaceae and the seeds are utilized as a food especially for the vegetarian people. They are rich in protein content than cereals and other crops. It constitutes the main source of essential amino acids for vegetarian population of India. Pulses are also rich in lysine content with an average of 65 ± 7 mg/g of protein as compared to 29 ± 7 mg/g in cereals. India plays a major role in pulse import and export and stands as one among the largest pulse growing country covering an area of about 23.63 mha and a production of 14.76 mha. Greengram being the third largest pulse crop covers an area of 34.4 lakhs ha (18.07%), production 14 lakh tonnes (11.48%) and a productivity of 406.98 kg/ha. In Tamil Nadu alone greengram covers an area of about 4.97 percent of total 3.41m ha, production of about 4.58 percent of total 1.21 m tonnes and with a productivity of 354.84 kg/ha [4]. The skewness represents the nature of gene action [3] and kurtosis denotes the number of genes controlling the traits [9]. The skewness and kurtosis of the trait are zero if it exhibits normal distribution. Deviation from the normal distribution provides information on genetic control of the trait. In general, the skewed distribution of the trait suggests that the trait is influenced by environmental variables and is governed by non-additive gene action, particularly epistasis [7]. The positive skewness is associated with complementary gene action and negative skewness is related to duplicate gene action. The trait with leptokurtic distribution is said to be governed by few numbers of genes while, the traits with platykurtic distribution is by larger number of genes [7]. In the present study, the main objective is aim to find the nature of gene action and the number of genes involved in trait expression and to make the selection effective.

Materials and methods

The materials chosen for this objective consisted of four greengram genotypes. The seed materials VBN2 (Cross derivative of VGG 4 x MH 309) and VRM (Gg)1 (Pure line selection from Vellore local) were obtained from the National Pulses Research Centre (NPRC), Vamban and RIL 165 and RIL 169 (F9 recombinant inbred lines (RIL) developed from VRM(Gg)1 X TNAU RED crosses.) were obtained from Agriculture Research Station (ARS), Virinjipuram. Three crosses namely VBN 2 x RIL 165, VBN 2 x RIL 169 and VRM(Gg)1 x RIL 165 were effected during October, 2017 and their F1s were raised during January, 2018. F_2 populations of these hybrids along with their parents were raised during June, 2018 at Agriculture College and Research Institute, Thanjavur. Each F_2 generation was sown on row of 4m length with a spacing of 30 x 10 cm, without replication. A total of 40 plants per row were uniformly maintained. Each F_2 population consisted of more than 160 plants. The recommended packages of practices were followed throughout the crop period. Observations were taken on in every F_2, populations for days to first flowering, plant height (cm), number of clusters per plant, number of pods per plants, number of seeds per pod, 100 seed weight (g) and single plant yield (g). The adjusted mean values of each accessions of quantitative trait were used to estimate co-efficient of skewness and kurtosis using SPSS 16.0 software programme.

Result and discussion

Skewness and kurtosis in F_2 population of VBN2 x RIL 165.

The range of mean for the traits recorded for the F_2 population of cross VBN2 x RIL 165 was from 21.00 to 36.00 for days to first flowering, 20.20 to 55.10 cm for

