RESEARCH ARTICLE

Legume Research- An International Journal, Volume 45 Issue 11: 1333-1343 (November 2022)

Evaluation of Mung Bean Germplasm [*Vigna radiata* (L.) Wilczek] for Yield in Transitional Plain of Inland Drainage Zone of Rajasthan, India

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10.18805/LR-4543

ABSTRACT

Background: Pulses are leguminous crops which not only increase the soil fertility, its fitness and maintain soil health but also essential to meet the nutritional demand of burgeoning human population particularly in developing countries. Mungbean is a major pulse crop of Zone IIa (Transitional Plain of Inland Drainage Zone) of Rajasthan state. Farm profitability can also be enhanced by augmenting farm productivity. Selection of high yielding genotypes may play a vital role to achieve sustainable high agricultural yield at farmer's field. Therefore, it is prerequisite to identify the suitable genotypes for this zone since the available varieties were not tested for its adaptability. The current study was aimed to evaluate twelve mung bean genotypes for seed yield with four checks in Zone IIa of Rajasthan.

Methods: The mung bean crop was raised during *Kharif* 2018 and 2019 at Agricultural Research Station, Fatehpur-Shekhawati, Sikar (Rajasthan). Seed yield and its ancillary characters have been observed by following standard protocols. Present experiment was conducted in randomized block design with three replications. The material was sown in a four row plot of 4 m length with a spacing of 30 cm between rows and 10 cm between plants.

Result: The performance of genotypes RMG 1098, RMG 1132, RMG 1134, RMG 1139 and RMG 1147 were superior to the zonal, state checks and other tested genotypes. The selected high yielding mung bean genotypes can increase farm output per se and farm profitability by sustaining soil health, fitness and productivity of this region.

Key words: Evaluation, Mung bean, Randomized block design, Yielding ability, Zone IIa.

INTRODUCTION

Pulses are extensively grown in tropical regions of the world as a major protein rich crop bringing considerable improvement in human diet and play an important role for alleviation of malnutrition particularly from developing African and Asian countries (Chandra *et al.,* 2019a). Average protein content in the pulse seed is around 24 per cent (Nair *et al.*, 2019). The protein is comparatively rich in the amino acid lysine which is deficient in cereal grains (Baskaran *et al.,* 2009; Garg *et al.*, 2017). Mung bean [*Vigna radiata* (L.) Wilczek] is one of the important pulse crop in arid regions of Indian subcontinent (Hanumantha *et al.*, 2016) because of its short maturity duration, high nitrogen fixation ability, barren tolerance (Zhou *et al.,* 2020; Muthu *et al.*, 2018; Patil *et al.*, 2011), adaptation to low water requirement and low soil fertility (Raturi *et al.*, 2015). It is favored for human consumption due to its high palatability, easy digestibility and low production of flatulence (Raghuvanshi *et al.*, 2011).

The mung bean secures third place in India after chickpea and pigeon pea in terms of cultivated area. In India, it is cultivated on 4.26 million ha (m ha) area with production of 2.01 million tones (mt) and productivity of 472 kg/ha (AICRP on MULLaRP, 2018). As per Department of Agriculture (Fourth Advance Estimate of 2020), the Rajasthan state comprised 2.32 m ha area, 1.30 mt production with a productivity of 559 kg/ha. Sikar district is having 0.07 mha, 0.05 mt with a productivity of 773 kg/ha. Hence, the data revealed that district level performance is better than national productivity which shows the suitability of mung bean in arid region of Rajasthan. The average productivity of mung bean is very low not only in India but also in the countries of tropical and sub-tropical Asia (Pratap *et al.,* 2012; Kumar *et al.,* 2005). Based on above studies, the aim of present study

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How to cite this article: Khatik, C.L., Chandra, K., Khan, M., Ved Prakash, Jatav, H.S., Khan, M.A., Chand, S. and Mishra, C.D. (2022). Evaluation of Mung Bean Germplasm [*Vigna radiata* (L.) Wilczek] for Yield in Transitional Plain of Inland Drainage Zone of Rajasthan, India. Legume Research. 45(11): 1333-1343. DOI: 10.18805/LR-4543.

Submitted: 05-11-2020 **Accepted:** 18-03-2021 **Online:** 02-04-2021

was to identify high yielding genotypes suitable for this zone. Such type of findings may help mung bean growers to have best choice from the basket and increase their farm profitability and also have great role in crop diversification and ecological sustainability.

MATERIALS AND METHODS

The present investigation was undertaken to study the seed yield and its ancillary characters. The experiment involved twelve genotypes with four checks of mung bean which were sown in randomized block design with three replications during *Kharif* 2018 and 2019 at research farm of Agricultural Research Station, Fatehpur-Shekhawati, Sikar (Rajasthan) and the experimental location is depicted in Fig 1. The location comes under Zone IIa of Rajasthan and known as" Transitional Plain of Inland Drainage Zone". These genotypes were obtained from All India Coordinated Research Project on MULLaRP, RARI, Durgapur (Jaipur). Twelve mung bean genotypes *viz.* RMG-1087, RMG-1094, RMG-1098, RMG-1132, RMG-1134, RMG-1137, RMG-1138, RMG-1139, RMG-1147, RMG-1148, RMG-1152, RMG-1154 along with two zonal checks (RMG-492, IPM-02-3) and two state checks (RMG-975, MSJ-118) were included for the experiment (Fig 2). The details of checks were presented in Table 1.

Each genotype was positioned in a four row plot of 4 m length with a spacing of 30 cm between rows and 10 cm between plants. Ten random plants were selected from each plot and data were recorded on five characters *viz*. plant height (cm), pod length (cm), number of seeds per pod, test weight (g) and seed yield (kg/ha). For days to 50% flowering and days to maturity data were recorded on whole plot basis.

