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Toker C (1998). Adaptation of kabuli chickpeas (*Cicer arietinum* L.) to the low and high lands in the West Mediterranean region of Turkey. Turk J Field Crop 3:10-15.

Toker C and Canci H (2003). Selection of chickpea (*Cicer arietinum* L.) genotypes for resistance to ascochyta blight [*Ascochyta rabie*i (Pass.) Labr.], yield and yield criteria. Turk J Agric For27: 277-283.

Toker C, Canci H and Ceylan FO (2006). Estimation of outcrossing rate in chickpea (*Cicer arietinum* L.) sown in autumn.Euphytica 151: 201-205.

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Yasar M, Ceylan FO, Ikten C and Toker C (2013). Comparison of expressivity and penetrance of the double podding trait and yield components based on reciprocal crosses of kabuli and desi chickpeas (*Cicer arietinum* L.). Euphyticadoi:10.1007/s001090000086

Book:

Toker C (2014). Yemeklik Baklagiller. BISAB, Ankara.

Book chapter:

Toker C, Lluch C, Tejera NA, Serraj R and Siddique KHM (2007). Abiotic stresses. In: Chickpea Breeding and Management,Yadav SS, Redden B, Chen W and Sharma B (eds.),CAB Int. Wallingford, pp: 474-496.

Online document:

FAOSTAT J (2013) http://faostat.fao.org/site/567/default.aspx#anchor. Accessed 15 May 2013.

Dissertation (Thesis):

Yasar M (2012). Penetrance and expressivity of double podding characteristic in chickpea (*Cicer arietinum* L.). Dissertation, Akdeniz University, Antalya.

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Abbreviations

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Determination of Variability for Grain Yield and Quality Traits in Gamma-Ray Irradiated Bread Wheat Populations

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ABSTRACT

The study was carried out in the experimental area of the Field Crops Department, Faculty of Agriculture, Namik Kemal University in the growing season of 2011-12. In the study, grain yield and its components and some quality traits such as 1000 grain weight, wet gluten content, gluten index, sedimentation value and protein content were investigated. The results exhibited significant differences among the tested genotypes, for all studied characters except spike length, indicating genetic variation among them. The genetic variation was higher for grain yield and its components when compared with quality characteristics. These differences show that the effects of increasing gamma irradiation are not systematically negative for plant height, while positive for all other characters in comparison with controls. In general, it is understood that the highest percent changes are achieved in 200 and 250 Gy of gamma radiation doses for yield components, while are in 300-350 Gy for the quality characteristics. The values of phenotypic coefficient of variation PCV were slightly higher than their corresponding values of GCV for all traits. Moderate estimates of genotypic coefficient of variation GCV were obtained by grain yield (12.50%), gluten content (11.20%) and grain weight per spike (10.20%), respectively. Low estimates of GCV (less than 10) were recorded for the other characters investigated. The h^2 values ranged from 37.3%, for sedimentation value, and 86.6%, for plant height, while the values of GA% ranged between 0.09 and 593.0.5% at 10% selection intensity for grain weight per spike and grain yield, respectively. The high values of heritability coupled with high values of genetic advance (%) were recorded by plant height, indicates the importance of the additive gene effects, so, selection would be effective in early generations for the trait. The high values of heritability coupled with moderate values of genetic advance (%) for harvest index and gluten index indicate selection would be a delay in later generations.

***Keywords*:** Bread wheat, gamma rays, yield, quality, mutated population

Introduction

The main purpose of using mutagens has been to induce genetic variation especially in homozygous genotypes of self-pollinated crops which is the first step in a breeding program (Galal et al. 1975). Genetic variation in major crops has been successfully unlocked, shuffled, recombined, and sometimes created, by plant breeders over the last century to achieve yield increase. The success of induced variation will mainly depend on the precision in selection techniques (Mac Key 1984 and Konzak 1987). The expected response to selection can be measured by determining the parameters like mean, coefficient of variation, standard deviation, heritability and genetic advance (Ibrahim and Sharaan 1974; Scossiroli 1977; Shabana et al. 1994 and Amer et al. 2001).

Changes in morphological, physiological and quality characters after mutation application are common, and therefore it has been demonstrated that induced mutation can increase yield as well as other agronomic characters such as stiffness of straw, time of maturity, adaptability, shattering resistance, disease

resistance, protein content, baking quality, malting quality and numerous other characters (Ibrahim and Sharaan 1974; Borojevic 1990; Brunner 1991). Several achievements in crop improvement through mutation breeding have resulted in two major outcomes: improved varieties that are directly used for commercial cultivation and new genetic stocks with improved characters or with better combining ability of traits (Roychowdhury and Tah 2013). More than 3,200 mutant varieties have been directly or indirectly derived through mutation induction, nearly 80% of these crop varieties are seed propagated, almost half of which (48%) are cereals (Jankowicz-Cieslak et al. 2017) including 274 bread wheat varieties (International Atomic Energy Agency, IAEA, 2018) and are being grown in different countries of the world. Considering the improvements in mutation breeding in the world, unfortunately, there is no mutant wheat variety in our country yet. This inferiority is that the mutation breeding work in our country is very limited. The primary aim of this study is to contribute to the accumulation of knowledge on mutation breeding. Knowledge of the high value of heritability and predicted genetic advance clarifies that the selection among genotypes would be effective for yield and yield components (Shabana et al. 1994, Tammam et al. 2000, Kashif and Khaliq 2004 and Baloch et al. 2013). High heritability in the broad sense associated with high genetic advance reveals a strong contribution of additive genetic variance for the expression of the traits and the selection based on these traits could play a vital role in improving grain yield (Laghari et al. 2010). Therefore, the present work was planned to estimate genetic variation, heritability (h^2) and genetic advance (% mean). The results may be helpful to plan appropriate selection strategies for improving the grain yield of wheat crop in Turkey.

Materials and Methods

Plant material

Three bread wheat (*Triticum aestivum* L.) advanced lines, BSB (Bezostaja 1 x Saraybosna; tall, mid-late, awnless, superior in flour quality for bread making, but inferior in lodging resistance and yield capacity), FA (Flamura 80 x Atilla 12;mid-tall, mid-early, awned and inferior in flour quality for bread making, disease resistance and superior in lodging and yield capacity), PK (Pehlivan x Kate A-1; tall, mid-late, awnless and inferior in flour quality for bread making, lodging and disease resistance) were used as the experimental material.

Gamma irradiation

The moisture contents of seeds of wheat genotypes (*Triticum aestivum* L.) used in the study were around 12.0%. Gamma treatment was applied in 0 (Control), 100, 150, 200, 250, 300 and 350 Gy obtained from ^{60}Cobalt, Ob-Servo Sanguis Co-60 Research Irradiator with isotope model, while the dose rate was 2.190 kGy h^{-1} in before the 2010-11 growing season sowing at the Turkish Atomic Energy Authority, Sarayköy Nuclear Research and Training Center, Ankara, Turkey. Right after irradiation, the experiment was set up using a total of 30 M_0 combination seeds together with the un-irradiated (control) in the experimental field of the Field Crops Department of the Faculty of Agriculture of Namik Kemal University during the growing season of 2010-11. The experiment was carried out in a randomized complete block design (RCBD) with 3 replicates. Plots were sown on Nov.15, 2010, by hand at the rate of 350 seeds per m^2 and were 2 m in length x 1.0 m wide, with 6 rows 0.2 m apart. The crop was kept free of weeds by hand hoeing when necessary. The seeds obtained from the harvested plants in M_1 generation were planted in M_2generation as 20 cm row distance in 5 meters of 6-row parcels with 4 replicates and as 400 seeds in each row. Morphological and yield characters were recorded on 15 random and guarded plants to study the effect of irradiation doses on the studied genotypes on plant height, spike length, the number of spikelets per spike, number of grains per spike, grain weight per spike and harvest index. Grain yield and some grain quality characters such as thousand grain weight, test weight, gluten content, gluten index, sedimentation value and protein content were investigated in each seed of M_2 generation.