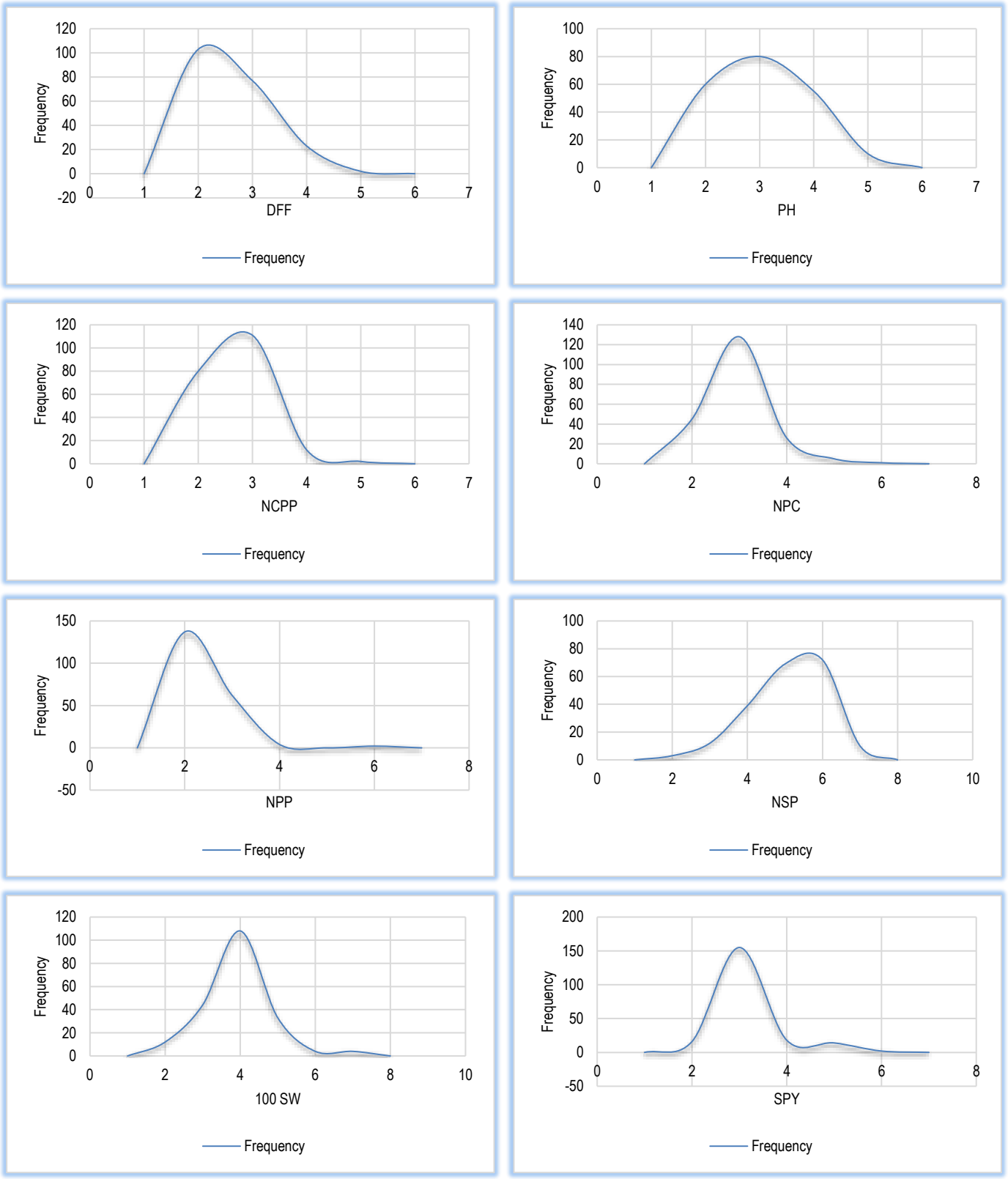

Fig-1 Frequency distribution of F_2 segregating population from VBN 2 x RIL 165

plant height, 2.00 to 18.00 for number of clusters per plant. 2.00 to 9.00 for number of pod per cluster, 7.00 to 89.00 for number of pods per plant, 4.00 to 14.00 for number of seeds per pod, 2.10 to 4.00 g for 100 seed weight and from 4.97 to 23.88 g for single plant yield [Fig-1]. In F_2 population of a cross VBN 2 x RIL 165 the traits namely days to first flowering, number of clusters per plant, number of pods per cluster and 100 seed weight were positively skewed with platy kurtic. It indicates that dominance based complementary gene interaction involving large number of genes having decrease effect. The skewness was positive indicating that predominance of dominant alleles as opinioned by [2]. The negative skewness with platy kurtic was observed in plant height and number of seeds per pod. These traits were controlled by large number of dominant genes with increasing effect and duplicate gene interaction in the inheritance. Number of pods per plant and single plant yield were leptokurtic with negative skewness, which showed that these traits were controlled by few segregating genes with majority of these exhibited decrease effects and dominance based complementary gene interaction [Table-1]. The similar results were reported by [1, 5, 6 and 11] also recorded negatively skewed and platykurtic.