Statistical analysis

All the characters were analyzed for PCV and GCV (Burton, 1952), heritability in broad sense (Falconer, 1981) and genetic advance as percent of mean (Johnson *et al.,* 1955). Analysis of variance (ANOVA) and Duncan's new multiple range test were carried out using Statistical Tool for Agricultural Research (STAR) software of International Rice Research Institute (IRRI). The data were subjected to the Best Linear Unbiased Predictors (BLUPs) using Multi-Environment Trial Analysis in R (META-R) software of CIMMYT. The R (version 4.0.2) software was used to display the scatter plots, correlograms, box plots and heat map.

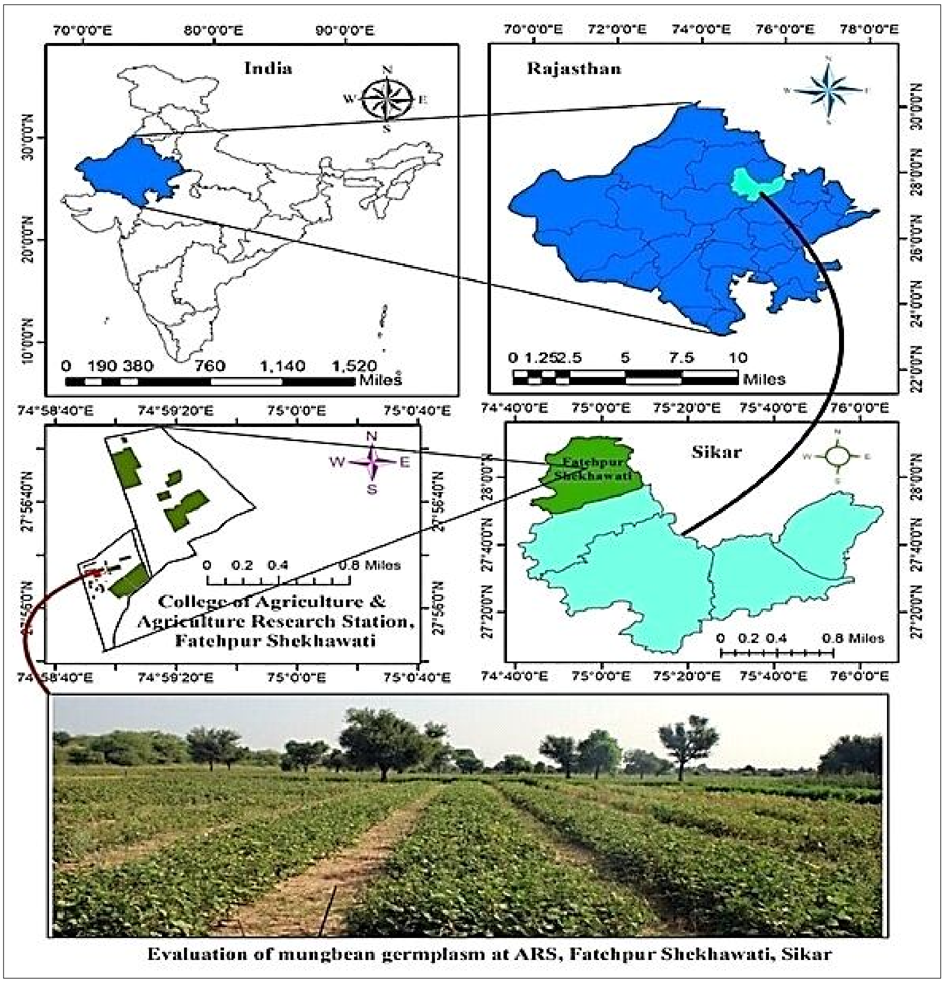


Fig 1: Experimental location of evaluating mungbean germplasm.

RESULTS AND DISCUSSION

The main objective of any plant breeding programme is to produce high yielding varieties suitable for the cultivation area and breeding strategy like selection can only be imposed when there is ample availability of desirable genetic variability (Chandra *et al.,* 2019b) and variability can be revealed through analysis of variance (ANOVA). Therefore, total variability was divided into different components presented in Table 2 for yield and its contributing characters of twelve mung bean genotypes along with four checks evaluated at Transitional Plain of Inland Drainage zone of Rajasthan. Results from individual ANOVA analysis for *kharif* 2018 and 2019 revealed that variability in mung bean germplasm found to be significant for all the characters under study. However, pooled analysis of both season exhibited variation only in pod length, test weight and seed yield. Whereas interaction effect of year × treatment showed that days to 50% flowering, days to maturity, plant height, number

Fig 2: Mung bean germplasm used for present experiment.

Table 1: Details of checks used for present experimental findings.

Checks	Released year	Characteristics	Reference
IPM-02-3	2009	▪ Developed from hybridization of IPM-99-125 × Pusa Bold 2 ▪ Grain medium size ▪ 100 seed weight = 3.4 g ▪ Susceptible to Yellow mosaic virus ▪ Maturity days = 70-72 days ▪ Yield = 11-12 q/ha (in favourable condition) ▪ Released by IIPR, Kanpur	Department of Agriculture, Important Improved Agricultural techniques for *Kharif* crops (Hindi) *Kharif*-2019. Sikar Zone: Zone IIa, Joint Director Agriculture (Extension). Pp. 38-39.
RMG-492	2003	▪ Maturity days = 65-70 days ▪ 100 seed weight = 4.1 g ▪ Bold seeded variety shiny green colour seed resistant to BLS.	
RMG-975 (Keshwan and Mung 1)	2016 (SVRC)	▪ Yield = 8-9 q/ha ▪ Days to maturity = 65-70 days ▪ Moderately tolerant to MYMV and tolerant to root knot nematode ▪ Released by RARI, Durgapura	State released varieties of Mungbean in India Project Coordinator's Report, AICRP on MULLaRP, ICAR, IIPR, Kanpur, 2017-18.
MSJ 118a (Keshwn and Mung 2)	2016 (SVRC)	▪ Yield = 7-8 q/ha ▪ Days to maturity = 66-65 days ▪ Moderately tolerant to MYMV ▪ Released by RARI, Durgapura	

of seeds/pod and test weight were only significant. Similar reports have been obtained from Belay *et al.* (2019) stating that analysis of variance for six mung bean varieties exhibited differences in varietal characters *viz.* days to 50% flowering, plant height, number of seeds per pod, seed yield and thousand seed weight ($p \leq 0.05$) except number of pods per plant.