Statistical analyses

Genetic parameters

The genotypic and phenotypic variances and their corresponding coefficients of variations were estimated, using the pertinent mean square expectations, according to the method, suggested by Johnson et al. (1955). Broad sense heritability (h^2), genetic advance as % of mean was calculated following Hanson et al. (1956) and Allard (1999).

Mean squares were used to estimate

$\boldsymbol{\sigma}_g^2 = (\text{MSS-MSE})/r$

$\boldsymbol{\sigma}_{ph}^2 = \boldsymbol{\sigma}_e^2 + \boldsymbol{\sigma}_g^2$, where broad-sense heritability (h_{bs}^2) was estimated as follows:

$h^2 = (\boldsymbol{\sigma}_g^2 / \boldsymbol{\sigma}_{ph}^2)$ x 100 and the phenotypic and genotypic coefficients of variation were computed as follows:

PCV = $100\ x\ \sqrt{\sigma_{ph}^2}/\bar{X}$ **GCV** = $100\ x\ \sqrt{\sigma_g^2}/\bar{X}$

Expected genetic advance: Expected genetic advance from direct selection for all studied traits was calculated according to Singh and Chaudhary (1999) as follows:

GA% at 10% (selection intensity)=$100 \chi k \chi h^2 \chi \sigma_{ph}/\bar{X}$,

Where $\bar{X}$: general mean and k is selection differential (k= 1.76 for 10% selection).

T-test was performed to compare the mean values obtained from treatments with different gamma irradiation with the untreated (control) means for each character studied.

Results and Discussion

Mean performance

The mean values of yield and quality characters for the three tested genotypes, evaluated in M_2 generation, are given in Table 1.

The grain yield means of M_2 populations of bread wheat genotypes varied between 367-589 gm^{-2}. Gamma irradiation caused significant increases for all three genotypes of bread wheat. The highest grain yield increases were obtained from 300 and 350 for BSB, FA and BK. There was an increase in thousand kernel weight in all doses except 100 gray. While the gluten ratio value was not significant affected by the application of gamma irradiation for the BSB mutated population, the other two mutated population resulted in significant increases in doses after 200 gray doses. The gluten index showed a significant decrease for the BK mutated population, but there was an increase for the BSB mutated population. However, there was no significant increase in the FA population for the traits. In terms of sedimentation value, the BSB mutated population showed an increase in only 350 gray applications, while BK increased in all doses. Protein ratio was increased statistically by application of mutagen in populations of all three varieties.

The results exhibited significant differences among the tested genotypes, for all studied characters except spike length, indicating genetic variation among them. But it can be said that this genetic variation is higher for grain yield and its components when compared with quality characteristics. These differences show that the effects of increasing gamma irradiation are not systematically negative for plant height, while positive for all other characters in comparison with controls. In general, it is understood that the highest percent changes (data was not shown) are achieved in 200 and 250 Gy of gamma radiation doses for yield components, while are in 300-350 Gy for the quality characteristics. Chen et al. (1997) observed wide differences between different irradiation doses. Similarly, a high contribution of genotypes to the total variance of seed yield was reported by (Dhillon et al. 1999, Gebeyehu and Assefa 2003 and Albokari et al. 2015).

Genotypic and phenotypic variances and their corresponding coefficient of variations, broad-sense heritability (h^2), and genetic advance (GA) expressed as a per cent of mean for the studied traits, evaluated in M_2 generation, are presented in Table 2.

Shivsubramanium and Madhavmenon (1973) are suggested for classified PCV and GCV as a per cent of mean as low (<10%), moderate (10-20%) and high (>20%). According to this classification, the GCV and PCV values obtained in our study are moderate and low. Moderate estimates of genotypic coefficient of variation GCV were obtained by grain yield (12.50%), gluten content (11.20%) and grain weight pers pike (10.20%) in M_2 generation, respectively. Low estimates of GCV (less than 10) were recorded for the other characters investigated.

On the other hand, the values of phenotypic coefficient of variation PCV were slightly higher than their corresponding values of GCV for all traits which reflect the somewhat environmental influence on the expression of characters in M_2 generation. These results indicated that the selection would be effective to improve these traits among the tested genotypes.

It is important to emphasize that, the heritability values (h^2) would not be practically valuable in the selection depends on phenotypic appearance without considering genetic advance (GA). (Johnson et al. 1955). Confirmed that heritability estimates, in conjunction with genetic advance would give the more reliable index of selection value.

In the present study, the h^2 values ranged from 37.3%, for sedimentation value, and 86.6%, for plant height, while the values of GA% ranged between 0.09 and 593.05 % at 10% selection intensity for grain weight per spike and grain yield, respectively. According to Singh (2001), the heritability of a trait is considered as high when the value is 80% or moderate when it ranged from 40-80% and when it is less than 40%, it is low. Deshmukh et al. (1986) classified genetic advance as per cent of mean as low (<10%), moderate (10-20%) and high (>20%).

The high values of heritability ($h^2 \geq 80\%$) coupled with high values of genetic advance (%), both at 10% selection intensity ($GA \geq 20\%$), were recorded by plant height. Such previous results indicated the importance of the additive gene effects, so, selection would be effective in early generations for the trait. The high values of heritability ($h^2 \geq 80\%$) coupled with moderate values of genetic advance (%), both at 10% selection intensity ($GA \geq 10\%$) for harvest index and gluten index indicate selection would be a delay in later generations.

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Table 1. Mean performance of wheat genotypes for some yield and quality characters during M_2 generation in 2011/12 season.

Genotypes	Gamma Doses	Plant Height (cm)	Spike Length (cm)	Number of Spikelets Per Spike (no)	Number of Grains Pers Pike (no)	Grain Weight Per Spike (g)	Harvest Index (%)	Thousand Grain Weight (g)	Grain Yield (gm^{-2})	Wet Gluten Content (%)	Gluten Index	Sedimentation Value (ml)	Protein Content (%)
BSB	Cont	121.5	10.2	20.2	46.2	1.820	37.8	38.8	367	30.0	89.0	50.0	12.70
	100	119.9*	10.0	21.0*	44.4*	1.857	38.5	39.8	397*	31.0	90.3	47.7*	13.07**
	150	118.5**	9.9	20.9	47.8*	2.187*	39.3*	40.0*	390*	29.7	91.0*	49.3	12.77
	200	115.6**	10.3	22.4**	48.7*	2.567**	40.2**	40.4**	445**	30.7	91.7*	50.0	12.87
	250	112.8**	10.5	21.6*	47.8*	2.440**	41.7**	41.0*	451**	31.7	91.0*	48.0	13.00*
	300	107.9**	10.4	21.4*	46.4	2.410**	42.1**	41.5**	459**	32.0	90.7	49.7	12.97*
	350	106.0**	10.2	21.2*	42.7**	2.377**	41.6**	41.7**	492**	29.0	92.0*	52.0	12.83
BK	Cont	116.7	9.7	19.2	45.2	2.053	34.9	38.9	378	24.7	95.0	46.0	11.90
	100	116.2	9.7	20.1*	50.4**	2.173*	37.1*	39.5	412**	26.0	92.7*	46.3	12.00
	150	112.3**	9.9	20.7**	48.3**	2.253**	37.8**	39.7*	425**	24.0	95.7	49.0*	12.03*
	200	109.9**	9.8	21.0**	52.4**	2.217**	39.1**	40.1**	443**	28.0**	91.0**	49.0*	12.40**
	250	104.6**	10.1	21.9**	53.7**	2.283*	39.4**	40.9*	455**	30.7**	90.7**	51.3**	12.87**
	300	102.8**	10.0	22.0**	52.2**	2.467**	41.0**	41.0**	469**	30.0**	90.7**	47.7	12.93**
	350	100.0**	9.6	20.6**	48.0**	2.660**	39.3**	39.7	434**	31.0**	91.7**	51.0**	13.00**
FA	Cont	105.9	7.9	19.1	38.1	1.757	39.4	37.2	457	22.3	85.0	47.3	11.87
	100	105.2	8.1	19.4*	40.4**	2.050**	41.5**	37.9	507**	21.7	85.0	45.0**	11.67*
	150	102.6**	7.9	19.9**	42.1**	2.073**	41.8**	38.8*	511**	24.0	86.0	46.3	12.00
	200	101.1**	8.2	20.3**	47.7**	2.107**	42.2**	39.6**	537**	24.7**	86.0	50.7**	12.53**
	250	97.7**	7.8	21.3**	47.5**	2.230**	42.6**	40.4**	574**	24.7**	85.0	48.0	12.63**
	300	97.0**	8.9**	20.8**	47.5**	2.410**	43.2**	41.7**	560**	27.7**	88.3**	49.0	12.80**
	350	90.2**	8.6**	20.8**	48.9**	2.560**	43.7**	42.6**	589**	28.7**	85.3	49.7**	12.77**

