

Genetic variation for seed yield and Yellow Mosaic Virus Resistance in Soybean [*Glycine max* (L.) Merrill]

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Abstract- Forty four genotypes of soybean (*Glycine max* (L.) Merrill) including indigenous germplasm of North East India were studied to evaluate genetic variation for seed yield and Yellow Mosaic Virus (YMV) resistance. All traits under study viz, Plant height (PH), Internodal length(IL), No. of trifoliolate leaves plant⁻¹ (TL), Pods plant⁻¹ (PP), Seeds plant⁻¹ (SP), 100-seed weight (SW), Pod weight (PW), Seed yield plant⁻¹ (SY), Days to 50% flowering (DF) and Days to maturity (DM) exhibited wide variation among the genotypes. 100-seed weight exhibited highest coefficient of variance at both genotypic (GCV) and phenotypic level (PCV) followed by seed yield plant⁻¹ and seeds plant⁻¹ indicating wide variation among the genotypes under study. High heritability coupled with high genetic advance was observed in 100-seed weight, seeds plant⁻¹, seed yield plant⁻¹, plant height and pod weight plant⁻¹ indicating their potential to be selected for the effectiveness of further improvement. Character association studies revealed significant and positive genetic correlation of seed yield plant⁻¹ with pod weight plant⁻¹ and 100-Seed weight. Screening for Yellow Mosaic Virus resistance revealed one highly susceptible variety viz. JS 335 and two highly resistant varieties viz. DS 9712 and DS9814.

Index Terms- Genetic variation, seed yield, Yellow mosaic virus resistance, soybean.

I. INTRODUCTION

Soybean [*Glycine max*] is the unique grain legume globally known for its dual purpose use as pulse and oilseed containing 38-44% protein and 18-22% oil. Soybean also finds place as the key component in a diverse range of industrial products like solvents, adhesives, inks, lubricants and insulating foams are. In a large section of vegetarian people in country like India, soybean plays an important role as a rich source of protein. Occupying an area of 12.03 mha with total production of 12.98 mt and productivity 1079 kg /ha soybean finds an important place in the Indian agriculture (Anonymous 2013). India is the third largest importer of soya oil in the world and is one of the major exporters of soya meal to the other Asian countries (Anonymous, 2013). The south and central India particularly the state of Madhya Pradesh and Maharashtra are the hubs of soybean production in India, where soybean has already been established as an important industrial crop.

Although Soybean is not a major crop for north- east India, the crop is traditionally grown by Tribal communities of the entire region, where soybean pods and seeds are consumed as either raw or cooked vegetables. However, due to non

availability of improved varieties and industrial support in the region it has not yet gained the status of a well established crop with desired degree of farmer's acceptance (Bhuyan and Sarma, 2007). Soybean was *already* demonstrated as a successful crop in north eastern region of India (Tiwari *et al.*, 2001). In spite of the feasibility of growing commercial soybean in the region and availability of indigenous cultivars, very less scientific efforts have been made so far for the genetic studies and development of improved varieties except the attempts for identification of few soybean varieties (Singh and Singh, 2002) for the region. It is in this context important to study the magnitude of genetic variability of the native soybean germplasm with respect to seed yield and other adaptive traits in the region for breeding improved soybean varieties. An attempt, therefore, was made to study the extent of genetic variation for quantitative traits associated with seed yield and resistance to yellow mosaic virus disease which appears to be the very serious disease of soybean in the entire country. Character association both at genotypic as well as phenotypic level was also studied so as to provide a basis for formulating selection criteria in breeding improved soybean genotypes for the region.

Knowledge of correlation between grain yield and other characters is helpful in selection of suitable plant type. (Aditya *et al.* 2011). The present investigation was aimed in deciding desirable traits for development of high yielding variety. We studied the genetic parameters of variation viz, Range, Mean, Standard error of Mean, CD%, Genotypic and phenotypic variance as well as coefficient of variance, Heritability and Genetic Advance of 44 Soybean germplasm comprising native genotypes of North East India along with varieties from all over India.