The significant differences revealed that there is ample genetic variability among mung bean germplasm. After exploitation of genetic variability in available germplasm, it is better to separate heritable portion from the non-heritable part and to plan the accurate breeding programme and this is the opportunity to a breeder that now he/she can improve characters with high heritability *via* selection (Parida *et al.,* 2018).

Piepho *et al.* (2008) explains that BLUP has good predictive accuracy in plant breeding experiments. Table 3 presents the summary statistics, heritability (broad sense) and BLUPs values of mung bean germplasm for yield and its ancillary characters. Where it clearly depicts that the seed yield drastically decreased *i.e.* 41.23% in 2019 compared to 2018 *kharif* season and days to maturity also revealed that the genotypes responded early in maturity in 2019 since there is 17.98% reduction in maturity days. Similarly other traits under study also revealed percent reduction in 2019 *viz.* test weight (8.85%), number of seed/pod (8.15%) and plant height (3.63%) whereas delayed days to 50% flowering (1.46%) and increased pod length (1.94%) have been observed. The reduction in yield in *kharif,* 2019 might be due to high rainfall coinciding with maturity stage of mung bean during 39th meteorological week (24th September- 30th September) and early crop maturity whereas no rainfall coincides with maturity in 2018 as depicted from Fig 7 and Fig 8.

Johnson *et al.* (1955) has classified heritability as low (below 30%); medium (30-60%) and high (above 60%). In both the seasons only days to 50% flowering and test weight shown high heritability (>60%). This implies that expected gain from selection will be high if these traits are to be used as selection criteria in mung bean crop improvement (Degefa *et al.*, 2014).

The data collected from present study were also used for estimating the variability, normality and character association for yield and ancillary characters of mung bean germplasm and presented in Fig 3, where distribution of each variable has been depicted diagonally. The bivariate scatter plots with a fitted line are given below the diagonal and correlation values above the diagonal. All the traits under study followed normal distribution. The x-axis represents column variable and y-axis represent row variable in each scatter plot. The correlation values under scatter plots were also supported using correlograms among yield and ancillary characters of mung bean genotypes (Fig 4). In 2018, seed yield was positively correlated with days to 50% flowering, days to maturity and number of seeds/pod, but negatively correlated with plant height. Similar findings reported from Makeen *et al.* (2007). However, in 2019 the similar pattern was not observed and seed yield was found to be negatively correlated with days to 50% flowering and number of seeds/pod, while positive correlation with plant height and pod length. Observing a negative correlation of seed yield with number of seeds/pod is not in agreement with other reports and this negative correlation might be due to shriveled and

Table 2: ANOVA (*Kharif* 2018, 2019 and pooled) of mung bean germplasm for yield and its ancillary characters.

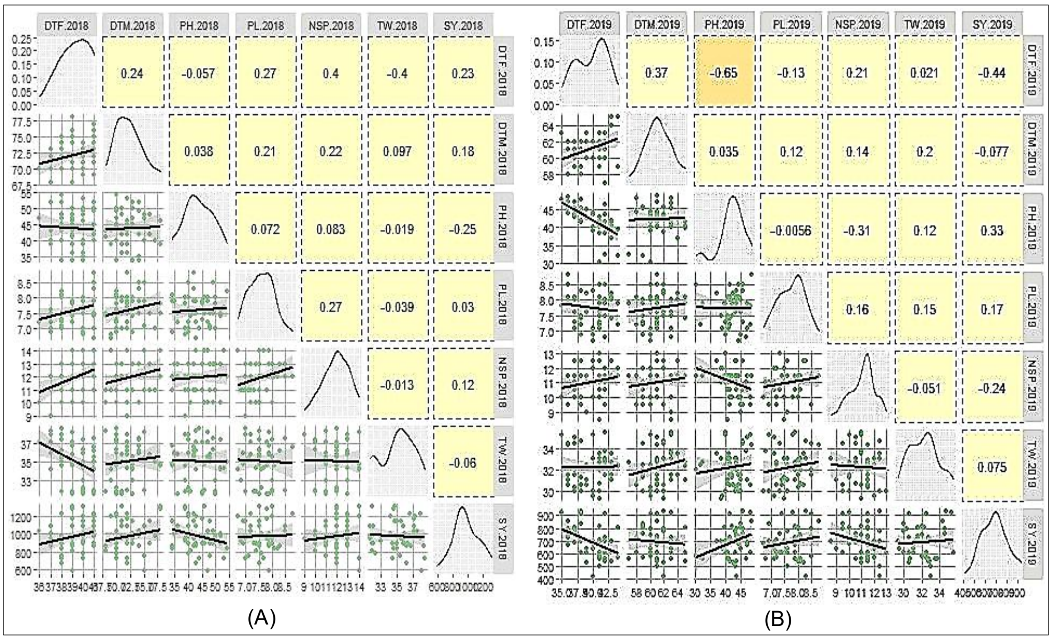
		Characters						
Sources of variation	Df	Days to 50% flowering	Days to maturity	Plant height	Pod length (cm)	No. of seeds/pod	Test weight (g)	Seed yield (kg/ha)
Year 2018								
Genotype	15	4.13**	8.18*	48.36*	0.38**	2.45**	13.88**	45055.14*
Replication	2	7.77	30.06	46.08	1.05	1.56	0.01	51109.33
Error	30	0.35	3.22	17.64	0.11	0.90	0.15	18490.82
CD (Genotype)	0.98	2.99	6.99	0.55	1.58	0.66	226.51	
Year 2019								
Genotype	15	17.02**	7.42**	41.34**	0.22**	1.52*	8.10**	32653.50**
Replication	2	5.40	6.81	4.04	3.21	2.27	0.08	11012.31
Error	30	0.80	1.35	1.81	0.08	0.67	0.26	4745.69
CD (Genotype)	1.50	1.96	2.24	0.46	1.38	0.86	114.77	
Pooled								
Year	1	8.17	2904.00**	56.27	0.52	19.26*	196.07**	1940290.67**
Replication within year	4	6.58	18.44	25.06	2.13	1.92	0.04	31060.82*
Genotype	15	9.31	2.55	52.75	0.52**	2.15	15.62**	57571.44*
Year × Genotype	15	11.83**	13.04**	36.95**	0.08	1.82**	6.36**	20137.20
Pooled error	60	0.57	2.28	9.72	0.09	0.78	0.21	11618.26
CD (Year)		1.39	2.33	2.72	0.79	0.75	0.11	95.67
CD (Genotype)		5.28	5.54	9.33	0.42	2.07	0.69	217.88
CD (Year × Genotype)		1.64	3.28	6.77	0.66	1.92	0.98	234.04

