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Studies on skewness and kurtosis of quantitative traits in green gram germplasm accessions [*Vigna radiata* (L.)] under drought condition

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Abstract

An experiment was conducted to evaluate 200 green gram germplasm accessions for drought tolerance using augmented design during summer 2015 by imposing drought stress condition. ANOVA revealed high significant differences among germplasm accessions for yield, yield component traits and also for drought tolerance traits. Mean squares attributable to 'Genotypes vs check entries' were significant for all the traits except seeds per pod and relative water content. All the quantitative traits studied in germplasm accessions exhibited skewness values between -0.5 and 0.5 except for the traits leaf water potential (0.69) and seed yield per plant (0.66) indicating normal distribution for these traits in the population. Similarly all the quantitative traits exhibited lesser than zero values for kurtosis except for the test weight (1.02) and threshing percentage (0.24) indicating that the tails of the distribution of these traits are platykurtic.

Keywords: Green gram germplasm, drought tolerance screening, skewness, kurtosis

1. Introduction

Green gram, alternatively known as the mung bean, or mugda is the third most important pulse crop after chickpea and pigeon pea in India. It is a fast-growing grain legume belonging to the family Fabaceae. Being a short-duration legume, it is an ideal legume for catch cropping, intercropping, and relay cropping (Pooja *et al.*, 2019) [1]. Mung bean has the ability to fix nitrogen via symbiosis with nitrogen-fixing Rhizobium bacterium (Allito *et al.*, 2015) [2]. Pulse crops are important valuable grain legumes that are widely used as food, fodder and feed. Pulses are important constituent of the Indian diet, green gram has excellent and easily digestible source of protein for humans and is said to be an alternate to animal protein such as meat, ultimately supporting food security. The mature seeds are rich in nutrients including carbohydrates, protein, fibers, minerals, antioxidants like flavonoids (Quercetin-3-Oglucoside), and phenolics (Guo *et al.*, 2012) [3]. Despite being an economically important pulse crop, overall production of mung bean in India is low due to abiotic and biotic stresses (Bangar *et al.*, 2018) [4].

Among abiotic stresses, drought stress is undoubtedly one of the most devastating environmental stresses especially in crop like green gram whose cultivation is mostly confined to marginal lands, low fertile soils and in rainfed condition. Drought is a multidimensional complex stress, simultaneously disturbing the metabolic, physiological, morphological, biochemical, and molecular states which control the growth and development of the crop and ultimately crop productivity (Basu *et al.*, 2016) [5]. The agricultural crops are frequently exposed to drought situations and this stress is aggravating worldwide as drought-stressed areas are expanding rapidly due to uneven rainfall, limited water sources, and other rapid and drastic changes in global environmental conditions (Fahad *et al.*, 2017) [6].

A measure of the standard error of skewness (SES) can roughly be estimated as the square root of $6/N$, where N represents the number of samples (Tabachnick, B.G and Fidell, 1996) [7]. If the skewness is more than twice this amount, then it indicates that the distribution of the data is non-symmetric and it can be assumed that the distribution is significantly skewed. If the skewness is within the expected range of chance fluctuations in that statistic (i.e. \pm SES), that would indicate a distribution with no significant skewness problem (Petar Čisar, 2010) [8].

2. Material and Methods

The experiment was conducted at experimental plot of College of Agriculture, Hassan, University of Agricultural Sciences, Bangalore. The experimental site is geographically located at Southern Transitional Zone (Zone-7) of Karnataka with an altitude of 827 m above Mean Sea Level (MSL) and at 33' N latitude and 75° 33' to 76° E38' longitude.

The study material consisted of 200 germplasm accessions collected from different research institutions/organizations representing different agro-climatic zones. List of germplasm

accessions used in the study with their source is given in table No 1.