*=Significant at 0.05% level, **=Significant at 0.01% level

Table 2. Range, mean, phenotypic and genotypic coefficient of variation, heritability and expected genetic advance for agronomic characters in M_2 bread wheat mutated populations.

Agronomic Characters	Range	Grand Mean	Coefficient of Variation (%)		h^2 (%)	GA Mean (10%)
			PCV	GCV		
Plant height (cm)	85.0-125.4	107.8	8.19	7.62	0.866	118.80
Spike length (cm)	7.2-11.2	9.4	10.51	9.49	0.817	1.40
Number of spikelets per spike (no)	18.2-23.7	20.7	5.62	3.54	0.398	0.95
Number of grains per spike (no)	35.5-57.5	47.0	10.39	6.91	0.442	18.56
Grain weight per spike (g)	1.500-3.040	2.236	12.81	10.20	0.637	0.09
Thousand grain weight (g)	36.8-43.4	40.1	3.68	3.08	0.701	2.69
Harvest index	34.57-44.42	40.20	5.85	5.43	0.863	8.39
Grain yield (gm^2)	329.0-625.0	464.4	15.61	12.50	0.641	593.05
Gluten content (%)	19.0-33.0	27.7	12.93	11.20	0.751	6.95
Gluten index	84.0-96.0	89.7	3.78	3.51	0.862	7.45
Sedimentation value (ml)	45.0-55.0	48.7	5.04	3.08	0.373	3.95
Protein content (%)	11.00-13.40	12.55	4.00	3.34	0.697	0.31

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Performance of Feed Barley Genotypes Assessed by AMMI Mixed with BLUP for North Western Plains Zone of the India

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ABSTRACT

AMMI analysis for feed barley genotypes evaluated North Western Plains Zone of India had expressed highly significant effects of environments (E), GxE interaction and genotypes (G). Interaction effects GxE accounted for 23.4 and 26.9%, while environment explained up to tune of 63.4 and 61.4%; during cropping seasons of 2018-19 and 2019-20, respectively. ASTAB measure achieved the desirable lower values for PL906, DWRB137, UPB1080. Composite measure MASV1 found PL906, DWRB137, RD2552, and as per MASV ranks desired PL906, DWRB137, and UPB1080 genotypes would be of choice for these locations of the zone. Superiority index while weighting 0.65 and 0.35 for average yield & stability found KB1707, PL906, RD2994 as of stable performance with high yield. Biplot graphical analysis as per 73.7% of variation of the measures exhibited MASV1 clubbed with ASTAB, EV, SIPC, Za, W3, WAASB and MASV measures. For the second-year lower value of WAASB measure had observed for KB1707, RD2994. Barley genotypes DWRB137, PL906 were selected as per values of ASTAB measure. MASV1 selected PL906, DWRB137 while PL906, DWRB137 identified by MASV as genotypes of choice. Superiority index pointed towards PL906, DWRB137 feed barley genotypes. About 64.3% of variation among the measures under biplot analysis seen AMMI based IPCA1, Za, W1, W2, W3, ASTAB, WAASB measures grouped in quadrant. Simultaneous utilization of AMMI and BLUP of genotypes would be more appropriate to recommend high-yielding stable genotypes.

***Keywords*:** AMMI, ASV, ASV1, HMGV, GAI, HMPRVG, biplot, barley

Introduction

Barley represents one of the ancient grain crops cultivated worldwide owing to its high adaptability; this plant grows in different global climates where common cereals fail to survive (Karkee et al. 2020). Barley plants are used for forage, pasture, or hay, as per the harvested stage (Badr et al. 2000). Straw after grain harvesting is a good source of fibre for animal feeding (Kendel et al. 2019). Since a long time by products of malting and brewing industries were used in animal feed (Newton et al. 2011). Multi-environment trials (MET) had been advocated to retrieve the maximum information from the best estimator of each genotype's performance in a given environment (Bocianowski et al. 2019). AMMI (additive main-effects and multiplicative interaction) is popular for analyzing MET data with fixed effect (Agahi et al. 2020). The genotypic effects regarded as random may be preferable and the assessment of it may be viewed as a problem of prediction rather than estimation (Piepho et al. 2008). The prediction of the outcome of random variables is commonly done by Best Linear Unbiased Prediction (BLUP). Advantages of both methods are combined in Superiority Index put forward by assigning weights to high yield and stability of genotypes as per the breeding objectives in crop improvement program (Olivoto et al. 2019).

Materials and Methods

The mega wheat growing area of the country comprises of parts of sub-humid Sutlej-Ganga Alluvial Plains and arid western plains, which comprises Punjab, Haryana, Delhi, Rajasthan (except Kota and Udaipur divisions), Western Uttar Pradesh (except Jhansi division and hilly areas), parts of Jammu and Kashmir (Jammu and Kathua districts) and parts of Himachal Pradesh (Paonta Valley and Una districts). Twenty-one feed barley genotypes at six locations and eight genotypes at eight locations were evaluated under research field trials during 2018-19 and 2019-20 cropping seasons, respectively. Field trials were conducted at research centres in randomized complete block designs with four replications. Recommended agronomic practices were followed to harvest good yield. Details of genotype parentage along with environmental conditions were reflected in Table 1 and Table 2 for ready reference.

Stability measure as Weighted Average of Absolute Scores calculated as

$$\text{WAASB} = \sum_{k=1}^{p} |IPCA_{ik} \times EP_k| \,/\, \sum_{k=1}^{p} EP_k$$

Where, WAASB_i was the weighted average of absolute scores of the *i*th genotype (or environment); IPCA_{ik} the score of the *i*th genotype (or environment) in the *k*th IPCA, and EP_k was the amount of the variance explained by the *k*th IPCA. Superiority index allowed variable weightage between yield and WAASB to select genotypes that combined high performance and stability as

$$\text{SI} = \frac{(rG_i \times \theta_Y) + (rW_i \times \theta_S)}{(\theta_Y + \theta_S)};$$

where rG_i and rW_i were the rescaled values for yield and WAASB, respectively, for the *i*th genotype; G_i and W_i were the yield and WAASB for *i*th genotype. SI superiority index for the *i*th genotype weighted between yield and stability, and θ*Y* and θ*S* were the weights for yield and stability would be of order 65 and 35 respectively for present study,