poor pod filling due to high humidity by rainfall at maturity stage of mung been (Fig 8).

Further to understand the significant difference between genotypes under study, Duncan's new multiple range test of mung bean germplasm for yield and its ancillary characters were studied and the results are presented in Table 4. Genotypes RMG 1098 and RMG 1132 were jointly ranked first for seed yield with the value of 1129.67 kg/ha during *kharif* 2018. However, genotypes RMG 1087, RMG 1094, RMG 1134, RMG 1137, RMG 1138, RMG 1139, RMG 1147 and RMG 492 were also statistically on par. In *kharif* 2019, genotype RMG 1147 ranked first for seed yield. Lowest yield was obtained from MSJ 118 in 2018 and IPM 02-3 in 2019. Therefore, during both the year, genotype RMG 1147 was found to be suitable and outperformed even in condition of rainfall coinciding with maturity (*kharif* 2019). The seed yield of genotypes RMG 1098, RMG 1132, RMG 1134, RMG 1139 and RMG 1147 were superior over the zonal and state checks.

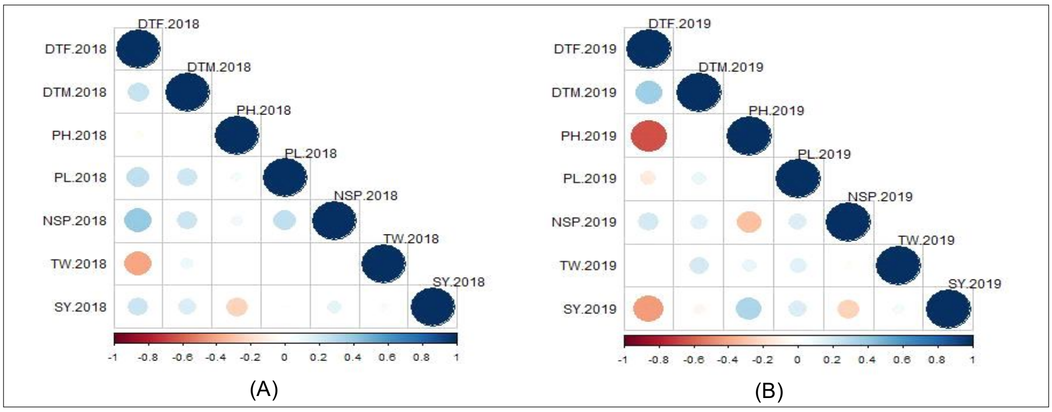
Fig 5 revealed box plot description of mung bean yield and its ancillary characteristics. Williamson *et al.* (1989) states that box plot convey the level, spread and symmetry of distribution of data. Fig 5(a) for days to 50% flowering depicts that a wide range has been observed in 2019 compare to 2018 and median value revealed delayed flowering in 2019 than 2018. This might be due to more rainfall in 2019 *i.e.* 414 mm total rainfall and 33 rainy days compare to 281.5 mm rainfall and 27 rainy days in 2018 which tends to extend of vegetative growth and lead to delay flowering (Fig 7 and Fig 8).

All the studied genotypes showed delayed maturity during 2018 as compared to 2019 (Fig 5b). Thus, during 2019, early maturity might be due to high humidity at critical stage tends to invite the infestation of disease and pest and plant forced to complete their life cycle under stress condition (Oplinger *et al.,* 1990; Nair *et al.*, 2019). Genotypes showed more number of seeds/pod during 2018 (Fig 5c). Hence, observed seed yield was less during 2019 than 2018 (Fig 5g).



(A) (B)

Fig 3: Scatter plot of yield and ancillary characters of mung bean genotypes during (A) 2018 and (B) 2019.



(A) (B)

Fig 4: Correlation among yield and ancillary characters of mung bean genotypes during (A) 2018 and (B) 2019.