Soybean production has been challenged by a number of biotic and abiotic stresses. Among the different biotic stresses, Yellow Mosaic Virus (YMV) disease is one of the predominant viral diseases, especially in North, North east and Central India. This YMV disease is transmitted by white fly *Bassimia tabacci*. The All India Coordinated Research Project on Soybean has identified YMV disease as one of the most biotic threats to soybean. Yield losses due to this disease are as high as 80% (Nene, 1972). In severe cases, the growing tip stops growing and becomes a clump of un-opened leaves. Pod setting gets drastically reduced with eventual loss of yield. The incidence of YMV disease in soybean is most pronounced in North Eastern India as well as Northern India (Annual Report, AICRP-Soybean, 2000-2002, 2004-05 and 2005-06, 2008-09, 2009-10). Yield losses due to its attack are as high as 80%. So, further spread of this disease may bring disaster towards soybean industry in our country. Therefore, resistance to YMV must be improved and

incorporated into selected germplasm to minimize yield loss. We tried to screen the germplasm resistance towards the infectivity of Yellow Mosaic Virus and hence can be considered for selection and breeding programme to design variety with YMV resistance.

II. MATERIALS AND METHOD

The materials for the present investigation comprised of a set of 44 soybean genotypes representing native soybean germplasm of North East India and some improved varieties and breeding lines procured from various organizations, viz., All India Coordinated Research Project on Soybean, ICAR Research Complex for North Eastern Hill Region, Borapani, Meghalaya and by personal collection from farmers' field of various parts of the region. The set of genotypes were grown in the experimental field of BN College of Agriculture, Biswanath Chariali during Kharif 2012 and 2013 as per Randomized Block design in three replications (Each variety in 3 rows with spacing of 30 cm between rows and 10 cm between plants). Observations were made on the eight quantitative traits viz., Plant height (PH), Internodal length (IL), Number of trifoliolate leaves plant⁻¹ (TL), Pods plant⁻¹ (PP), Seeds plant⁻¹ (SP), 100-seed weight (SW), Pod weight (PW), and Seed yield plant⁻¹ (SY) based on five randomly selected plants per plot. Days to 50% flowering (DF) and Days to maturity (DM) were recorded on whole plot basis. Data on the above traits were recorded based on the standard criteria.

Frequency distributions for all the traits were computed. Number of intervals was considered 10 as per convenience using the software STIATISTICA. Observed data of 10 quantitative traits were subjected to Analysis of Variance (ANOVA) of Randomised Complete Block Design with three replications following Panse and Sukhatme (1967). The mean sum of squares obtained from ANOVA was subjected to estimation of genetic parameters of variation as per Singh & Choudhury (1985). Estimates of variability parameters, heritability and genetic advance were calculated using standard methods of Burton and Devane (1953) and Johnson *et al.* (1955). Phenotypic and genotypic correlation coefficients were calculated using the method adopted by Johnson *et al.* (1955). For identification of stable source of resistance for YMV disease in soybean, 44 genotypes comprising the germplasm accessions as well as varieties were used and scoring was done using 0-9 scale (Table 1). Based on the disease symptom, score were assigned and the genotypes were grouped accordingly.

Table 1: Scoring criteria for YMV incidence

Score	Symptom
0	No symptoms on any plant
3	Yellow mottle on 10% or fewer plant
5	Necrotic mottle on most plants, no reduction in plant growth, no yield loss.
7	Yellow mottle not covering whole leaf on most plants, reduction in leaf and plant growth
9	Yellow mottle on most plant, severe reduction in leaf and plant growth as well as yield.