Zobel	Averages of the squared eigenvector values
$\text{EV} = \sum_{n=1}^{N} \lambda_{in}^2 \,/n$	
Sneller et al.	Sums of the absolute value of the IPC scores
$\text{SIPC} = \sum_{n=1}^{N} \lambda_n^{0.5} \gamma_{in}$	
Rao and Prabhakaran	AMMI based stability parameter
$ASTAB = \sum_{n=1}^{n} \lambda_n \gamma_{ni}^2$	
Zali et al.	Modified AMMI stability value
$MASV = \sqrt{\sum_{n=1}^{N-1} \frac{SSIPC_n}{SSIPC_{n+1}} (PC_n)^2 + (PC_{n+1})^2}$	
Zali et al.	Absolute value of the relative contribution of IPCs to the interaction
$Z_a = \sum_{n=1}^{N} \lvert\lambda_n \gamma_{in}\rvert$	
Ajay et al.	MASV1
$\text{MASV1} = \sqrt{\sum_{n=1}^{N-1} (\frac{SSIPC_n}{SSIPC_{n+1}} PC_n)^2 + (PC_{n+1})^2}$	
Olivato	Superiority Index
$\text{SI} = \frac{(rG_i \times \theta_Y) + (rW_i \times \theta_S)}{(\theta_Y + \theta_S)}$	

AMMI analysis was performed using AMMISOFT version 1.0, available at https://scs.cals.cornell.edu/people/ hugh-gauch/ and SAS software version 9.3.

Results and Discussion

AMMI analysis of barley genotypes

In first year (2018-19), highly significant GxE interaction, environment (E) and genotypes (G) effects had observed by AMMI analysis. Environment accounted for 63.4% of the total sum of squares due to treatments indicating that diverse environments caused most of the yield variations (Table 3). Genotypes explained only 9.1% of total sum of squares, whereas GxE interaction contributed about 23.4% of treatment variations in yield. Significant GxE interaction demanded the stable estimation of genotypes yield over the studied environments (Ajay et al. 2020). Larger magnitude of GxE interaction sum of squares as compared to genotypes indicated the presence of genotypic differences across environments and complex GxE interaction for yield (Gauch 2013). GxE interaction further revealed that the first four multiplicative terms (IPCA1, IPCA2, IPCA3, and IPCA4) of AMMI were highly significant and explained 37.6%, 25.8%, 19.1%, and 10.7% of interaction sum of squares, respectively. Total of the significant multiplicative components were

93.2% and remaining 6.8% was the discarded residual (Oyekunle et al. 2017).

In second year (2019-20), highly significant effects of environment (E), GxE interaction and genotypes (G) had been achieved by analysis for multi-location evaluation of feed barley genotypes. Environment contributed maximum to the tune of 61.4%; GxE interaction accounted for 26.9% whereas genotypes contributed only 3.6% of total treatment variations in yield (Table 4). Further GxE interaction observed only two out of six multiplicative terms had explained about 39.3%, 27.8%, 14.4%, 11.6%, 4.4% and 2.4% of interaction sum of squares, respectively. Moreover, the total of these components were to the tune of 99.8% and remaining was noise that was discarded.

Ranking of barley genotypes as per AMMI based stability measures

In first year (2018-19), least value of absolute IPCA1 expressed by NDB1723, NDB1709, HUB266 and higher value achieved by KB1707 and RD2991 (Table 5). Low values of (EV) associated with stable behaviour of the barley genotypes NDB1723 followed by DWRB137, NDB1709 and unstable yield by RD2899, BH 946 genotype. Measure SIPC identified NDB1723 followed by NDB1709, DWRB137 as of stable nature, whereas RD2899, DWRB205 would be of least stable type. Za measure considered absolute value of the relative contribution of IPCs to the interaction revealed NDB1723, NDB1709, and DWRB137 as genotypes with descending order of stability, whereas DWRB205, KB1707 genotype with the least stability. ASTAB measure observed genotypes NDB1723, NDB1709 and DWRB137 as stable and KB1707, RD2899 was least stable in this study (Rao and Prabhakaran 2005). MASV1 and MASV measures considered all the significant IPCAs. Values of MASV1 showed that the genotypes, NDB1723, NDB1709 and BH1024 were most stable and RD2899, BH 946 would express unstable while, NDB1723, NDB1709 and BH1024 would be stable and RD2899 along with DWRB205 by MASV measure respectively (Ajay et al. 2019). Measure W1 favoured KB1707, RD2991, RD2786 while as per W2, genotypes identified were KB1707, DWRB205, RD2991while W3 favoured DWRB205, RD2991, RD2899 whereas finally lower values of WAASB associated with stable nature of DWRB205, KB1707, RD2991genotypes as for considered locations of the zone at the same time maximum deviation from the average performance across environments obtained by NDB1723, NDB1709 genotypes.

In second year (2019-20), genotypes UPB1080, PL906 expressed least absolute values of IPCA1 measure and higher value achieved by KB1707 (Table 6). Stable behaviour of PL906, UPB1080 genotypes anticipated as per minimum values of EV measure and maximum value had by KB1707, genotype. PL906, followed by UPB1080 identified for the lower value SIPC measure, whereas KB1707 would be of least stable behaviour. Preference order of genotypes PL906, UPB1080 revealed by Za measure in descending order of stability, whereas KB1707 would express the least stability. ASTAB measure observed genotypes PL906, and UPB1080 as the stable whereas RD2552 genotype was of least stable performance (Rao and Prabhakaran 2005). PL906, UPB1080 genotypes were of choice by of MASV1 and MASV measure pointed for PL906, RD2994 as the stable genotypes while BH946 would be unstable. W1 measure selected KB1707, RD2994 while measure W2 favoured KB1707, BH946 whereas genotypes KB1707, UPB1080 selected by W3 measure. Lower value of WAASB measure had observed for KB1707, RD2994 whereas large value by PL906.

Superiority indexes as per AMMI and BLUP barley genotypes

In first year (2018-19), average yield of genotypes as per BLUP values selected KB1707, HUB266, RD2994 where PL906, KB1707, RD2994 selected by Geometric adaptability index while Harmonic mean of genotypic values pointed for PL906, RD2994, and UPB1080 as suitable genotypes as far as higher production are concerned. More yields alone is not a desirable selection criterion as high yielders genotypes may not be of stable performance, simultaneous use of yield and stability in a single measure has considered by (Kang 1993; Farshadfar et al. 2008). Simultaneous Selection Index also referred to as genotype stability index (GSI) or yield stability index (YSI) (Farshadfar et al. 2011) was computed by adding the ranks of mean yield of genotypes and ranks of stability measure. Least ranks for IPCA1 measure exhibited by DWRB137, PL906, HUB266 were considered as stable with high yield, whereas high values suggested as least stable high yield of RD2991 genotype (Table 7). EV measure identified PL906, DWRB137 and PL909 whereas ranks as per SPIC measure favoured DWRB137, PL906&PL909 genotypes. Genotypes DWRB137, PL906&UPB1080 possessed lower value of Za measure. ASTAB measure achieved the desirable lower values for PL906, DWRB137, UPB1080. Composite measure MASV1 found PL906, DWRB137, RD2552, and as per MASV ranks desired PL906, DWRB137, UPB1080 genotypes would be of choice for these locations of the zone. Superiority index while weighting 0.65 and 0.35 for average yield and stability found

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KB1707, PL906, RD2994 as of stable performance with high yield. Least magnitude of SIgm ranked PL906, KB1707, RD2994 as desirable genotypes while values of SIhm measure favoured PL906, RD2994, KB1707 feed barley genotypes.