Table 1: List of germplasm accessions used in the study and their source

Sl. No.	Germplasm	Location
1	KM13-16	ARS, Bidar
2	KM13-19	ARS, Bidar
3	KM13-39	ARS, Bidar
4	GG13-7	ARS, Bidar
5	GG13-6	ARS, Bidar
6	KM13-44	ARS, Bidar
7	GG13-10	ARS, Bidar
8	SML-668	ARS, Bidar
9	KM13-9	ARS, Bidar
10	IPM99-125	ARS, Bidar
11	LGG-596	RARS, Guntur
12	LGG-572	RARS, Guntur
13	LGG-450	RARS, Guntur
14	LGG-583	RARS, Guntur
15	LGG-590	RARS, Guntur
16	LGG-588	RARS, Guntur
17	LGG-589	RARS, Guntur
18	LGG-579	RARS, Guntur
19	LGG-562	RARS, Guntur
20	LGG-582	RARS, Guntur
21	LGG-585	RARS, Guntur
22	AKL-170	NBPGR, Akola
23	PLM-110	UAS, Bangalore
24	LGG-577	RARS, Guntur
25	IC-436624	IIPR, Kanpur
26	IC-436723	IIPR, Kanpur
27	IC-413316	IIPR, Kanpur
28	IC-436746	IIPR, Kanpur
29	VGG10-010	TNAU, Coimbatore
30	VGG04-011	TNAU, Coimbatore
31	VGG04-007	TNAU, Coimbatore
32	COGG-93	TNAU, Coimbatore
33	VBNGG-2	TNAU, Coimbatore
34	TARM-2013	TNAU, Coimbatore
35	VGG04-005	TNAU, Coimbatore
36	COGG-920	TNAU, Coimbatore
37	VGG07-003	TNAU, Coimbatore
38	VGG10-002	TNAU, Coimbatore
39	VGG-112	TNAU, Coimbatore
40	IC-92048	NBPGR, Akola
41	AKL-103	NBPGR, Akola
42	AKL-39	NBPGR, Akola
43	AKL-106	NBPGR, Akola
44	AKL-225	NBPGR, Akola
45	AKL-95	NBPGR, Akola
46	AKL-194	NBPGR, Akola
47	AKL-212	NBPGR, Akola
48	AKL-195	NBPGR, Akola
49	AKL-211	NBPGR, Akola
50	KM13-11	ARS, Bidar
51	KM13-30	ARS, Bidar
52	KM13-45	ARS, Bidar
53	KM13-18	ARS, Bidar
54	KM13-5	ARS, Bidar
55	KM13-02	ARS, Bidar
56	KM13-37	ARS, Bidar
57	KM13-23	ARS, Bidar
58	KM13-55	ARS, Bidar
59	KM13-12	ARS, Bidar
60	GG13-9	ARS, Bidar
61	KM13-49	ARS, Bidar
62	GG13-4	ARS, Bidar

63	GG13-54	ARS, Bidar
64	KM13-20	ARS, Bidar
65	GG13-5	ARS, Bidar
66	Chinamung	ARS, Bidar
67	GG13-2	ARS, Bidar
68	KM13-26	ARS, Bidar
69	KM13-47	ARS, Bidar
70	KM13-41	ARS, Bidar
71	KM13-11	ARS, Bidar
72	KM13-42	ARS, Bidar
73	GG13-11	ARS, Bidar
74	GG13-8	ARS, Bidar
75	GG13-12	ARS, Bidar
76	KM13-48	ARS, Bidar
77	IPM2-3	ARS, Bidar
78	IPM2-14	ARS, Bidar
79	PDM-139	ARS, Bidar
80	LGG-580	RARS, Guntur
81	PM-112	TNAU, Coimbatore
82	LGG-578	NBPGR, Akola
83	LGG-563	NBPGR, Akola
84	LGG-594	NBPGR, Akola
85	TM-96-2	NBPGR, Akola
86	LGG-593	NBPGR, Akola
87	LGG-591	NBPGR, Akola
88	PM-115	NBPGR, Akola
89	LGG-587	NBPGR, Akola
90	PM-113	NBPGR, Akola
91	LGG-586	NBPGR, Akola
92	IC-436775	NBPGR, Akola
93	IC-413311	NBPGR, Akola
94	IC-398984	NBPGR, Akola
95	IC-436767	NBPGR, Akola
96	IC-436573	NBPGR, Akola
97	LGG-584	NBPGR, Akola
98	LGG-592	NBPGR, Akola
99	LGG-555	NBPGR, Akola
100	LGG-564	NBPGR, Akola
101	LGG-460	RARS, Guntur
102	LGG-595	RARS, Guntur
103	LGG-566	RARS, Guntur
104	IC-553514	IIPR, Kanpur
105	IC-413319	IIPR, Kanpur
106	IC-436542	IIPR, Kanpur
107	IC-546493	IIPR, Kanpur
108	IC-436594	IIPR, Kanpur
109	IC-436630	IIPR, Kanpur
110	IC-436668	IIPR, Kanpur
111	IC-436555	IIPR, Kanpur
112	IC-413314	IIPR, Kanpur
113	AKL-20	NBPGR, Akola
114	AKL-89	NBPGR, Akola
115	AKL-228	NBPGR, Akola
116	AKL-184	NBPGR, Akola
117	AKL-182	NBPGR, Akola
118	AKL-230	NBPGR, Akola
119	AKL-229	NBPGR, Akola
120	AKL-86	NBPGR, Akola
121	IC-436646	IIPR, Kanpur
122	IC-343964	IIPR, Kanpur
123	IC-436528	IIPR, Kanpur
124	IC-436723	IIPR, Kanpur
125	IC-546491	IIPR, Kanpur
126	IC-546481	IIPR, Kanpur
127	IC-398988	IIPR, Kanpur
128	VGG10-005	TNAU, Coimbatore
129	VBN-223	TNAU, Coimbatore
130	COGG-912	TNAU, Coimbatore
131	VBN(G9)-3	TNAU, Coimbatore