III. RESULT & DISCUSSION

The Soybean genotypes under observation exhibited significant variability among the traits (Table 2). The variability among all the quantitative traits under study was clearly demonstrated in the form of histograms of the frequency distributions (Fig 1-10). Observation on days to 50% flowering revealed that most of the genotypes showed flowering at 26-28 days. When we talk about days to maturity, it was observed that maximum number of genotype was matured during the period of 90-92 days. For plant height, maximum number of genotypes (17) was observed between 40 to 60 cm. Very few genotypes occupied extreme phenotypic classes. Likewise only four genotypes were of less than 40 cm height. Observation on internodal length indicated that the varieties were widely diverse. It was observed that 47.7% of total genotypes showed internodal length of 4-6 cm while only one variety exhibited internodal length of more than 12 cm. In case of number of trifoliolate leaves, maximum frequency was found in intermediate classes and 13 genotypes showed 25-30 numbers of trifoliolate leaves. Only three genotypes were found having trifoliolate leaves more than 35 while only one variety occupied extreme phenotypic class. The genotypes showed remarkable difference with respect to the trait Pods plant⁻¹. Only three genotypes occupied extreme high phenotypic class. While seven genotypes occupied extreme less frequency. Maximum number of genotypes exhibited 30-40 Pods plant⁻¹. Eight genotypes were found to fall in the class, 40-50 Pods plant⁻¹ while three, four, two and one genotypes occupied the classes 50-60, 60-70, 70-80, 80-90, respectively. Similar observation was recorded in case of the trait seeds plant⁻¹. Only three genotypes belonged to extreme less and two genotypes belonged to extreme high phenotypic class. Nineteen numbers of genotypes occupied the class 50-100 followed by 13 genotypes occupying the class 100-150. In case of the trait Pod weight, intermediate classes were observed to show high frequencies. Only one variety exhibited lowest pod weight class (less than 10 g) as well as highest pod weight class (more than 80 g). Observation on seed weight revealed that the varieties widely differed in their seed weight. About 25% of the total genotypes showed less than 10 g of seed weight while about 45.4% exhibited seed weight in the class 10-20 having the highest frequency. Five genotypes were found to exhibit seed weight in the range of 20-30 g while four and three varieties belong to the class 30-40 and 40-50, respectively. Only one genotype was observed to occupy the highest phenotypic class. The trait seed yield also exhibited diverse variation. The intermediate classes exhibited highest seed yield. Twenty seven *per cent* of total genotypes exhibited seed yield of more than 10 g and less than 20 g. Only three genotypes occupied the highest phenotypic class and nine genotypes belong to the lowest phenotypic class.

The significant mean sum of squares indicated the high degree of variability among the genotypes for the traits under study. The considerable range of variation expressed for the traits indicated good scope for genetic improvement which is clearly revealed in Table 3. Good agreement was observed between the magnitudes of phenotypic as well as genotypic variance. Highest genotypic variance was observed for the attribute number of seeds plant⁻¹ followed by plant height and pods plant⁻¹. Mere study of the magnitude of variance does not justify the

comparison of variability exhibited by different traits. Estimation of Coefficient of variation which takes into account the mean of each characters, gives the real basis for comparison. In the present study, 100-seed weight exhibited highest coefficient of variance both genotypic (GCV) and phenotypic level (PCV) followed by seed yield plant⁻¹ and seeds plant⁻¹. Malik *et al.* 2011 reported high variability for pods plant⁻¹, 100-seed weight and seed yield plant⁻¹ in a set of germplasm of Japan, Pakistan, USA, North Korea and other Asian countries. Wide genetic diversity among soybean genotypes with respect to Leaf area (cm), Days to flowering initiation, Days to flowering, Days to maturity, Plant height (cm) Pods plant⁻¹, Branches plant⁻¹ 100-seed weight (g) Seed yield plant⁻¹(g) Oil content (%) were observed by various workers in different countries (Sihag *et al.* 2004, Chettri *et al.* 2005, Muhammad *et al.* 2003, Malik *et al.* 2006, etc.). High GCV did not provide a clear picture of genetic gain to be achieved from selection of phenotypic trait unless the heritable fraction of variation was known (Burton 1952). Here lies the essence of estimation of heritability and genetic advance (Sarma and Richharia 1995). Johnson *et al.* 1955 and Gandhi *et al.* 1964 suggested that high heritability should be accompanied with high genetic advance for effectiveness of selection. In the present investigation 100-seed weight, seeds plant⁻¹, seed yield plant⁻¹, plant height and pod weight plant⁻¹ exhibited high heritability coupled with high genetic advance. Considering the magnitude of genetic variability, the traits 100-seed weight, seeds plant⁻¹, and seed yield plant⁻¹ were observed to be the most potential for further improvement.