In second year (2019-20), simultaneous ranking of barley genotypes as per IPCA1 measure favoured DWRB137, PL906 as per the least values, whereas large values of KB1707 suggested unstable high yield (Table 8). EV measure ranked for PL906 and BH946 barley genotypes. Minimum ranks as per SPIC favoured PL906 and DWRB137 genotypes. Lower value of Za ranks possessed by PL906 and DWRB137 genotypes for stable higher yield as compared to other genotypes. Barley genotypes DWRB137, PL906 were selected as per values of ASTAB measure accounted the AMMI analysis with BLUP of genotypes yield values. Composite measure MASV1 selected PL906, DWRB137 while PL906, DWRB137 identified by MASV as genotypes of choice for these locations of the zone. Maximum average yield expressed by DWRB137, PL906 genotypes and good variation had been observed from 45.5 to 50.9 q/ha among feed barley genotypes. Higher value of genotypes adaptability index achieved by DWRB137, PL906 whereas harmonic mean of genotypic values ranked DWRB137, PL906 barley genotypes. Superiority index measures pointed towards PL906, DWRB137 and large value by KB1707. Superiority index while weighting 0.65 and 0.35 for GAI and stability found PL906, DWRB137 as of stable performance with high yield. While considering harmonic mean and stability corresponding ranks identified DWRB137, PL906 genotypes.

Biplot graphical analysis

In first year (2018-19), loadings of studied measures as per first two significant principal components were reflected in Table 9. Biplot graphical analysis considered these PCAs as accounted for 73.7% of variation of the measures (Bocianowski et al. 2019). Three major clusters of the studied measures observed in graphical analysis (Figure 1). MASV1 clubbed with ASTAB, EV, SIPC, Za, W3, WAASB and MASV measures. Yield based measures clubbed with corresponding SI measures. Measure IPCA1 and W2 maintained distance from measures and observed as outliers in different quadrant. Nearly right angles between group of AMMI based and Superiority Index had reflected all together performance of these measures.

The second year (2019-20**)** results are given in Table 10 which reflected the loadings of the measures as per first two significant principal components. Graphical Biplot analysis as per these PCAs accounted for 64.3% of the total variation among the measures (Figure 2). Measures had grouped all together into three major clusters. MASV1 clubbed with ASTAB, EV, SIPC, and MASV measures. Average yield measures clubbed with corresponding SI measures. Others AMMI based measures IPCA1, Za, W1, W2, W3, ASTAB, WAASB observed in adjacent quadrant.

Conclusions

Simultaneous utilization of AMMI and BLUP of genotypes would be more appropriate to recommend high-yielding stable genotypes. The main advantages of AMMI and BLUP had been combined to increase the reliability of multi-locations trials analysis by Superiority Indexes. An additional advantage was to assign desirable weights to the yield and stability performance based on the goal of crop breeding trials.

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Conflict of interest

The authors declared no conflict of interests.

Table 1. Parentage details of barley genotypes and environmental conditions (2018-19).

Code	Genotype	Parentage	Code	Location	Latitude	Longitude	Altitude
G1	RD2991	RD2592 /RD2503//RD 2715	E1	Karnal	29°43'N	70°58'E	245
G2	KB1707	Manjula/DWRUB52	E2	Hisar	29°10'N	75°46'E	229
G3	RD2994	RD2624 / NDB1173	E3	Durgapura	26°51'N	75°47'E	390
G4	RD2992	RD2660 /13thEMBGSN-4	E4	Ludhiana	30°54'N	75°48'E	247
G5	KB1713	IBON-19 (2011-12)/RD2885	E5	Pantnagar	29°02'N	79°48'E	243.8
G6	UPB1077	AHOR1489.58//GLORIA-BAR/ COPAL/3/PRO-/4/CAPUL/TOCTE/5/ ICARO	E6	Tabiji	26°35'N	74°61'E	508
G7	UPB1080	AHOR1489.58//GLORIA-BAR/ COPAL/3/PRO-/4/CAPUL/TOCTE/5/ ICARO					
G8	HUB266	DL 70 / 25th IBYT-22-1					
G9	PL906	RD2503/WSA353 (*H. spontaneum*)					
G10	DWRB205	CDC MANLEY/BCU2881					
G11	NDB1709	INBYT-HI-2 (2016)					
G12	PL909	RD2740/BL194					
G13	BH 946	BHMS22A/BH549//RD2552					
G14	NDB1723	3rd GSBSN-35 (2016)					
G15	DWRB203	P.STO/3/LBIRAN/UNA80// LIGNEE640/4/BLLU/5/PETUNIA 1/6/ M111					
G16	RD2552	RD2035/DL472					
G17	BH1023	NBGSN-4 (2011-12)/RD 2552					
G18	RD2786	RD2634/NDB1020//K425					
G19	DWRB137	DWR28/DWRUB64					
G20	BH1024	NBGSN-12 (2011-12)/BH 393					
G21	RD2899	RD2592/RD2035//RD2715					

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Table 2. Parentage details of barley genotypes and environmental conditions (2019-20).

Code	Genotype	Parentage	Code	Location	Latitude	Longitude	Altitude (m)
G1	BH946	BHMS22A/BH549//RD2552	E1	Durgapura	26°51'N	75°47'E	390
G2	RD2994	RD2624 / NDB1173	E2	Hisar	29°10'N	75°46'E	229
G3	DWRB137	DWR28/DWRUB64	E3	Karnal	29°43'N	70°58'E	245
G4	PL906	RD2503/WSA353 *(H. spontaneum)*	E4	Ludhiana	30°54'N	75°48'E	247
G5	BH902	BH495/RD2552	E5	Modipuram	29°05'N	77°70'E	226
G6	RD2552	RD2035/DL472	E6	Pantnagar	29°02'N	79°48'E	243.8
G7	UPB1080	AHOR1489.58//GLORIA-BAR/ COPAL/3/PRO-/4/CAPUL/ TOCTE/5/ICARO	E7	Tabiji	26°35'N	74°61'E	508
G8	KB1707	Manjula/DWRUB52	E8	Udaipur	24°34'N	73°41'E	585

Table 3. AMMI analysis and percentage contribution of significant interaction principal components (2018-19).

Source	Degree of Freedom	Mean Sum of Squares	Level of Significance	Proportional Contribution of Factors	GxE Interaction Sum of Squares (%)	Cumulative Sum of Squares (%) by IPCA's
Treatments	125	638.79	0.0000000***	95.94		
Genotype (G)	20	378.02	0.0000000***	9.08		
Environment (E)	5	10555.55	0.0000000***	63.42		
GxE interactions	100	195.11	0.0000000***	23.44		
IPC1	24	305.44	0.0000000***		37.57	37.57
IPC2	22	228.62	0.0000000***		25.78	63.35
IPC3	20	186.59	0.0000000***		19.13	82.48
IPC4	18	116.28	0.0000000***		10.73	93.21
Residual	16	82.85	0.0000000***			
Error	252	13.40				
Total	377	220.75				

***=Highly significant effects, IPC1, IPC2, IPC3=Interaction Principal Components 1 , 2 and 3

Table 4. AMMI analysis and percentage contribution of significant interaction principal components (2019-20).

Source	Degree of Freedom	Mean Sum of Squares	Level of Significance	Proportional Contribution of Factors	GxE Interaction Sum of Squares (%)	Cumulative Sum of Squares (%) by IPCA's
Treatments	63	425.98	***	91.93		
Genotype (G)	7	150.36	***	3.61		
Environment (E)	7	2559.33	***	61.37		
GxE interactions	49	160.59	***	26.95		
IPC1	13	237.81	***		39.29	39.29
IPC2	11	198.94	**		27.81	67.10
IPC3	9	126.06	0.613385		14.42	81.51
IPC4	7	130.13	0.96681		11.58	93.09
IPC5	5	68.54	0.973109		4.36	97.45
IPC6	3	63.48	0.904934		2.42	99.87
Residual	1	10.58	0.739886			
Error	128	18.42				
Total	191	152.85				

Table 5. AMMI stability measures and Weighted average of absolute scores for barley genotypes (2018-19).