132	ML-1165	TNAU, Coimbatore
133	VGG04-025	TNAU, Coimbatore
134	VGG04-004	TNAU, Coimbatore
135	VGG04-149	TNAU, Coimbatore
136	COGG-954	TNAU, Coimbatore
137	VGG08-002	TNAU, Coimbatore
138	VBN-1	TNAU, Coimbatore
139	VGG-119	TNAU, Coimbatore
140	VC3890-A	TNAU, Coimbatore
141	DGGV-4	UAS, Raichur
142	KPS-1	UAS, Raichur
143	CGG-973	UAS, Raichur
144	CN9-5	UAS, Raichur
145	KPS-2	UAS, Raichur
146	VC-6173	UAS, Raichur
147	VC-6368	UAS, Raichur
148	CO-6	UAS, Raichur
149	Harsha	UAS, Raichur
150	PLM-92	UAS, Bangalore
151	MH-709	UAS, Raichur
152	LGG-460	RARS, Guntur
153	KGS-5	UAS, Raichur
154	Barimung-4	UAS, Raichur
155	AKL-189	NBPGR, Akola
156	AKL-168	NBPGR, Akola
157	AKL-218	NBPGR, Akola
158	AKL-179	NBPGR, Akola
159	AKL-185	NBPGR, Akola
160	AKL-163	NBPGR, Akola
161	COGG-912	TNAU, Coimbatore
162	IC-73451	NBPGR, Akola
163	IC-105690	NBPGR, Akola
164	IC-73534	NBPGR, Akola
165	IC-73412	NBPGR, Akola
166	IC-39605	NBPGR, Akola
167	IC-73472	NBPGR, Akola
168	IC-92053	NBPGR, Akola
169	IC-73779	NBPGR, Akola
170	IC-73462	NBPGR, Akola
171	IC-118992	NBPGR, Akola
172	IC-53783	NBPGR, Akola
173	IC-73456	NBPGR, Akola
174	IC-73458	NBPGR, Akola
175	AKL-105	NBPGR, Akola
176	AKL-213	NBPGR, Akola
177	AKL-169	NBPGR, Akola
178	AKL-220	NBPGR, Akola
179	AKL-84	NBPGR, Akola
180	AKL-82	NBPGR, Akola
181	AKL-97	NBPGR, Akola
182	AKL-226	NBPGR, Akola
183	AKL-24	NBPGR, Akola
170	IC-73462	NBPGR, Akola
171	IC-118992	NBPGR, Akola
172	IC-53783	NBPGR, Akola
173	IC-73456	NBPGR, Akola
174	IC-73458	NBPGR, Akola
175	AKL-105	NBPGR, Akola
176	AKL-213	NBPGR, Akola
177	AKL-169	NBPGR, Akola
178	AKL-220	NBPGR, Akola
179	AKL-84	NBPGR, Akola
180	AKL-82	NBPGR, Akola
181	AKL-97	NBPGR, Akola
182	AKL-226	NBPGR, Akola
183	AKL-24	NBPGR, Akola
184	AKL-174	NBPGR, Akola
185	AKL-161	NBPGR, Akola
186	AKL-180	NBPGR, Akola

187	AKL-222	NBPGR, Akola
188	AKL-187	NBPGR, Akola
189	AKL-216	NBPGR, Akola
190	AKL-29	NBPGR, Akola
191	AKL-90	NBPGR, Akola
192	AKL-227	NBPGR, Akola
193	AKL-200	NBPGR, Akola
194	AKL-92	NBPGR, Akola
195	AKL-183	NBPGR, Akola
196	AKL-176	NBPGR, Akola
197	AKL-191	NBPGR, Akola
198	AKL-165	NBPGR, Akola
199	AKL-164	NBPGR, Akola
200	AKL-192	NBPGR, Akola

2.1 Layout of the experiment

The experiment was conducted in an Augmented Randomized Complete Block Design with 200 germplasm accessions and 5 check varieties. As per the augmented RCBD, the check entries were replicated twice randomly in each block. There were 5 blocks, each block had 5 plots of size 3x3 m² thus each block size was 15 m². The gross area of experimental plot was 75 m². The row spacing was 30 cm and inter plant distance was 10 cm. The experiment was conducted during *summer* 2015. Recommended crop production practices were followed during the crop growth period to raise healthy crop.

2.2 Imposing drought condition

Drought condition was imposed by withholding irrigation 25 days after sowing (Baroowa and Gogoi, 2015; Pooja *et al.*, 2019) ^[9, 1]. Since the experiment was conducted during *summer* season, there were no unpredicted rains during the entire cropping period hence the drought condition was effectively imposed. The rainfall data of experimental site during the cropping period is given in table No.2.