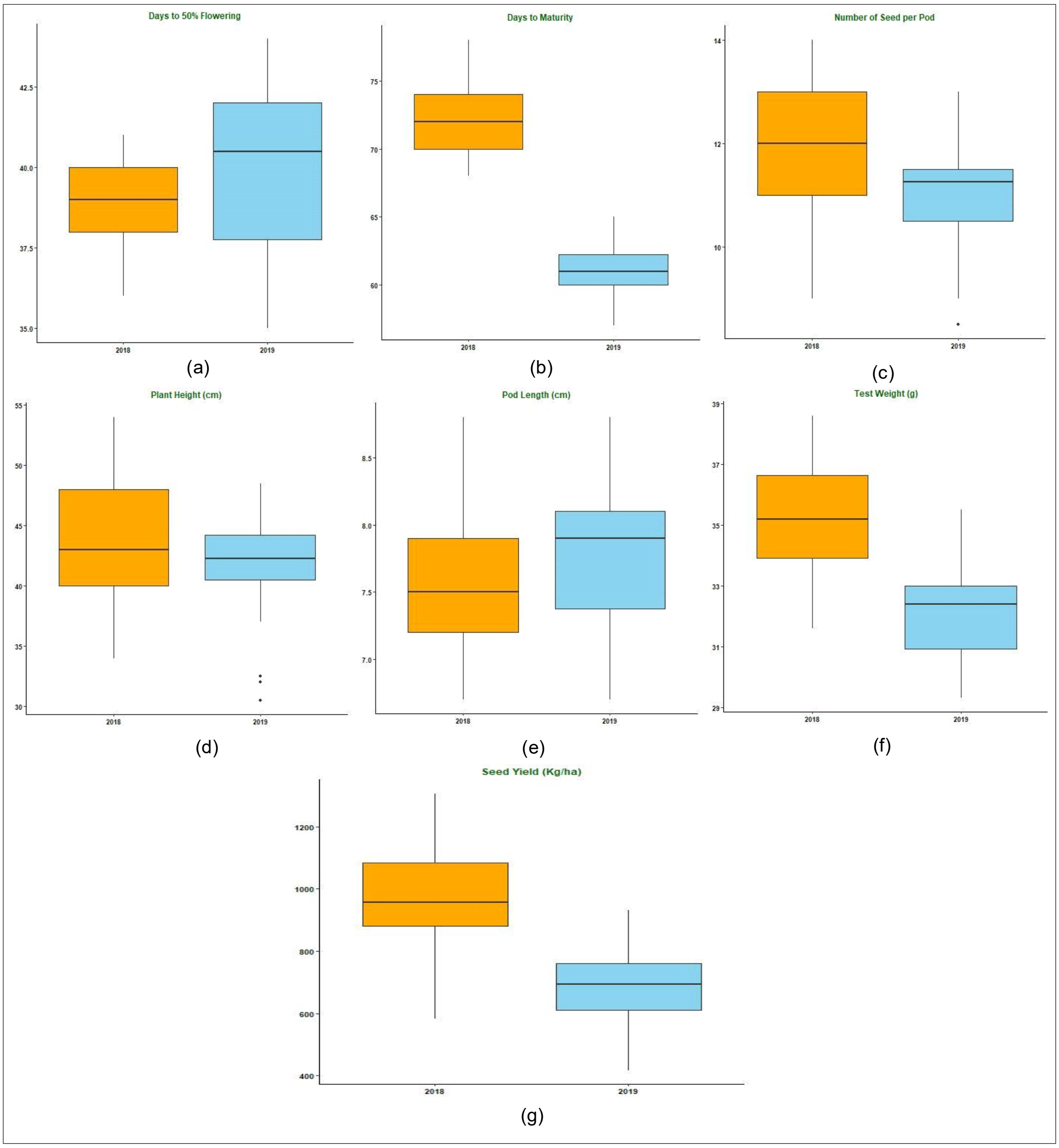
Table 3: Summary statistics, heritability (broad sense) and best linear unbiased predictors (BLUPs) of mung bean genotypes for yield and ancillary characters over the years 2018 and 2019.

Genotypes	Days to 50% flowering		Days to maturity		Plant height (cm)		Pod length (cm)		No. of seed/pod		Test weight (g)		Seed yield (kg/ha)	
	2018	2019	2018	2019	2018	2019	2018	2019	2018	2019	2018	2019	2018	2019
IPM-02-3(C)	38.41	40.94	73.69	61.85	46.21	42.64	7.55	7.78	11.98	11.39	35.59	33.10	907.33	531.82
MSJ-118(C)	38.10	42.85	71.47	63.22	44.30	38.50	7.50	7.82	12.19	11.58	38.36	32.91	825.38	725.26
RMG-1087	37.19	40.31	72.07	61.31	45.15	41.69	7.33	7.54	10.50	10.46	37.51	32.72	978.28	673.70
RMG-1094	39.93	42.21	73.29	59.12	39.86	32.12	7.55	7.82	11.98	11.39	35.79	32.39	1032.92	586.81
RMG-1098	39.93	37.13	74.50	59.40	39.86	44.08	7.33	7.69	11.55	10.93	34.80	30.33	1065.74	768.85
RMG-1132	39.93	36.18	72.07	61.85	44.30	46.63	7.96	7.78	12.40	10.46	37.38	34.85	1065.74	783.95
RMG-1134	40.54	38.40	71.47	61.03	46.21	42.80	7.19	7.42	12.82	11.20	34.54	30.23	1032.92	775.40
RMG-1137	38.71	37.13	72.88	60.22	41.97	43.12	7.77	7.93	12.40	10.93	34.80	31.62	994.79	721.27
RMG-1138	38.10	37.13	72.07	59.67	40.70	46.47	7.48	7.71	11.98	10.65	37.31	31.04	1021.91	693.92
RMG-1139	40.54	41.58	72.68	60.22	42.18	42.32	7.98	7.97	12.19	10.65	31.84	32.39	1060.23	796.77
RMG-1147	40.54	37.13	72.07	60.76	44.09	46.31	8.03	7.99	11.77	11.30	36.39	34.43	983.78	823.26
RMG-1148	38.10	40.94	71.47	61.31	42.40	40.57	7.48	7.67	11.98	10.93	35.99	34.52	891.02	673.70
RMG-1152	39.32	42.53	70.86	63.49	44.94	41.37	7.69	7.78	10.92	11.30	31.84	31.36	918.34	677.69
RMG-1154	40.24	41.90	70.86	62.67	43.24	43.60	7.26	7.59	11.77	11.39	32.36	33.10	923.84	555.47
RMG-492(C)	39.32	40.63	71.67	61.03	43.67	39.30	7.60	7.46	12.19	11.58	32.16	29.68	978.28	654.04
RMG-975(C)	38.41	39.67	71.87	61.85	49.60	42.64	7.77	7.88	12.40	10.55	34.54	30.78	901.83	591.08
Mean	39.21	39.79	72.19	61.19	43.67	42.14	7.59	7.74	11.94	11.04	35.07	32.22	973.90	689.56
CV	1.51	2.24	2.49	1.90	9.62	3.19	4.28	3.63	7.93	7.42	1.10	1.59	13.96	9.99
LSD	0.94	1.45	2.33	1.75	5.58	2.19	0.46	0.37	1.26	1.02	0.64	0.84	174.11	106.20
Genotypic variance	1.26	5.41	1.65	2.03	10.24	13.18	0.09	0.05	0.52	0.28	4.58	2.61	8854.77	9302.60
Error variance	0.35	0.80	3.22	1.35	17.64	1.81	0.11	0.08	0.90	0.67	0.15	0.26	18490.82	4745.69
Broad sense heritability	0.78	0.87	0.34	0.60	0.37	0.88	0.47	0.37	0.37	0.30	0.97	0.91	0.32	0.66

A higher mean pod length was shown by horizontal line in box plot for 2019 compare to 2018 which can be revealed from Fig 5(e).