Genotype	IPCA1	EV	SIPC	Za	ASTAB	MASV1	MASV	W1	W2	W3	WAASB
RD2991	2.72	0.040	5.923	20.00	104.23	5.72	4.76	2.7154	2.0018	1.9058	1.7306
KB1707	3.63	0.047	5.494	20.06	140.86	5.86	4.95	3.6299	2.7088	1.6174	1.7986
RD2994	1.72	0.041	6.321	19.15	82.17	4.80	4.21	1.7214	1.6838	1.4834	1.5885
RD2992	0.55	0.027	4.384	13.31	55.27	5.07	4.23	0.5487	0.8536	1.4376	1.0881
KB1713	2.13	0.029	5.154	17.09	72.68	4.91	4.09	2.1333	1.6306	1.6327	1.4672
UPB1077	1.40	0.038	6.008	17.88	71.98	4.69	4.08	1.3988	1.4137	1.4442	1.4680
UPB1080	1.36	0.020	3.845	13.15	51.14	3.95	3.51	1.3591	1.6186	1.1236	1.1416
HUB266	0.20	0.016	3.501	10.27	32.37	3.55	3.09	0.2037	0.7371	0.9570	0.8295
PL906	1.06	0.014	3.730	11.58	30.39	2.95	2.60	1.0628	1.1184	0.9058	0.9700
DWRB205	2.10	0.043	6.506	21.35	107.62	5.91	5.12	2.1002	2.2141	1.9171	1.8227
NDB1709	0.11	0.012	2.020	4.88	16.19	1.64	1.61	0.1113	0.2463	0.1526	0.3645
PL909	1.01	0.014	3.571	11.35	32.56	3.10	2.77	1.0110	1.2197	0.8806	0.9598
BH 946	0.69	0.047	5.963	17.10	86.07	6.10	5.11	0.6854	0.9000	1.6655	1.3688
NDB1723	0.02	0.003	1.298	3.39	4.24	1.14	1.00	0.0211	0.1402	0.2602	0.2602
DWRB203	0.96	0.037	5.581	16.18	66.61	4.28	3.87	0.9644	1.3227	1.1716	1.3143
RD2552	1.04	0.016	3.672	11.21	33.21	2.91	2.63	1.0373	1.1489	0.7496	0.9356
BH1023	1.02	0.018	3.607	10.37	32.30	3.10	2.66	1.0209	0.6227	0.8385	0.8415
RD2786	2.21	0.033	5.339	16.82	74.39	4.15	3.62	2.2089	1.7508	1.1666	1.4278
DWRB137	0.73	0.010	3.069	9.69	22.50	2.74	2.41	0.7316	0.9435	0.8383	0.8136
BH1024	1.20	0.015	3.392	10.04	28.83	2.65	2.30	1.2039	0.7679	0.7386	0.8295
RD2899	0.51	0.058	6.884	19.79	110.92	6.44	5.59	0.5141	1.3199	1.7525	1.5864

IPCA1=Interaction Principal Components Axis 1 used for stabe performance of genotypes, MASV=Modified AMMI Stability Value, WAASB=Weighted Average of Absolute Scores

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Table 6. AMMI stability measures and Weighted average of absolute scores of barley genotypes (2019-20).

Genotype	IPCA1	MASV1	MASV	Za	EV	SIPC	ASTAB	W1	W2	W3	W4	WAASB
BH946	0.83	8.27	6.58	23.20	0.078	7.898	95.89	0.829	1.879	1.677	1.482	1.435
RD2994	3.04	6.96	5.40	24.21	0.082	8.002	100.72	3.041	1.788	1.563	1.595	1.509
DWRB137	0.19	7.56	6.07	18.02	0.084	6.635	71.37	0.194	1.153	1.108	0.995	1.058
PL906	0.11	5.65	3.89	9.34	0.025	3.480	23.68	0.111	0.110	0.209	0.530	0.509
BH902	1.67	8.21	5.88	21.90	0.057	6.991	73.82	1.673	1.474	1.390	1.603	1.382
RD2552	0.51	8.26	6.31	23.42	0.084	7.944	88.26	0.515	1.510	1.437	1.511	1.402
UPB1080	0.05	6.31	5.83	15.30	0.083	5.888	87.38	0.047	0.194	0.989	0.902	0.852
KB1707	4.36	7.31	6.08	26.73	0.084	7.782	167.15	4.365	3.144	2.493	2.074	1.837

Table 7. Superiority index measures and corresponding ranking of genotypes (2018-19).

Genotype	IPCA1	EV	SIPC	Za	ASTAB	MASV1	MASV	Mean	R_k	SIam	R_k	GM	R_k	SIgm	R_k	HM	R_k	SIhm	R_k
RD2991	40	36	36	39	38	37	37	41.34	20	6.98	20	38.81	20	9.57	20	36.31	20	11.77	20
KB1707	22	20	15	21	22	19	19	55.97	1	65.63	1	52.86	2	64.74	2	50.14	4	63.01	3
RD2994	19	20	22	20	19	17	18	54.07	3	57.96	3	52.08	3	61.60	3	50.17	2	63.06	2
RD2992	26	32	32	32	32	37	37	39.75	21	0.38	21	36.53	21	0.38	21	33.30	21	0.38	21
KB1713	32	26	26	28	28	29	28	47.18	16	30.30	15	46.67	12	40.31	11	46.24	10	48.43	10
UPB1077	32	32	35	33	30	30	30	46.50	17	27.58	17	44.84	17	33.13	17	43.28	16	37.49	16
UPB1080	18	14	14	14	14	14	14	53.94	4	57.28	4	51.96	4	60.96	4	50.14	3	62.80	4
HUB266	15	19	17	17	19	21	21	47.85	12	32.76	12	46.72	11	40.30	12	45.71	12	46.26	12
PL906	14	6	11	11	7	8	7	55.35	2	62.88	2	53.09	1	65.34	1	50.85	1	65.34	1
DWRB205	33	34	36	37	35	35	36	47.26	14	30.72	14	46.15	14	38.41	14	45.07	13	44.22	13
NDB1709	17	18	17	17	17	17	17	47.18	15	29.93	16	45.78	15	36.43	15	44.50	15	41.63	15

Continuing Table 7

Genotype	IPCA1	EV	SIPC	Za	ASTAB	MASV1	MASV	Mean	R_k	SIam	R_k	GM	R_k	SIgm	R_k	HM	R_k	SIhm	R_k
PL909	16	12	13	15	15	14	15	51.57	7	47.71	7	49.68	7	51.97	7	47.92	6	54.49	6
BH 946	17	31	28	26	28	31	30	48.40	11	35.13	11	45.48	16	35.63	16	42.68	17	35.21	17
NDB1723	20	20	20	20	20	20	20	44.82	19	20.42	19	43.40	18	27.06	18	42.07	18	32.59	18
DWRB203	18	24	25	22	22	22	22	49.18	10	38.26	10	47.53	10	43.62	10	45.95	11	47.32	11
RD2552	19	16	16	15	17	13	14	49.73	8	40.34	8	48.07	9	45.62	9	46.44	9	49.00	9
BH1023	19	18	16	15	15	17	16	49.57	9	39.64	9	48.32	8	46.55	8	47.08	8	51.35	8
RD2786	25	19	19	19	21	17	17	52.21	6	50.45	6	49.97	6	53.25	6	47.85	7	54.41	7
DWRB137	12	7	8	8	8	9	9	52.47	5	51.27	5	50.55	5	55.33	5	48.76	5	57.55	5
BH1024	31	24	22	22	22	21	21	45.00	18	21.34	18	43.33	19	26.97	19	41.75	19	31.59	19
RD2899	17	34	34	31	33	34	34	47.69	13	32.37	13	46.25	13	38.71	13	44.82	14	43.22	14

AMu, GMu, HMu=Arithmetic, Geometric, Harmonic Mean for BLUP values; SI au, SI gu, SI hu=Superiority index as per Arithmetic, Geometric, Harmonic Mean; RPGVu, MHRPGVu=Relative performance and Harmonic mean of Relative Performance as per BLUP of genotypes; R_k=Rank of genotypes

Table 8. Superiority index measures and corresponding ranking of genotypes (2019-20).