Table 2: Meteorological data of experimental site for the year 2015

Year	Months	Temperature (°C)	Relative humidity (%)	Rainfall (mm)
2015	January	21.32	61.03	0.59
	February	23.10	50.72	Nil
	March	25.34	58.70	2 mm (25.03.2015)
	April	25.87	66.55	Nil

2.3 Plant sampling and data collection

Observations were recorded on five randomly chosen competitive plants from each germplasm accession for all the characters except days to 50 percent flowering and days to maturity, which were recorded on plot basis. The values of five competitive plants were averaged and expressed as mean of the respective characters. The observations were taken on the traits like; Days to 50% flowering, Days to maturity, Plant height (cm), Clusters per plant, Pods per cluster, Pods per plant, Pod length (cm), Seeds per pod, test weight, Threshing %, Harvest index (%), SCMR (SPAD Chlorophyll meter reading), Leaf water potential (Mpa), Proline content (µg g⁻¹), Relative water content, Specific leaf area and Seed yield per plant.

2.4 Test of normality

Test of normality for all the data sets of observations was carried out to check whether the data is following normal distribution or not. The normal distribution function is determined by the following formula

$$F(x) = 1/[(2*\pi)^{1/2} * \sigma] * e^{-1/2*(x-\mu)^2 / \sigma^2}$$

-∞ to + ∞

Where

‘μ’ is the mean of population

‘σ’ is the standard deviation of population

‘e’ is the Euler’s constant 92.71

‘x’ is the constant Pi (3.14)

The mean values of observations recorded on five plants were computed and these mean values were used in statistical analysis through computer based statistical software SAS 9.3 version and SPSS

3. Results and Discussion

Test of normality has to be conducted to know whether the quantitative traits are normally distributed in the population or not. This information is very much required to apply suitable statistical parameters and methods to analyze the data.

3.1 Analysis of variance

Analysis of variance revealed highly significant mean squares attributable to germplasm accessions for all the traits. Significant mean squares were recorded for all the traits. (Table 3). Mean squares attributable to ‘Genotypes vs check entries’ were significant for all the traits except seeds per pod and relative water content. These results suggest significant differences among the germplasm accessions. The germplasm accessions as group differed significantly for all of the traits under investigation, similarly, check entries as group differed significantly for most the traits under study.

3.2 Studies on distribution pattern of skewness and kurtosis

Skewness and kurtosis will help to understand relative mean performance and nature of distribution of traits (Table 4). Studies on distribution properties such as skewness and kurtosis provides insight about distribution pattern of the traits under study in the population. Skewness is the *degree of distortion* from the symmetrical bell curve or the normal distribution. It measures the lack of symmetry in the data distribution. If the skewness is between -0.5 and 0.5, the data is fairly distributed and is symmetrical. Kurtosis is about the distribution of tails whether it is peakedness or flatness. It is actually the *measure of outliers* present in the distribution. Lower kurtosis values in a data set is an indicator that data has light tails or lack of outliers. If the kurtosis is close to 0, then a normal distribution is often assumed. These are called mesokurtic distributions.

Table 3: Summary of augmented ANOVA for grain yield and component traits of germplasm accessions under drought condition

Sources of Variations	DF	DFE	DM	PH	CPP	PPC	PPP	PL	SPP	TW
Blocks (b)	4	14.74 **	8.18***	65.31**	2.23**	0.11*	25.23**	1.49**	5.05**	1.77 **
Entries (e) (Genotypes + Checks)	204	17.10 **	18.01**	84.47**	3.60**	0.51**	72.94**	0.75**	2.70**	0.35 **
Checks	4	34.57 **	37.01**	22.56**	1.40**	0.42**	12.50**	0.87**	3.98**	0.81 **
Genotypes	199	14.215 **	15.14**	85.71**	3.67**	0.51**	73.91**	0.73**	2.69**	0.31 **
Checks vs Genotypes	1	521.64 **	513.06**	85.01**	0.16**	1.45**	121.60**	4.52**	0.03	5.42 **
Error	16	1.32	0.74	0.98	0.04	0.02	0.98	0.009	0.05	0.05

Sources of Variations	DF	TP	HI	SCMR	LWP	PC	RWC	SLA	SYPP
Blocks (b)	4	37.12*	247.54 **	396.55 **	1.17 **	470.90 **	423.68 *	4067.34 *	2.11 **
Entries (e) (Genotypes + Checks)	204	37.20 **	54.41 *	98.71 **	2.45 **	1707.90 **	425.40 **	4283.10 **	7.01 **
Checks	4	17.09	64.39 *	24.49	0.82 **	942.07 **	63.06	1924.20	3.76 **
Genotypes	199	27.67 *	53.01 *	79.58 *	2.33 **	1712.67 **	433.68 **	4294.15**	7.10 **
Checks vs Genotypes	1	2014.79 **	293.20 **	4203.25 **	32.57 **	3822.09 **	227.32	11518.68**	0.42*
Error	16	9.83	19.57	31.14	0.03	1.48	130.64	1339.95	0.09

*Significant at P =0.05, ** Significant at P=0.01

DFE: Days to 50% flowering Pods plant⁻¹ HI: Harvest index (%) SLA: Specific leaf area
 DM: Days to maturity PL: Pod length (cm) SCMR: SPAD Chlorophyll meter reading SYPP: Seed yield plant⁻¹
 PH: Plant height (cm) SPP: Seeds per pod LWP: Leaf water potential (Mpa)
 CPP: Cluster plant⁻¹ TW: test weight (g) PC: Proline content (µg g⁻¹)
 PPC: Pods cluster⁻¹ TP: Threshing % RWC: Relative water content (%)