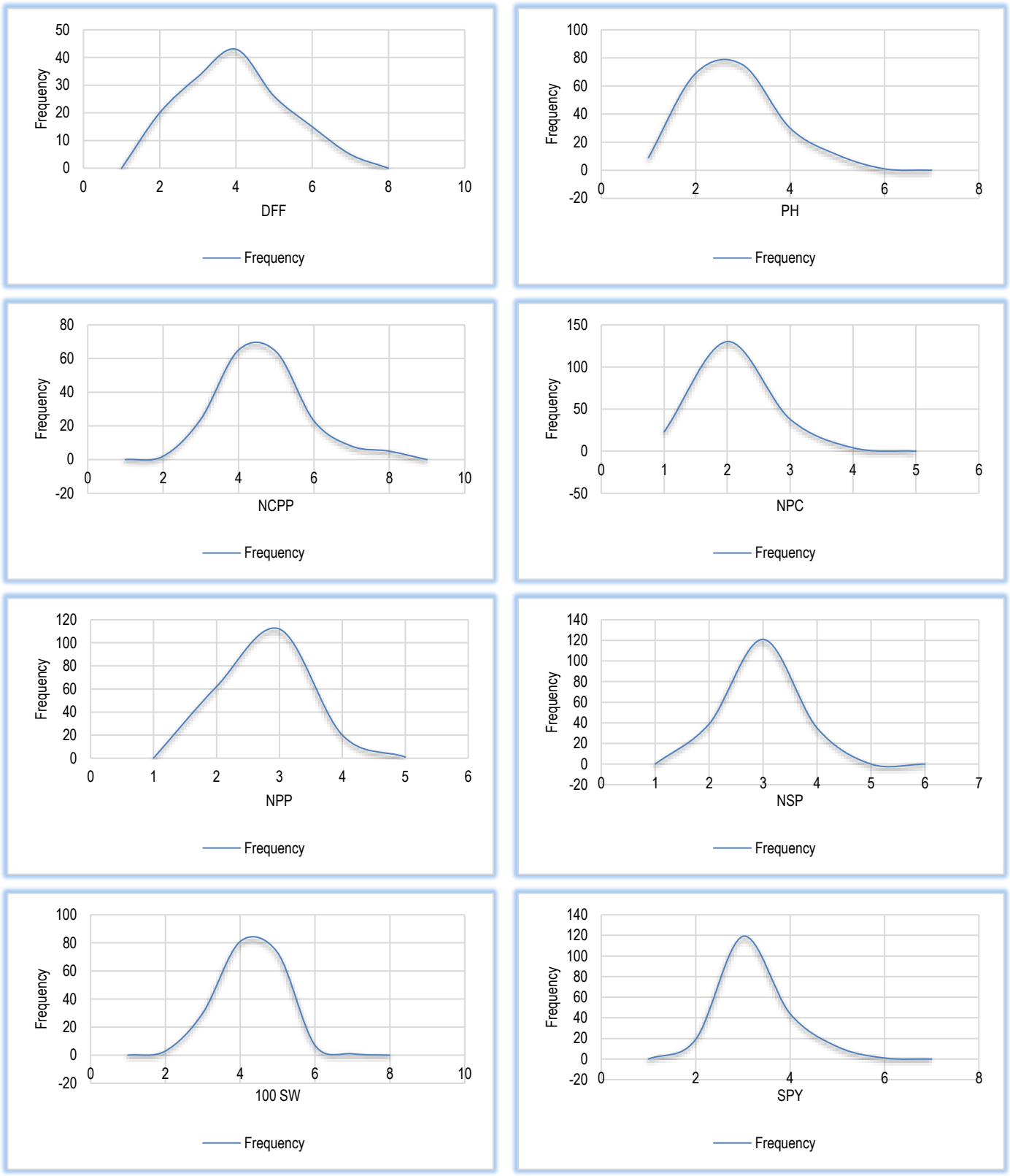

Fig-2 Frequency distribution of F_2 segregating population from VBN 2 x RIL 169

Skewness and kurtosis in F_2 population VBN 2 x RIL 169

For the F_2 population of VBN 2 x RIL 169, the mean for traits ranged from 20.00 to 28.00 for days to first flowering, 22.00 cm to 62.50 cm for plant height, 2.00 to 14.00 number of clusters per plant, 2.00 to 7.00 for number of pod per cluster, 8.00 to 63.00 for number of pods per plant, 5.00 to 14.00 for number of seeds per pod, 2.18 to 4.55 for 100 seed weigh and from 2.64 to 23.00 g for single plant yield [Fig-2]. Plants in F_2 population of a cross VBN 2 x RIL 169 are presented in fig-2. In F2 generation of VBN 2 x RIL 169, showed positively skewed with platykurtic for DAS, PH, NCPP, NPPC, NPP and SPY. It indicated that dominance based complementary gene interaction involving large number of genes having decreasing effect in the inheritance of these traits. Number of seeds per pod and 100 seed weight exhibited positively skewed with platykurtic [Table-1]. Hence, these traits were controlled by large number of dominant genes with increasing effect and duplicate interaction in the inheritance. The similar results were reported by [1, 8 and 10] for days to flowering in rice.