It is inevitable that pod length, number of seeds/pod and seed yield are interrelated characters. High humidity (Fig 7 and Fig 8) at critical plant stages may attract disease and pest. In 2019, genotypic seed yield was less compare than 2018 due to infestation of fungal even though there was higher pod length. It tends to incomplete pod filling and less number of seeds per pod and resulted in yield penalty. Apart from this, lack of sunlight facilitated vegetation to grow between the sown seeds that used most of the nutrients. Medium value shows that there was no much difference with reference to plant height as depicted from Fig 5(d). However, a wide range has been observed in 2018 compared to 2019. A higher test weight has been observed in 2018 compared to 2019 as depicted in Fig 5(f). Therefore, it clearly depicts that the grain formed in 2019 were shriveled and small. Kumar *et al*. (2013) also reported that heavy rain leads to yield loss in green gram.

Clustered heat map of yield and ancillary characters of mung bean genotypes during 2018 and 2019 has been presented in Fig 6. Heat map is a two way display of data

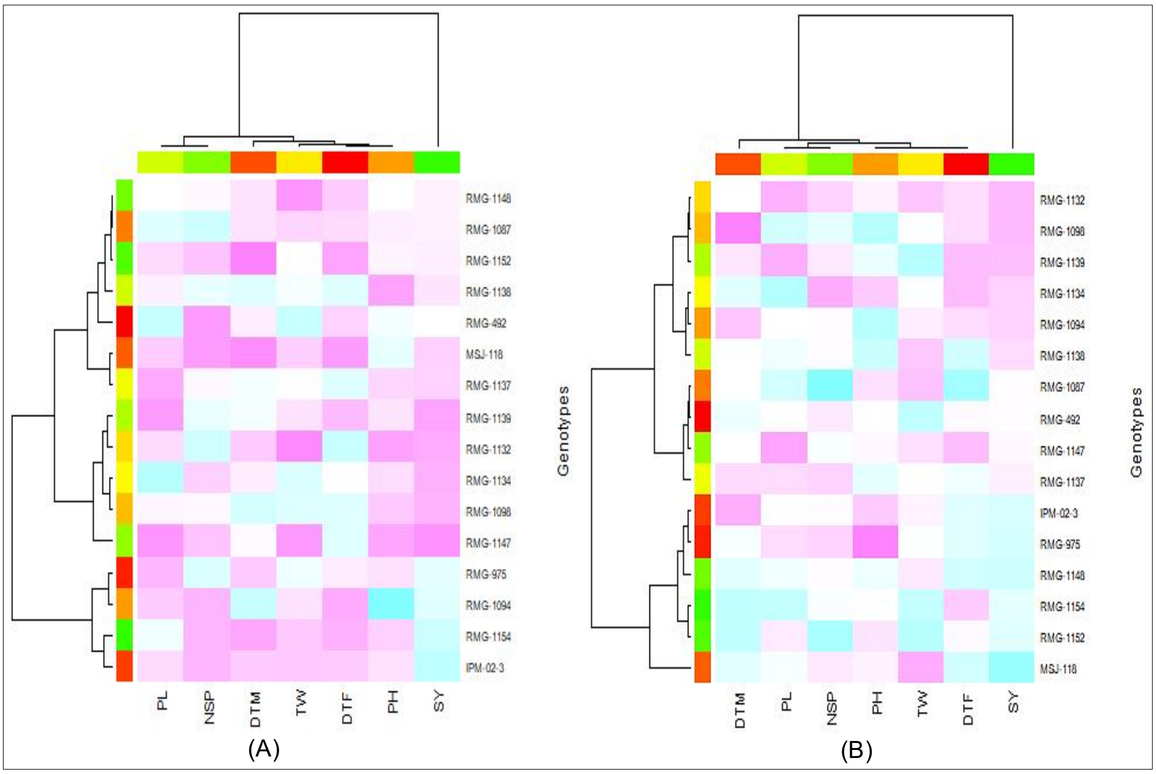


(a) (b) (c)

(d) (e) (f)

(g)

Fig 5: Box plot of yield and ancillary characters of mung bean genotypes during 2018 and 2019 for (a) days to 50% flowering, (b) days to maturity, (c) no. of seed per pod, (d) plant height, (e) pod length, (f) test weight and (g) seed yield.



(A) (B)

Fig 6: Heat map of yield and ancillary characters of mung bean genotypes during (A) 2018 and (B) 2019.