Table 4: Descriptive statistics for grain yield and its component traits of germplasm accessions under drought condition

Descriptive	DFE	DM	PH	CPP	PPC	PPP	PL	SPP	TW
Mean	41.61	69.14	37.74	5.00	3.23	16.81	5.83	6.63	3.45
Std. Error	0.26	0.27	0.58	0.12	0.04	0.54	0.56	0.10	0.03
Variance	15.93	17.37	78.13	3.32	0.47	66.93	0.71	2.55	0.35
Skewness	0.38	0.30	-0.31	-0.11	-0.18	0.23	0.08	-0.13	-0.04
Kurtosis	-0.28	-0.31	-0.41	-1.18	-1.09	-0.96	-0.83	-0.99	1.02

Descriptive	TP	HI	SCMR	LWP	PC	RWC	SLA	SYPP
Mean	62.03	35.11	55.55	-5.74	120.98	68.59	156.52	4.02
Std. Error	0.39	0.49	0.66	0.10	2.63	1.34	4.25	0.16
Variance	35.25	55.37	99.21	2.25	1563.92	404.32	4069.02	6.42
Skewness	-0.24	0.01	0.35	0.69	0.319	-0.20	-0.17	0.66
Kurtosis	0.24	-1.00	-0.43	-0.46	-1.24	-1.57	-0.97	-0.37

DFE: Days to 50% flowering PL: Pod length (cm)
 DM: Days to maturity SPP: Seeds per pod
 PH: Plant height (cm) TW: test weight (g)
 CPP: Cluster plant⁻¹ TP: Threshing %
 PPC: Pods cluster⁻¹ HI: Harvest index (%)
 PPP: Pods plant⁻¹ SCMR: SPAD Chlorophyll meter reading

If the kurtosis is less than zero, then the distribution is light tailed and is called a platykurtic distribution. If the kurtosis is greater than zero, then the distribution has heavier tails and is called a leptokurtic distribution. Positive kurtosis indicates a relatively peaked distribution. Negative kurtosis indicates a relatively flat distribution. As with skewness, if the value of kurtosis is too big or too small, there is concern about the normality of the distribution. These measures of skewness and kurtosis are one method of examining the distribution of the data. However, they are not definitive in concluding normality. What should also be examined is a graph (histogram) of the data; and further, one should consider performing other tests for normality such as the Shapiro-Wilk or the Kolmogorov-Smirnov test.

All the quantitative traits studied in germplasm accessions exhibited skewness values between -0.5 and 0.5 except for the traits leaf water potential (0.69) and seed yield per plant (0.66) indicating the fact that these traits are normally distributed in the population. Similarly all the quantitative traits exhibited lesser than zero values for kurtosis except for the test weight (1.02) and threshing percentage (0.24) indicating that the tails of the distribution of these traits are platykurtic with no

outliers in the data set. Mariyammal *et al.*, (2019) [10], has reported positive skewed and platykurtic for the traits; days to first flowering, plant height, number of clusters per plant and number of pods per cluster in Green gram. Sumathi *et al.* (2018) [11], has reported positive skewness for days to 50% tasseling, days to 50% silking, days to maturity, cob diameter, 100 grain weight and grain yield per plant in Maize.