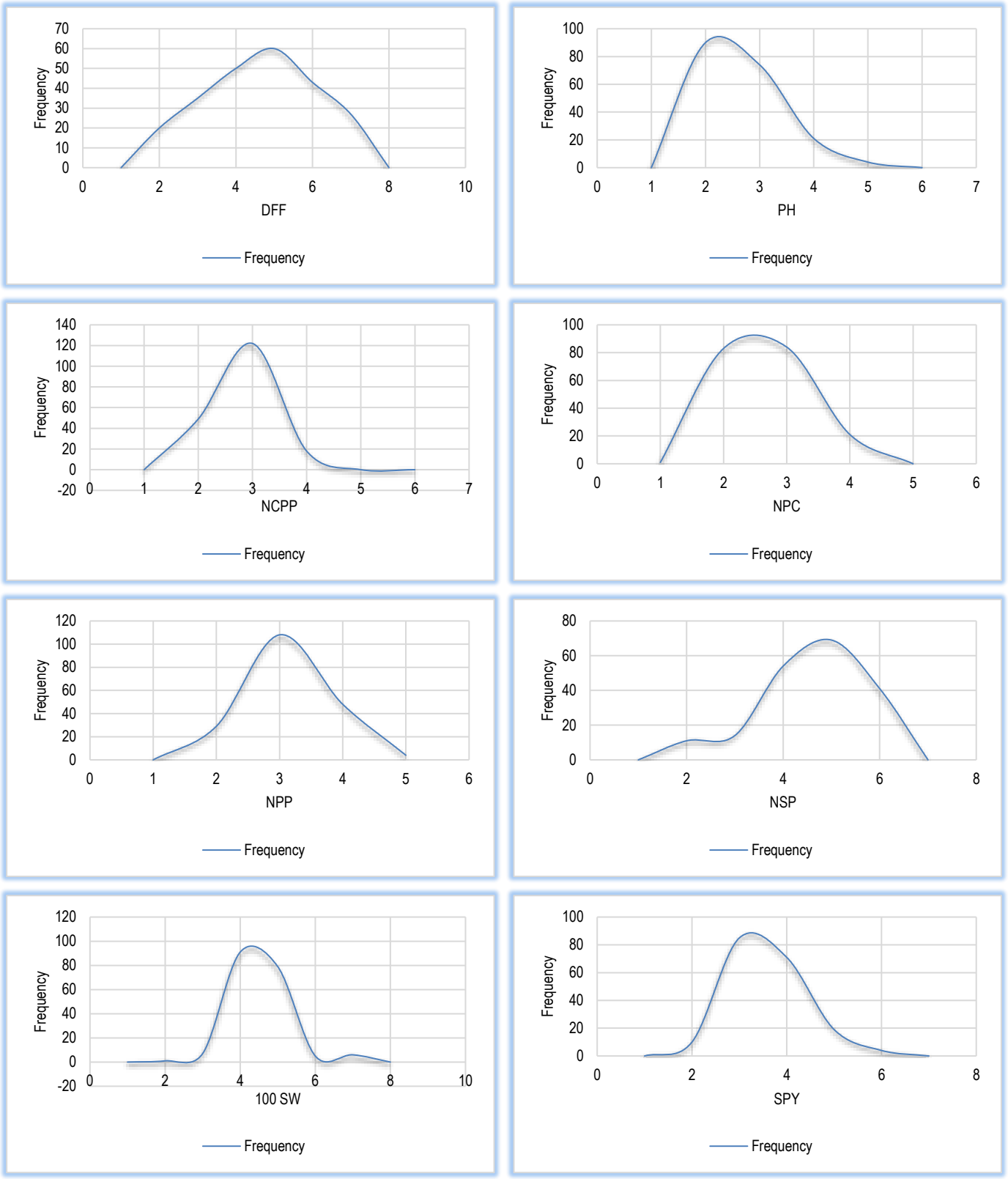

Fig-3 Frequency distribution of F_2 segregating population from VRM (Gg)1 x RIL 165

Skewness and kurtosis in F_2 population VRM (Gg)1 x RIL 165

The range of mean for the F_2 population of a cross VRM (Gg)1x RIL 165 recorded from 20.00 to 29.00 for days to first flowering, 22.00 cm to 56.50 cm for plant height, 2.00 to 15.00 number of clusters per plant, 2.00 to 7.00 for number of pod per cluster, 9.00 to 66.00 for number of pods per plant, 3.00 to 15.00 for number of seeds per pod, 2.33 to 4.86 for 100 seed weigh and from 2.97 to 21.78 g for single plant yield [Fig-3]. In F_2 population of a cross VRM (Gg)1 x RIL 165, number of seeds per pod had negative skewness with platykurtic, it indicated that dominance gene with increasing effect and duplicate interaction of inheritance. days to first flowering, plant height, number of clusters per pod, number of pod per cluster, number of pods per plant, 100 seed weight and single plant yield exhibited positive skewness and platykurtic, which showed the presence of complementary gene interaction with large number of gene having decreasing effect [Table-1]. Thus, similar to this findings frequency distribution for agronomic traits inherited quantitatively were described by [1 and 10]. Based on this study, the results were concluded that the characters such as days to first flowering, plant height, number of clusters per plant and number of pods per cluster were positive skewed and platykurtic for all three crosses.