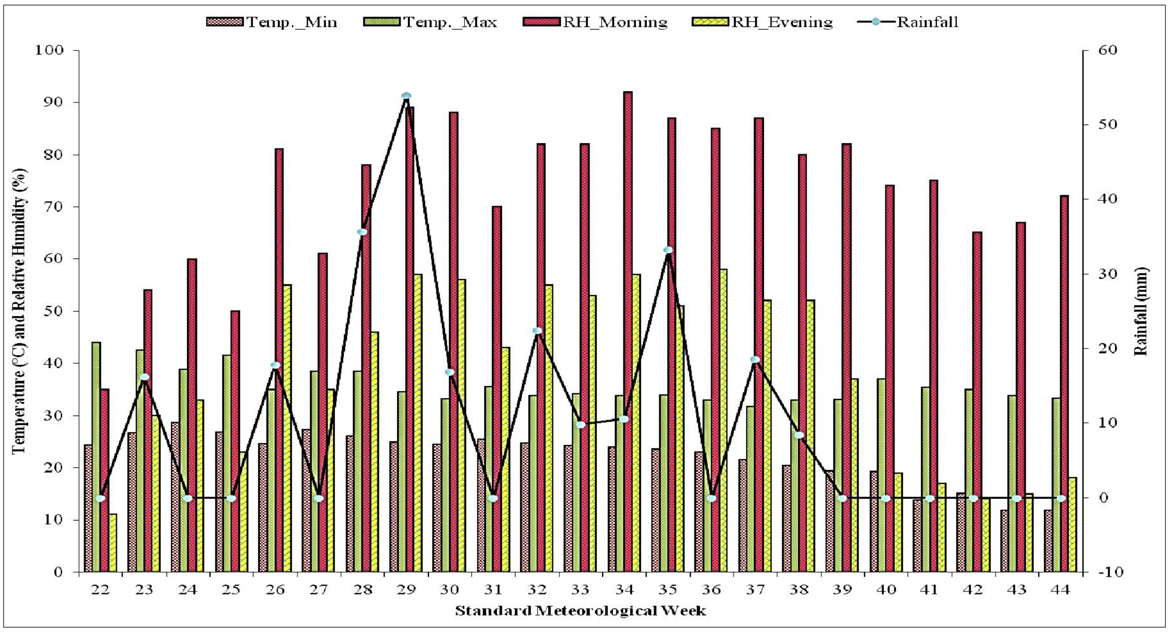


Fig 7: Meteorological data during 2018 *kharif* of crop growth period.

matrix in which the individual cells are displayed as coloured rectangles. The colour of a cell is proportional to its position along a colour gradient. Column variable of the matrix represents as the column of heat map and row of matrix as rows of the heat map. The order of rows is determined by performing hierarchical cluster analysis of the row tends to position similar rows together on the plot. The order of the column is determined similarly. Heat map clustered seed yield in one cluster and remaining all the characters in other clusters. Looking at the dendrogram we can see the two clusters for genotypes during both the seasons which explain that all the experimental material can be classified into two major groups. However, again if we look into the sub clustering then complexity of classification will be increased.

Table 4: Duncan's new multiple range test of 16 mung bean genotypes for yield and ancillary characters over the years 2018 and 2019.

Genotypes	Days to 50% flowering		Days to maturity		Plant height (cm)		Pod length (cm)		No. of seed/pod		Test weight (g)		Seed yield (kg/ha)	
	2018	2019	2018	2019	2018	2019	2018	2019	2018	2019	2018	2019	2018	2019
IPM-02-3(C)	38.33^{cd}	41.00^{bcd}	74.67^{ab}	62.00^{abc}	47.67^{ab}	42.67^{bcd}	7.53^{bcde}	7.80^{abcd}	12.00^{abc}	11.67^{ab}	35.60^{d}	33.13^{b}	861.00^{bcd}	505.00^{g}
MSJ-118(C)	38.00^{de}	43.00^{a}	71.00^{cd}	63.67^{a}	44.67^{bcd}	38.33^{f}	7.47^{cde}	7.87^{abc}	12.33^{ab}	12.00^{a}	38.40^{a}	32.93^{b}	722.00^{d}	731.33^{abcd}
RMG-1087	37.00^{e}	40.33^{cd}	72.00^{bcd}	61.33^{bcd}	46.00^{abc}	41.67^{bcd}	7.23^{cde}	7.43^{cde}	9.67^{d}	10.00^{c}	37.53^{b}	32.73^{b}	981.33^{abcd}	671.00^{cde}
RMG-1094	40.00^{ab}	42.33^{ab}	74.00^{abc}	58.67^{f}	37.67^{d}	31.67^{g}	7.53^{bcde}	7.87^{abc}	12.00^{abc}	11.67^{ab}	35.80^{cd}	32.40^{bc}	1074.00^{abc}	569.33^{efg}
RMG-1098	40.00^{ab}	37.00^{fg}	76.00^{a}	59.00^{ef}	37.67^{d}	44.17^{b}	7.23^{cde}	7.67^{abcde}	11.33^{bc}	10.83^{abc}	34.80^{e}	30.27^{ef}	1129.67^{a}	782.33^{abc}
RMG-1132	40.00^{ab}	36.00^{g}	72.00^{bcd}	62.00^{abc}	44.67^{bcd}	46.83^{a}	8.10^{ab}	7.80^{abcd}	12.67^{ab}	10.00^{c}	37.40^{b}	34.93^{a}	1129.67^{a}	800.00^{abc}
RMG-1134	40.67^{a}	38.33^{ef}	71.00^{cd}	61.00^{bcde}	47.67^{ab}	42.83^{bcd}	7.03^{e}	7.23^{e}	13.33^{a}	11.33^{abc}	34.53^{e}	30.17^{ef}	1074.00^{abc}	790.00^{abc}
RMG-1137	38.67^{cd}	37.00^{fg}	73.33^{abcd}	60.00^{cdef}	41.00^{bcd}	43.17^{bc}	7.83^{abc}	8.03^{ab}	12.67^{ab}	10.83^{abc}	34.80^{e}	31.60^{cd}	1009.33^{abc}	726.67^{abcd}
RMG-1138	38.00^{de}	37.00^{fg}	72.00^{bcd}	59.33^{def}	39.00^{cd}	46.67^{a}	7.43^{cde}	7.70^{abcde}	12.00^{abc}	10.33^{bc}	37.33^{b}	31.00^{de}	1055.33^{abc}	694.67^{bcde}
RMG-1139	40.67^{a}	41.67^{abc}	73.00^{abcd}	60.00^{cdef}	41.33^{bcd}	42.33^{bcd}	8.13^{ab}	8.10^{a}	12.33^{ab}	10.33^{bc}	31.80^{f}	32.40^{bc}	1120.33^{ab}	815.00^{ab}
RMG-1147	40.67^{a}	37.00^{fg}	72.00^{bcd}	60.67^{cdef}	44.33^{bcd}	46.50^{a}	8.20^{a}	8.13^{a}	11.67^{abc}	11.50^{abc}	36.40^{c}	34.50^{a}	990.67^{abc}	846.00^{a}
RMG-1148	38.00^{de}	41.00^{bcd}	71.00^{cd}	61.33^{bcd}	41.67^{bcd}	40.50^{def}	7.43^{cde}	7.63^{abcde}	12.00^{abc}	10.83^{abc}	36.00^{cd}	34.60^{a}	833.33^{cd}	671.00^{cde}
RMG-1152	39.33^{bc}	42.67^{a}	70.00^{d}	64.00^{a}	45.67^{abcd}	41.33^{cde}	7.73^{abcd}	7.80^{abcd}	10.33^{cd}	11.50^{abc}	31.80^{f}	31.33^{d}	879.67^{abcd}	675.67^{cde}
RMG-1154	40.33^{ab}	42.00^{abc}	70.00^{d}	63.00^{ab}	43.00^{bcd}	43.67^{bc}	7.13^{de}	7.50^{bcde}	11.67^{abc}	11.67^{ab}	32.33^{f}	33.13^{b}	889.00^{abcd}	532.67^{fg}
RMG-492(C)	39.33^{bc}	40.67^{bcd}	71.33^{bcd}	61.00^{bcde}	43.67^{bcd}	39.17^{ef}	7.60^{abcde}	7.30^{de}	12.33^{ab}	12.00^{a}	32.13^{f}	29.60^{f}	981.33^{abcd}	648.00^{def}
RMG-975(C)	38.33^{cd}	39.67^{de}	71.67^{bcd}	62.00^{abc}	53.00^{a}	42.67^{bcd}	7.83^{abc}	7.97^{abc}	12.67^{ab}	10.17^{bc}	34.53^{e}	30.73^{de}	851.67^{cd}	574.33^{efg}
SE(m)	0.34	0.52	1.04	0.68	2.43	0.78	0.19	0.16	0.55	0.48	0.23	0.30	78.75	39.90
SE(d)	0.48	0.73	1.46	0.95	3.43	1.10	0.27	0.23	0.77	0.67	0.32	0.42	111.03	56.25
LSD	0.98	1.50	2.99	1.96	6.99	2.24	0.55	0.46	1.58	1.38	0.66	0.86	226.51	114.77