Estimation of correlation coefficients among the traits under study at both genotypic and phenotypic level is presented in table 4. Knowledge of correlation between grain yield and other characters is helpful in selection of suitable plant type. (Aditya *et al.* 2011). Correlation studies at both phenotypic and genotypic level revealed that the magnitude of genotypic and phenotypic coefficient was found to be almost collinear indicating less environmental influence on the traits under study. It was observed that seed yield plant⁻¹ exhibited varied degree of association with other traits among different sets of genotypes studied. Seed yield plant⁻¹ exhibited significant and positive correlation coefficient at both genotypic and phenotypic level with pod weight plant⁻¹ and 100-Seed weight. Selection for these traits would be effective for improving seed yield plant⁻¹. Mukhekar *et al.* 2004, Chandel *et al.* 2005 & Turkec 2005 also reported similar pattern of correlation between seed yield plant⁻¹ and 100-seed weight. Significant and negative correlation was observed among 100-Seed weight, pods plant⁻¹, and seeds plant⁻¹. This undesirable negative association must be broken in order to improve seed yield in the present set of Germplasm under study. There is a possibility of getting soybean variety with early maturing and high seed yield plant⁻¹ as seed yield plant⁻¹ is negatively correlated with days to maturity and days to 50% flowering. Pod weight was significantly and positively correlated with seeds plant⁻¹ and pods plant⁻¹. It was observed that a significant and positive correlation is present between days to flowering and days to maturity. Similar result regarding days to maturity and days to flowering were recorded by Malik *et al.*, 2011. A trend was observed that seeds plant⁻¹ increased with increase in plant height, days to maturity and days to flowering. Number of pods and number of trifoliolate leaves showed

significant correlation with plant height and days to maturity. The present investigation indicated that intermodal length is of no significance as a yield attribute.

It was revealed that increased seed yield plant⁻¹ was associated with increase in 100-seed weight which in turn showed negative correlation with number of pods plant⁻¹ and seeds plant⁻¹. From this observation, it was indicated that higher seed weight is related with less number of seeds which was not desirable. Hence breaking off this negative correlation is required which can be achieved by recombination breeding between genotypes with contrasting values for these traits. The positive significant association of pods plant⁻¹ with plant height indicated that pods plant⁻¹ could be increased by selecting tall plants. Similar pattern was also observed by Malik *et al.* 2006.

The set of 44 genotypes were screened for incidence of yellow mosaic virus (YMV) resistance (Table 5). A moderate to severe incidence of the disease was observed only in a limited number of entries (Nine moderate and one highly susceptible). It was observed that all the native genotypes of North East India showed moderate susceptibility where infection is present but no yield loss due to infection was recorded. The frequency distribution of YMV resistance (Fig 11) showed that 31 genotypes exhibited moderate susceptibility without any yield loss followed by nine genotypes scoring 7. The genotype JS335 has been identified as the highly susceptible having the highest degree of disease incidence. Rest of the genotypes exhibited either zero or very low incidence of YMV. The genotypes DS 9712 and DS 9814 were found to be highly resistant to YMV infection.

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Table 2 : Frequency distribution of different morphological and agronomic traits in Soybean Germplasm under study

Traits	Phenotypic classes	Number of genotypes	Percent of genotypes
Days to 50%flowering (DF)	22-24	4	9.0
	24-26	10	22.7
	26-28	15	34.0
	28-30	12	27.2
	30-32	2	4.5
	32-34	1	2.2
Days to Maturity	Less than 84		
	84-86	4	9.0
	86-88	10	22.7
	88-90	12	27.2
	90-92	13	29.5
	92-94	2	4.5
	94-96	2	4.5
Plant Height	96-98	1	2.2
	20-40	4	9.0
	40-60	17	38.6
	60-80	9	20.4
	80-100	7	15.9
	100-120	5	11.3
Internodal length	120-140	2	4.5
	2-4	9	20.4
	4-6	21	47.7
	6-8	7	15.9
	8-10	4	9.0