Table-1 *Skewness and kurtosis in F_2 populations of selected cross*

SN	Trait	F_2 generation								
		VBN2 x RIL 165			VBN2 x RIL 169			VRM (Gg)1 x RIL 165		
		Skewness	Kurtosis	Types	Skewness	Kurtosis	Types	Skewness	Kurtosis	Types
1	DAS	0.98	0.37	Platy kurtic	-0.41	-0.50	Platy kurtic	-0.39	0.151	Platy kurtic
2	PH (cm)	-0.06	-1.02	Platy kurtic	0.38	0.11	Platy kurtic	0.55	0.42	Platy kurtic
3	NCPP	1.03	2.13	Platy kurtic	0.83	0.18	Platy kurtic	0.88	0.88	Platy kurtic
4	NPPC	1.85	6.99	Leptokurtic	0.47	0.48	Platy kurtic	0.18	-0.90	Platy kurtic
5	NPP	1.24	1.58	Platy kurtic	0.91	0.66	Platy kurtic	0.59	-0.11	Platy kurtic
6	NSP	-0.53	-0.10	Platy kurtic	-0.37	0.04	Platy kurtic	-0.62	0.05	Platy kurtic
7	100 SW (g)	0.38	1.82	Platy kurtic	-0.36	1.09	Platy kurtic	0.54	1.38	Platy kurtic
8	SPY (g)	1.95	4.13	Leptokurtic	1.09	1.45	Platy kurtic	0.59	-0.11	Platy kurtic

Skewness: positive (+) and negative (-), Kurtosis value less than 3 indicates platykurtic, more than 3 leptokurtic and three indicates mesokurtic

It showed that stringent selection process in advised to achieve quick genetic gain since they are governed by large number of genes with complimentary gene action. Likewise, the trait, number of seeds per pod negatively skewed with platykurtic for these crosses.