Genotype	IPCA1	EV	SIPC	Za	ASTAB	MASV1	MASV	MEAN	R_k	SIam	R_k	GM	R_k	SIgm	R_k	HM	R_k	SIhm	R_k
BH946	8	6	9	8	9	11	11	49.84	3	62.14	3	49.11	3	69.15	3	46.96	4	55.53	4
RD2994	12	9	13	12	12	8	7	48.54	5	44.55	5	47.55	4	48.18	5	46.72	5	51.81	5
DWRB137	4	8	4	4	3	6	6	50.95	1	85.54	2	49.64	1	85.54	2	49.66	1	85.54	1
PL906	4	3	3	3	3	3	3	50.38	2	93.11	1	49.31	2	95.98	1	47.18	2	81.59	2
BH902	10	6	8	8	7	10	8	48.78	4	50.78	4	47.54	5	51.39	4	42.47	7	23.50	7
RD2552	11	15	14	13	12	14	14	46.89	7	27.43	6	45.28	7	23.31	8	40.93	8	11.48	8
UPB1080	9	13	10	10	12	10	11	45.57	8	25.98	7	44.31	8	25.98	6	45.49	6	59.94	3
KB1707	14	12	11	14	14	10	12	47.45	6	22.71	8	46.3	6	24.27	7	46.96	3	44.95	6

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Table 9. Loadings of measures as per two Principal Components (2018-19).

Measure	PC1	PC2
Karnal	0.0473	0.2939
Hisar	0.1332	0.1144
Durgapura	0.0490	0.2393
Ludhiana	0.0736	0.3190
Pantnagar	0.0632	0.0544
Tabji	-0.0667	0.1624
Mean	0.0772	0.3989
IPCA1	0.2553	0.0513
MASV1	0.2894	-0.1353
MASV	0.2915	-0.1241
Za	0.3128	-0.0667
EV	0.2857	-0.1078
SIPC	0.2945	-0.0899
ASTAB	0.3089	-0.0710
WAASB	0.3162	-0.0533
W1	0.2553	0.0513
W2	0.2949	0.0566
W3	0.3112	-0.0543
Siam	0.0800	0.3980
Sigm	0.0657	0.4014
Sihm	0.0513	0.3955
73.69	45.92	27.77

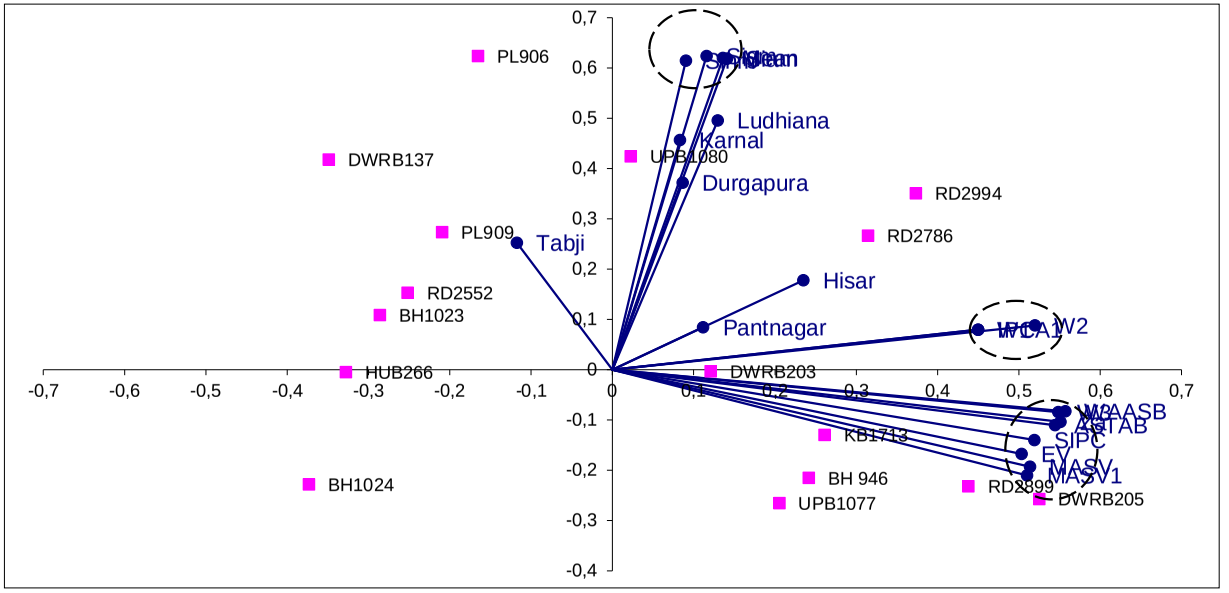

Figure 1. Biplot analysis of superiority index and other measures of barley genotypes 2018-19.

Table 10. Loadings of measures as per two Principal Components (2019-20).

Measure	PC1	PC2
Durgapura	0.0407	0.2748
Hisar	0.0905	-0.4187
Karnal	0.1184	-0.1296
Ludhiana	-0.0598	-0.2978
Modipuram	0.1598	-0.2997
Pantnagar	-0.1372	-0.0706
Tabiji	0.0083	-0.0275
Udaipur	-0.1011	-0.3696
MEAN	0.1482	-0.3316
IPCA1	-0.2330	-0.1913
MASV1	-0.1708	0.0355
MASV	-0.2086	0.0670
Za	-0.2857	-0.0207
EV	-0.2152	0.1150
SIPC	-0.2636	0.0566
ASTAB	-0.2840	-0.1005
WAASB	-0.2888	-0.0751
W1	-0.2330	-0.1913
W2	-0.2690	-0.2059
W3	-0.2928	-0.1181
W4	-0.2892	-0.0648
Siam	0.2399	-0.2419
Sigm	0.2322	-0.2663
64.28	47.5	16.79

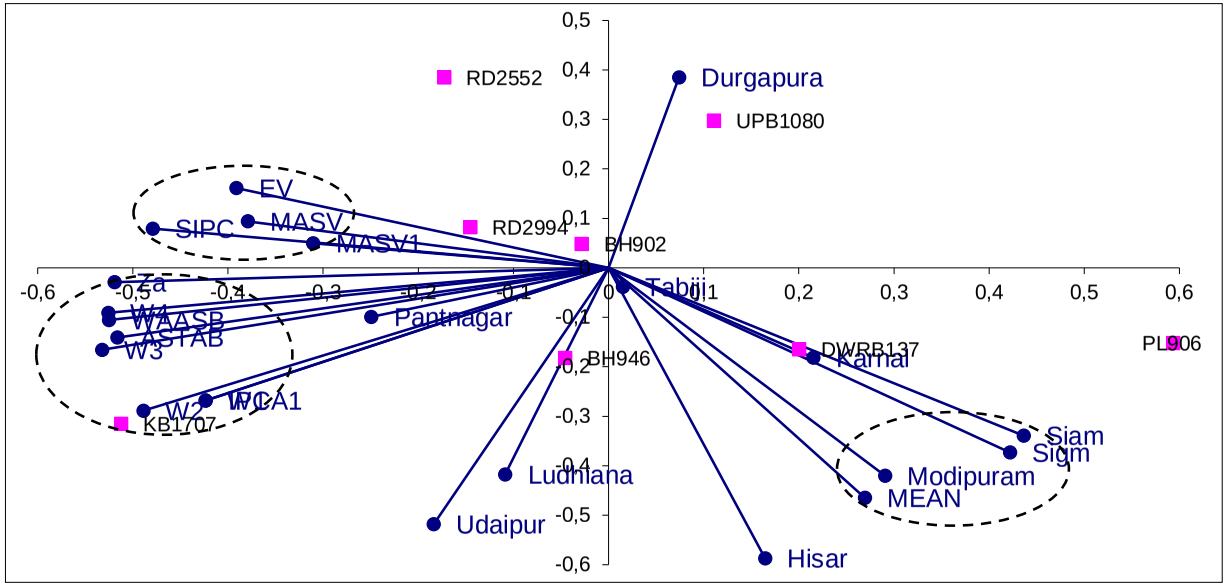

Figure 2. Biplot analysis of stability and adaptability measures of barley genotypes 2019-20.