	10-12	3	6.8
	12-14	1	2.2
Trifoliolate leaves	5-10	1	2.2
	10-15	7	15.9
	15-20	6	13.6
	20-25	8	18.1
	25-30	13	29.5
	30-35	6	13.6
	35-40	3	6.8
Pods plant ⁻¹	20-30	7	15.9
	30-40	16	36.3
	40-50	8	18.1
	50-60	3	6.8
	60-70	4	9.0
	70-80	2	4.5
	80-90	1	2.2
	90-100	3	6.8
Seeds plant ⁻¹	Less than 50	3	6.8
	50-100	19	43.1
	100-150	13	29.5
	150-200	6	13.6
	200-250	1	2.2
	250-300	2	4.5
Pod Weight	Less than 10	1	2.2
	10-20	7	25.9
	20-30	9	20.4
	30-40	13	29.5
	40-50	7	15.9
	50-60	4	9.0
	60-70	2	4.5
	70-80	1	2.2
Seed Weight	Less than 10	11	25.0
	10-20	20	45.4
	20-30	5	11.3
	30-40	4	9.0
	40-50	3	6.8
	50-60	1	2.2
Seed yield plant ⁻¹	5-10	9	20.4
	10-15	10	22.7
	15-20	10	22.7
	20-25	5	11.3
	25-30	5	11.3
	30-35	2	4.5
	35-40	3	6.8

Table 3: Genetic parameters of variation in Soybean germplasm under study for 10 quantitative traits.

Parameters	Days to 50 %flowering	Days to Maturity	Plant height	Internodal length	No. of Trifoliolate leaves	Pod No plant ⁻¹	Seed No plant ⁻¹	Pod weight plant ⁻¹	100-Seed Weight plant ⁻¹	Seed Yield plant ⁻¹
Range (Minimum)	23.50	85.50	32.10	3.00	9.10	22.50	46.00	9.13	3.95	6.24
Range(Maximum)	32.50	94.50	124.00	12.02	40.00	97.50	285.00	74.84	57.48	37.23
Mean	27.31	89.60	68.56	5.78	23.78	46.45	115.23	34.56	18.69	17.88
SEm (±)	1.39	2.26	2.75	0.63	0.99	2.02	5.00	3.84	1.92	1.00
CD 5%	2.34	3.80	4.62	1.05	1.65	3.40	8.40	6.45	3.22	1.68
Genotypic Variance	4.036	4.04	637.14	4.50	69.18	391.90	3098.43	219.42	163.31	74.98
Phenotypic Variance	5.99	5.99	644.71	4.90	70.16	396.00	3123.46	234.20	166.99	75.99
Genotypic Coefficient of Variance	7.35	2.25	36.82	36.67	34.97	42.61	48.30	42.85	68.35	48.42
Phenotypic Coefficient of Variance	8.96	2.74	37.03	38.24	35.22	42.836	48.49	44.27	69.12	48.74
Environmental Coefficient of variation (CV)	5.11	1.56	4.01	10.85	4.15	4.36	4.34	11.12	10.26	5.61
Heritability (Hb%)	67.39	44.67	98.82	91.98	98.61	98.96	99.19	93.69	97.79	98.67
Genetic Advance (GM PS)	12.44	3.80	75.39	72.43	71.54	87.33	99.10	85.45	139.24	99.08

Table 4: Genotypic, phenotypic and environmental correlation coefficient among the 10 quantitative traits of soybean under study.