Application of research: Study indicated that the number of seeds per pod is controlled by large number of dominant genes with increasing effect and duplicate gene interaction in the inheritance.

Research Category: Plant Breeding and Genetics

Abbreviations:
DAS: days to first flowering, PH: plant height, NCPP: number of clusters per plant, NPPC: number of pods per clusters, NPP: number of pods per plant, NSP: number of seeds per pod, 100 SW: 100 seed weight, SPY: single plant yield

Acknowledgement / Funding: Financial support from SERB/F/1406/2013-2014 is greatly acknowledged. Authors are also thankful to Agricultural College and Research Institute, Madurai, 625104, Tamil Nadu Agricultural University, Coimbatore, 641003, Tamil Nadu, India.

***Principal Investigator or Chairperson of research: Dr M. Pandiyan**
University: Tamil Nadu Agricultural University, Coimbatore, 641003, Tamil Nadu
Research project name or number: Development and validation of SNP marker platform for Vigna complex to map the MYMV and bruchids resistance" (SERB/F/1406/2013-2014)

Author Contributions: All authors equally contributed

Author statement: All authors read, reviewed, agreed and approved the final manuscript. Note-All authors agreed that- Written informed consent was obtained from all participants prior to publish / enrolment

Study area / Sample Collection: National Pulses Research Centre (NPRC), Vamban, Agriculture Research Station (ARS), Virinjipuram and Agricultural College and Research Institute, Thanjavur, Tamil Nadu 613006

Cultivar / Variety name: *Vigna radiata* L. Wilzeck, VBN2, RIL169, VRM (Gg)1 and RIL165

Conflict of Interest: None declared

Ethical approval: This article does not contain any studies with human participants or animals performed by any of the authors.
Ethical Committee Approval Number: Nil

References

[1] Cayalvizhi B. (2013) *An investigation on genomic and proteomic approaches for Mungbean yellow mosaic virus (mymv) resistance in mungbean [vigna radiata (l.) Wilczek] ohwi and ohashi]. Ph.D. Thesis.TNAU.*
[2] Darbeshwar Roy (2000) *Plant breeding analysis and exploitation of variation,*300- 304.
[3] Fisher R.A., Immer F.R. and Tedin O. (1932) *Genetics* 17, 107-124.
[4] NFSM-Pulses (2015) *Central Pulses Development Pogrammes / Schemes, Integrated Scheme on Oilseeds, Pulses, Oil Palm and Maize (ISOPOM) and Integrated Crop Development Programme (ICDP).*
[5] Pandiyan M., Senthil N., Ramamoorthi N., Muthiah A.R., Tomooka N., Duncan V. and Jayaraj T. (2010) *Electronic J. Plant Breeding*, 1(4), 600-610.
[6] Ganguly P.R. and Bhat K.V. (2012) *DHR-IJBLS*, 3(1).
[7] Poorni H.S., Jinks J.L. and Cornish M.A. (1977) *Heredity* 38, 329-338.
[8] Rani C.S., Anandakumar C.R., Raveendran M., Subramanian K.S. and Robin S. (2016) *Int. J. Agril.Sci.*, 8(15), 1733-1735.
[9] Robinson H.F., Comstock R.E. and Harvey P.H. (1949) *Agron. J.*, 41, 353-359.
[10] Sompong U., Kaewprasit C., Nakasathien S. and Srinives P. (2012) *Euphytica*, 171, 389-396.
[11] Tamil Kumar P. (2012) *Development of low phytate maize through marker assisted selection and evaluation of its seed quality. Ph.D. Thesis, submitted to Tamil Nadu Agricultural University, Coimbatore (India).* pp 95.