*Means with the same letter are not significantly different.

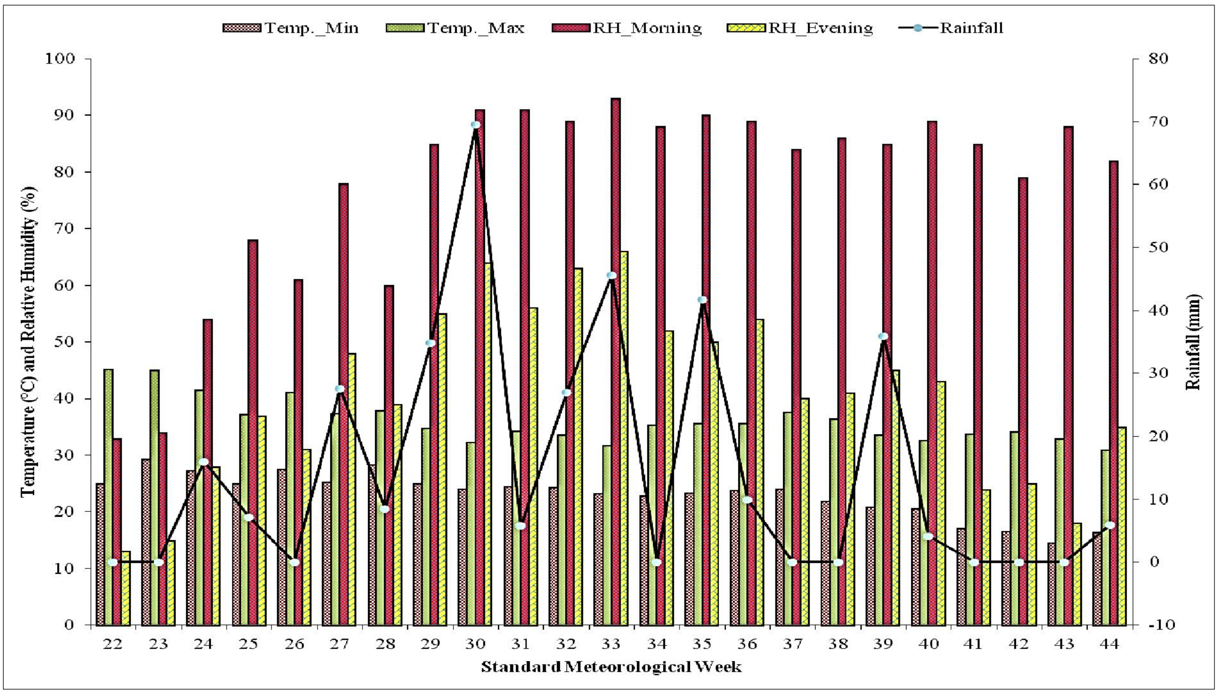


Fig 8: Meteorological data during 2019 *kharif* of crop growth period.

CONCLUSION

Environmental fluctuations play an important role in plant growth, development and productivity. Therefore to identify high yielding genotypes suitable to specific region, we must interpret the meteorological data. However if we summaries the data for both the season; genotypes RMG 1098, RMG 1132, RMG 1139 RMG 1139 and RMG 1147 performed well. These high yielding genotypes can be used by farmers for their farm profitability and can be utilized by plant breeders as parent in future breeding programme for green gram improvement.

ACKNOWLEDGEMENT

The authors are highly thankful to All India Coordinated Research Project on MULLaRP, RARI, Durgapura (Jaipur) for providing material; Zonal Director Research, Agricultural Research station, Fatehpur-Shekhawati for providing all the farm facilities and expert team of College of Agriculture, Fatehpur who supported to bring out this systematic manuscript.

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