Parameters	Correlation coefficient	DF	DM	PH	IL	TL	PP	SP	PW	SW	SY
Days to 50 %flowering (DF)	r _g	1.00	1.03**	0.34*	-0.18	0.39**	0.38*	0.38*	-0.16	-0.40*	-0.29
	r _p	1.00	0.77**	0.27	-0.17	0.31*	0.32*	0.32*	-0.13	-0.33*	-0.24
	r _e	1.00	0.49**	0.01	-0.18	-0.15	0.13	0.15	-0.01	-0.12	-0.06
Days to Maturity	r _g		1.00	0.54**	-0.20	0.47**	0.63**	0.58**	0.01	-0.40**	-0.28
	r _p		1.00	0.35*	-0.12	0.33*	0.43**	0.40**	-0.02	-0.33	-0.19
	r _e		1.00	-0.12	0.02	0.26	0.19	0.23	-0.15	-0.12	-0.03
Plant height	r _g			1.00	0.04	0.41**	0.40**	0.33	0.08	-0.19	-0.12
	r _p			1.00	0.04	0.40**	0.40**	0.33	0.08	-0.19	-0.12
	r _e			1.00	0.05	-0.07	0.06	0.03	0.09	-0.19	0.12
Internodal length	r _g				1.00	0.25	-0.07	-0.11	-0.10	0.04	-0.06
	r _p				1.00	0.25	-0.07	-0.10	-0.09	0.06	-0.05
	r _e				1.00	0.15	0.05	0.04	0.13	0.36*	0.10
No.of Trifoliate leaves	r _g					1.00	0.30*	0.25	0.25	0.11	0.31*
	r _p					1.00	0.30*	0.25	0.25	0.11	0.30*
	r _e					1.00	0.06	0.08	0.08	0.04	0.10
Pod No plant ⁻¹	r _g						1.00	0.89**	0.34*	-0.55**	-0.04
	r _p						1.00	0.89**	0.33*	-0.54**	-0.04
	r _e						1.00	0.98**	0.38*	0.08	0.31
Seed No plant ⁻¹	r _g							1.00	0.36*	-0.53**	0.11
	r _p							1.00	0.36*	-0.52**	0.11
	r _e							1.00	0.31*	0.15	0.33
Pod weight plant ⁻¹	r _g								1.00	0.13	0.48**
	r _p								1.00	0.12	0.47**
	r _e								1.00	-0.18	0.27
100-Seed Weight plant ⁻¹	r _g									1.00	0.67**
	r _p									1.00	0.66**
	r _e									1.00	0.06
Seed Yield plant ⁻¹	r _g										1.00
	r _p										1.00
	r _e										1.00

r=0.304 at 5% level of significance, r= 0.393 at 1% level of significance, *= Significant at P=0.05, **= Significance at P=0.0

Table 6: Screening of genotypes for YMV resistance

Score	No.of genotypes	Percent of genotypes	Percent of yield loss
0	2	4.5	NIL
3	31	70.4	NIL
5	1	2.2	20%
7	9	20.4	65%
9	1	2.2	85%

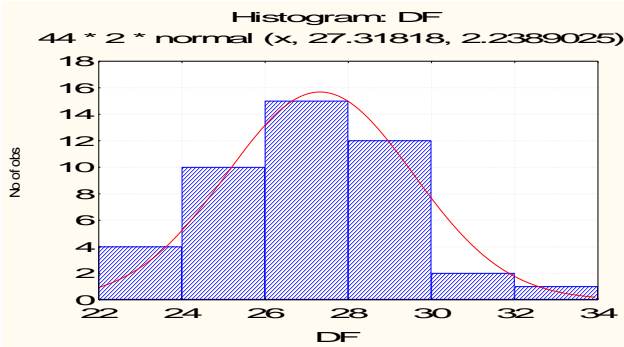


Figure 1: Histogram of Days to 50% flowering

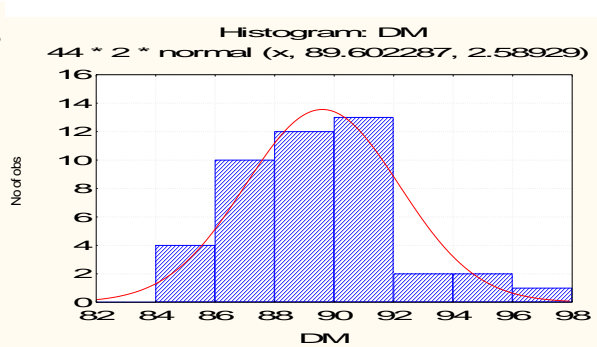


Figure 2: Histogram of Days to Days to maturity

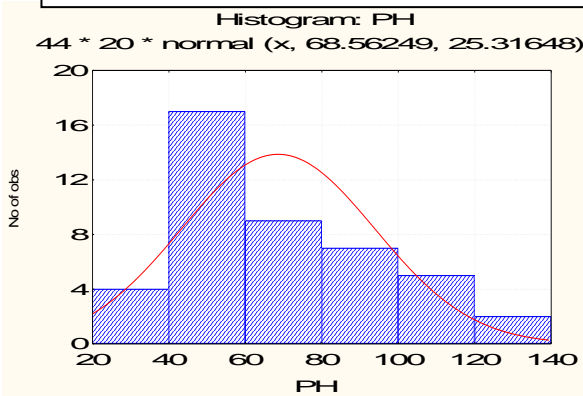


Figure 3: Histogram of Plant height (PH)