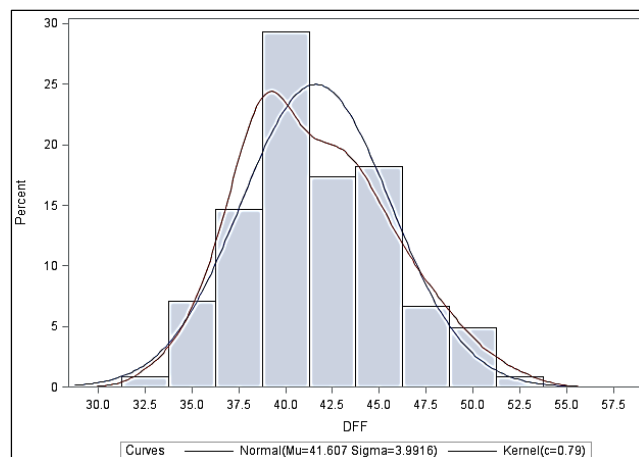


Fig 1: Distribution of DFF

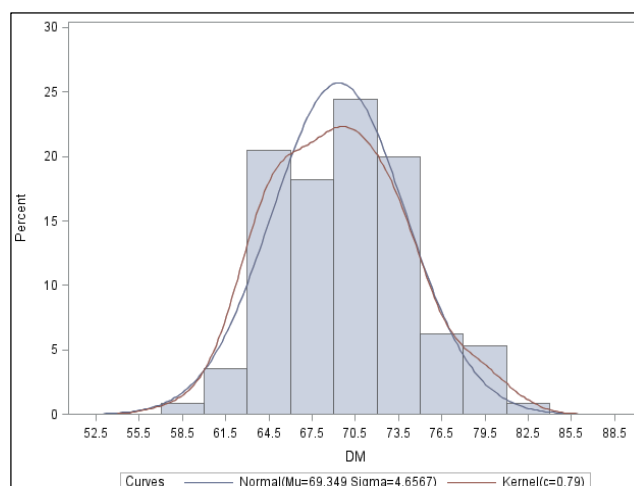


Fig 2: Distribution of DM

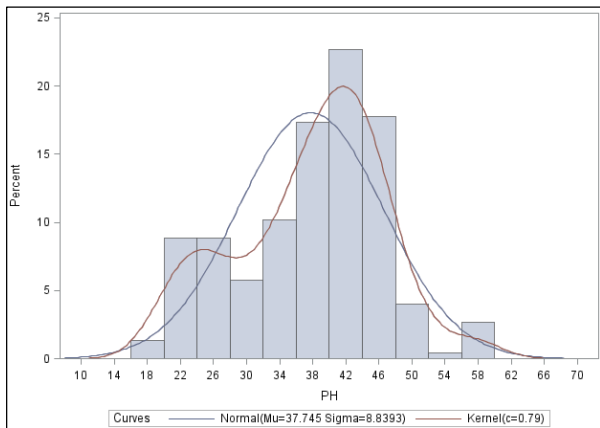


Fig 3: Distribution of PH

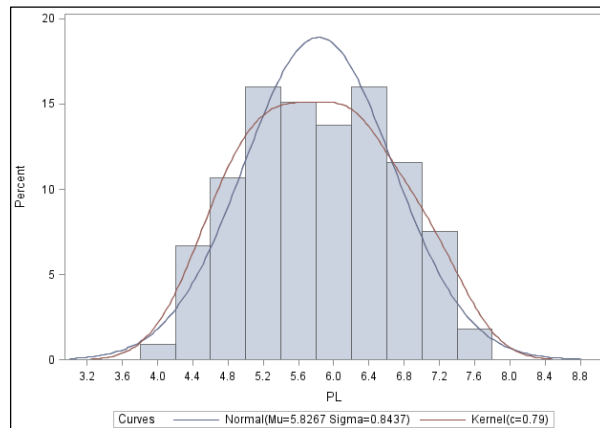


Fig 7: Distribution of PL

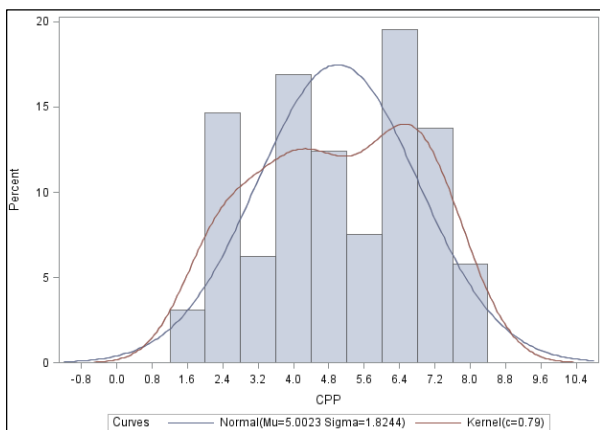


Fig 4: Distribution of CPP

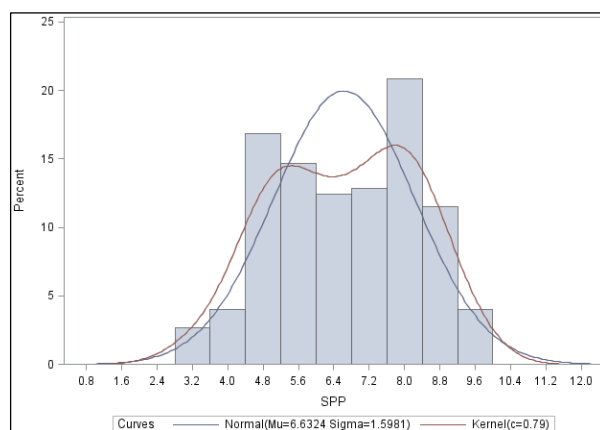


Fig 8: Distribution of SPP

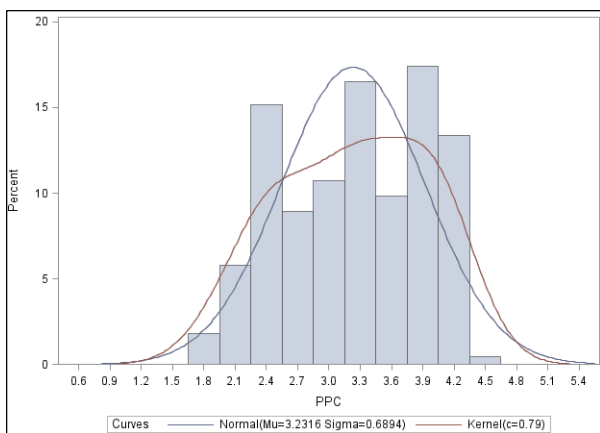


Fig 5: Distribution of PPC

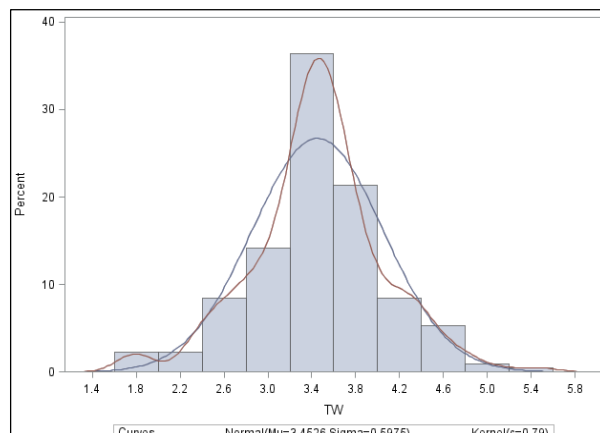


Fig 9: Distribution of TW

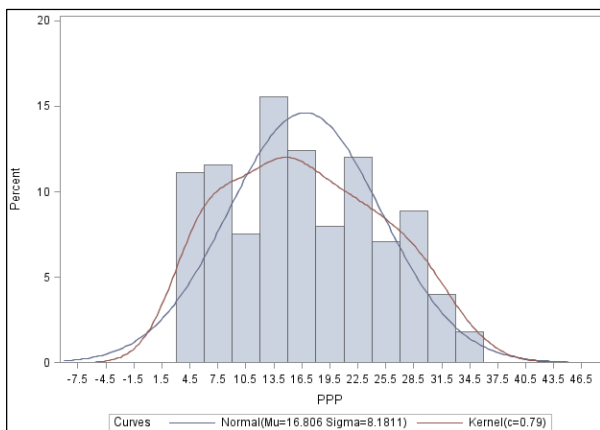