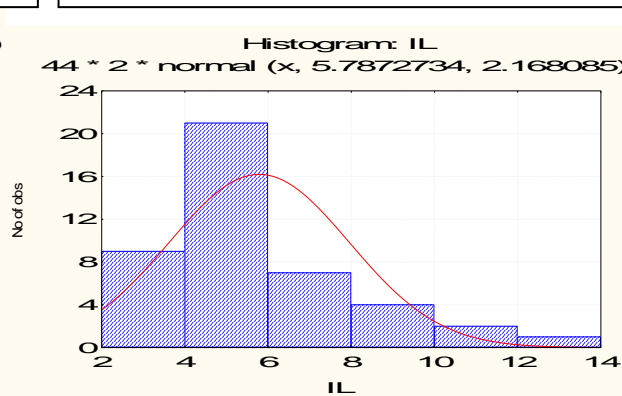


Figure 4: Histogram of Internodal

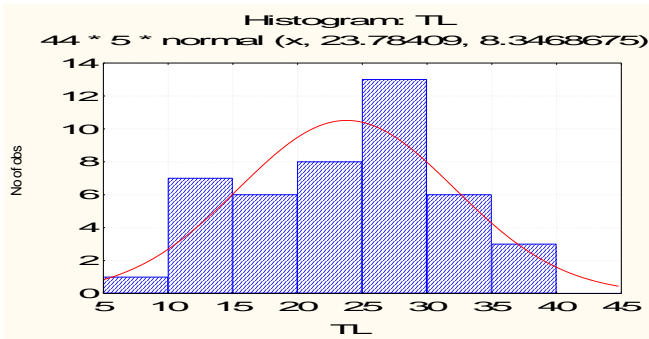


Figure 5: Histogram of Number of Trifoliolate leaves(TL)

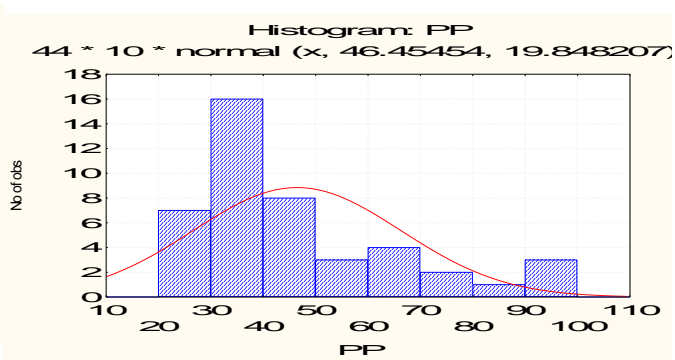


Figure 6: Histogram of Pods plant⁻¹ (PP)

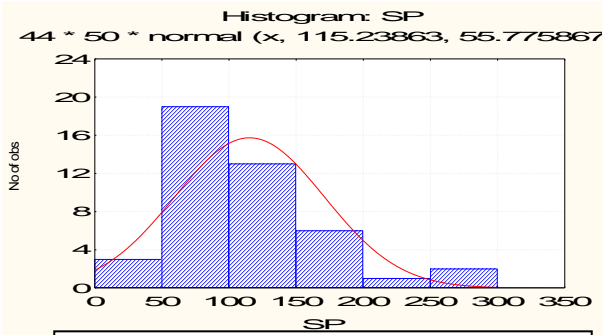


Figure 7: Histogram of Seeds plant⁻¹. (SP)

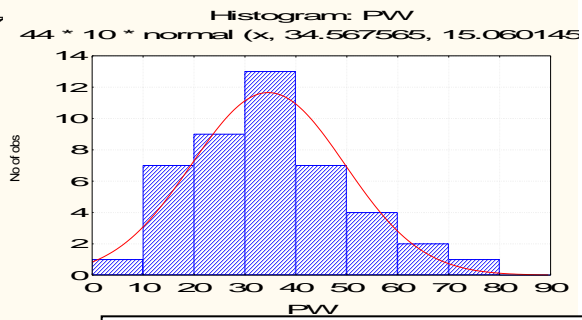


Figure 8: Histogram of Pod weight (PW)

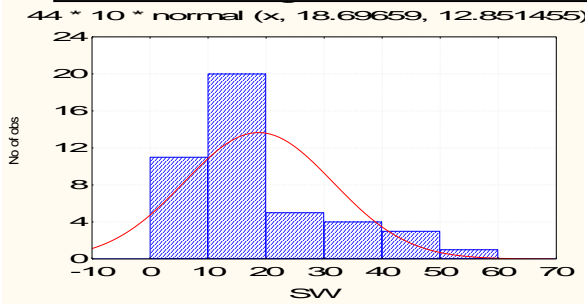


Figure 9: Histogram of Seeds weight (SW)

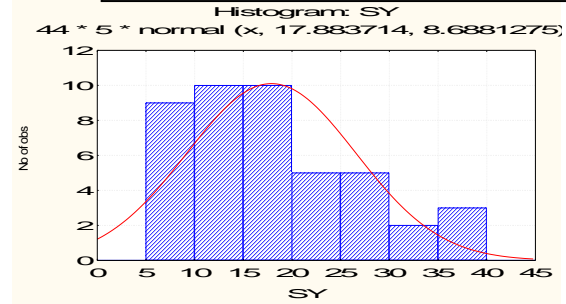


Figure 10: Histogram of Seed Yield plant⁻¹. (SY)

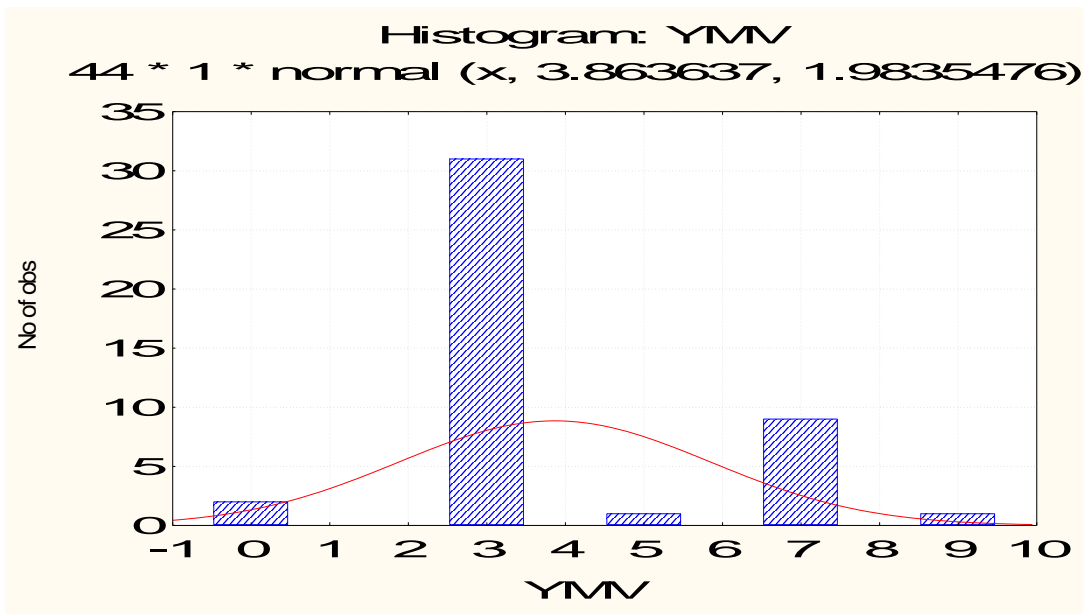


Figure 11: Histogram of YMV infection