Fig 6: Distribution of PPP

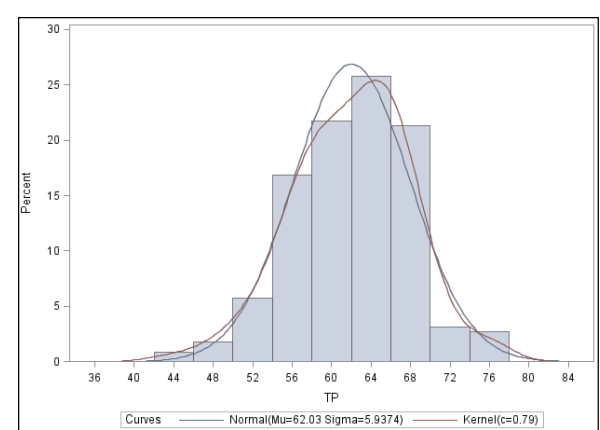


Fig 10: Distribution of TP

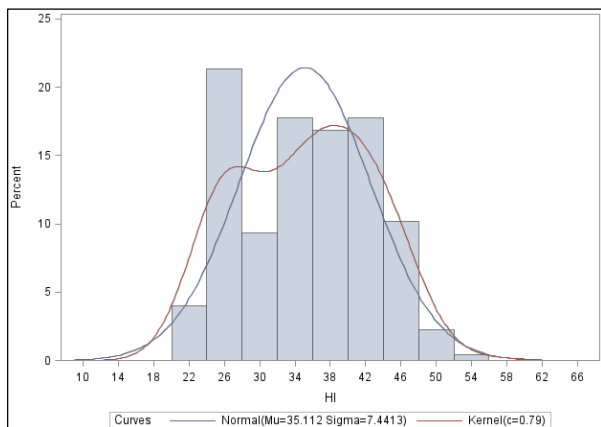


Fig 11: Distribution of HI

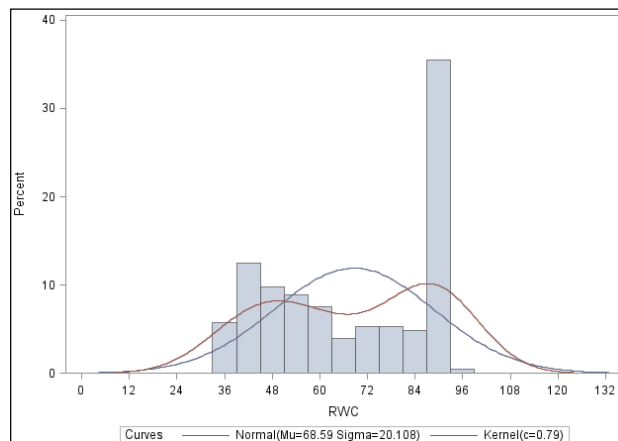


Fig 15: Distribution of RWC

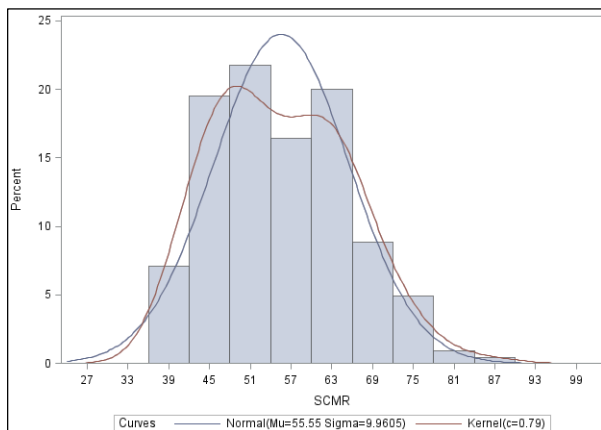


Fig 12: Distribution of SCMR

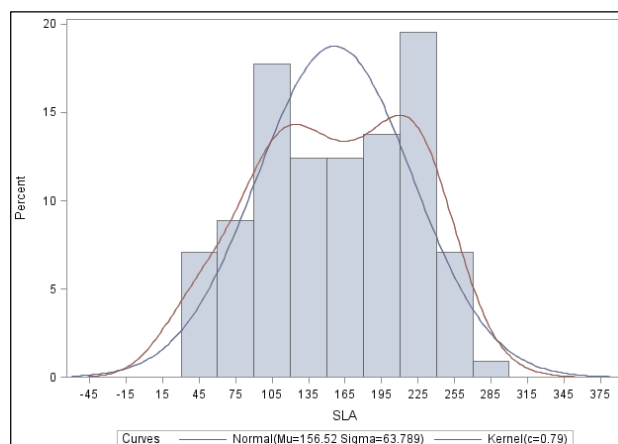


Fig 16: Distribution of SLA

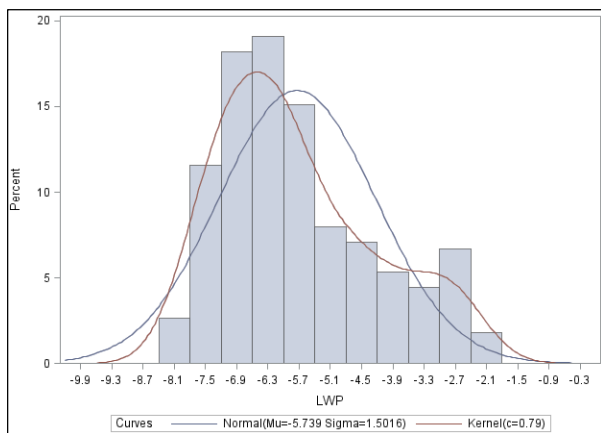


Fig 13: Distribution of LWP

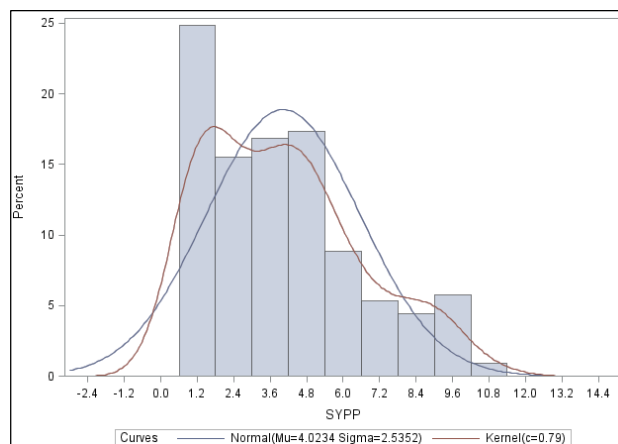


Fig 17: Distribution of SYPP

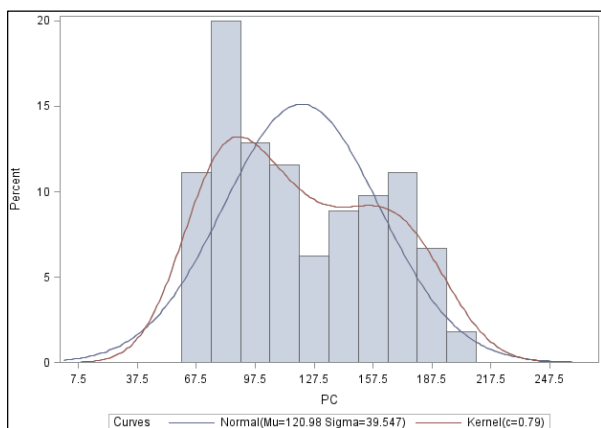


Fig 14: Distribution of PC

4. Conclusions

The study revealed that quantitative traits studied under drought condition in germplasm accessions of Green gram exhibited skewness values between -0.5 and 0.5 indicating the fact that these traits are normally distributed in the population. All the quantitative traits exhibited lesser than zero values for kurtosis indicating that the tails of the distribution of these traits are platykurtic with no outliers in the data set.

5. Acknowledgement

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6. References

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