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Determination of Morphological Variation by Principal Component Analysis and Characterization of the *Capsicum chinense* Genetic Resources

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ABSTRACT

The characterization of plant genetic resources and genetic diversity levels are determined with the morphological descriptors and molecular analysis methods. *Capsicum chinense* populations show a high level of variation in terms of fruit size, fruit width, fruit shape, fruit colour and bitterness. This study aimed to define the plant characteristics of the *C. chinense* genetic resources collected from different locations of the world according to the UPOV (International Union for the Protection of New Varieties of Plants) criteria and to determine the morphological variation levels in the current population within the species. In the first stage of this study, a gene pool consisting of 75 genotypes of the *C. chinense*s pecies was created. It was found that genotypes belonging to the *C. chinense* species show a high level of phenotypic diversity in terms of morphological identification criteria. Cluster and principal component analysis (PCA) were performed to determine relationships among populations. A dendrogram clustered into seven groups was prepared to evaluate morphological differences among *C. chinense* genotypes. In addition, the principal component (PC) analysis showed that the first six PC axes explained 70.99% of the total multivariate variation. It revealed high morphological variation among the *C. chinense* genotypes. In conclusion, this identified *C. chinense* genetic resources to be evaluated as qualified breeding materials for developing new variety candidates in the near future.

Keywords*: Capsicum chinense*, population, characterization, classification, variation

Introduction

The pepper (*Capsicum annuum* L.) belongs to the genus *Capsicum*, which is one of the 98 genera in the Solanaceae family (Greenleaf 1986; Eshbaugh 2012). The number of species within the *Capsicum* genus, which was 38, has been systematically updated to 43 species with the determination of 5 new species as a result of the botanical classification made by taxonomists (Barboza et al. 2019). Today, only 5 of these species (*C. annuum* L., *C. baccatum* L. var *pendulum*, *C. chinense* Jacq., *C. frutescens* L. and *C. pubescens* Ruiz & Pav.) have been cultivated (Eshbaugh 2012; Barboza et al. 2019). In the literature, the primary gene center of *C. annuum* is stated as Mexico and the secondary gene center as Guatemala. The primary gene center of the *C. chinense* and *C. frutescens* is accepted as the Amazon Basin (Ramchiary et al. 2014). Otherwise, the primary gene center of *C. baccatum* and *C. pubescens* species is Peru and Bolivia.

The origin of the pepper is known as Central America. However, studies conducted on the pepper species have revealed that the different origin according to the *Capsicum* species. In the literature, especially hot peppers have been reported to originate from South Brazil and Bolivia (McLeod et al. 1983; Pickersgill 1984). *C. chinense* is the most grown and consumed hot pepper in Brazil. It is also widely spread in the Central and South American countries (Eshbaugh 2012). Today, there are also transitional forms along with the forms that are cultivated. Therefore, *C. chinense* species; shows high phenotypic diversity in terms of fruit shape, fruit colour, fruit size, and bitterness levels.

The chromosome number of *C. chinense* was determined as 2n=24 (Moscone et al. 2007). *Capsicum* species are classified into three main groups according to their flower colours. Accordingly, peppers with white flowers were defined as the *C. annuum* complex, with yellow flowers as the *C. baccatum* group, and purple flowers as the *Capsicum eximium* complex. *C. chinense* species are included in the *C. annuum* complex in terms of flower characteristics (Ince et al. 2009).

Genetic resources are the greatest help to breeders in developing new varieties with high yield and superior qualities in agricultural production and the creation of breeding programs (Balkaya and Yanmaz 2001; Karaağaç and Balkaya 2017). In addition, they are unique resources for breeding programmes due to their adaptability to different ecologies, the resistance ability to diseases and pests, and many desired quality characteristics (Hawkes, 1983). Genetic resources also include both cultivated plants and their wild relatives (Engels et al. 1995). Ortiz and Delgado (1990) searched the morphological characteristics of five different cultured from the *Capsicum* genus found in different seed gene banks (UNA, Peru; CATIE, Costa Rica; INIA, Mexico and CIRF, Mexico), and they grouped genotypes belonging to *C. annuum* L., *C. chinense* Jacq., *C. frutescens* L., *C. pubescens* and C. *baccatum* species based on their plant characteristics to be used in breeding programmes.

Breeders carry out interspecific hybridization studies to benefit from the superior properties of interspecific crosses in the plant breeding programs. The information and data to be obtained from interspecific crosses are very important to increase yield, high resistance to abiotic and biotic stress factors, to develop varieties that can be used as rootstocks and to improve the quality of the cultivars, especially root rot disease (Mavi 2020). The success rate in interspecific hybridization studies changes depending on the genetic relationships between the species (Kurt 2001). It was stated in the literature that *Capsicum* species in wild form carry characters that constitute many resistance properties, especially resistance/tolerance to biotic and abiotic stress factors (Grubben 1977; Pickersgill 1980). The first known interspecific hybridization studies were done between *C. annuum* and *C. frutescens* in *Capsicum* species (Halstead 1912). Nowadays, *C. annuum* and *C. chinense* interspecific hybrids are utilized in F_1 hybrid variety breeding and rootstock breeding programs due to their resistance to low temperatures and viruses for grafted pepper seedlings (Balkaya 2013).

Over time, a high level of genetic diversity has emerged in countries where pepper is cultivated commonly, and as a result, traditional landraces with many different qualities have been formed. The local populations are genotypes of remarkable functional value. Introduction materials arriving in a region by various means adapt to their location. During the time they spend there, genetic diversity arises in its existing genetic structure with environmental factors (Karaağaç 2006). The cross-pollination rate varies between 9-32% in peppers (Bayraktar 1970). If plant isolation techniques are not followed in pepper seed production, a high level of genetic diversity may occur between genotypes (Karaağaç and Balkaya 2010).

Morphological variations have great importance in plant breeding studies. Determination of variation shown by available genetic resources for quantitative and qualitative traits is important for vegetable breeding programmes (Bliss 1981; Gil and Ron 1992; Escribano et al. 1998). Phenotypic diversity within landraces and populations of *Capsicum* is high, including variations in fruit shape, fruit weight, fruit size (length, diameter), fruit flavors, bitterness, fruit colour, and the number of seeds/fruit (García-Neria and Rivera-Bustamante 2011). The number of studies on the *C. chinense* species that demonstrate the level of variation in current populations is quite a few. Vasconcelos et al. (2012) reported the presence of a high level of variation and genetic diversity in terms of flower characteristics. Knowledge of the extent of genetic diversity, identification, differentiation, and characterisation of genotypes and populations, respectively, provides an information tool for detecting duplicates in the collection, their effective extension, and better characterisation and use in breeding (Hornakova et al. 2003). A morphological characterization is the first step in describing and classifying of local genetic resources (Smith and Smith 1989). There was a need to characterize the pepper populations collected so that they could then be used as lines for the development of new varieties (Balkaya and Yanmaz 2001; Karaağaç 2006; Karaağaç and Balkaya 2010). Objective descriptors based on morpho-agronomic characters are considered reliable traits to verify or assess genetic distance or conformity among populations (Hunter 1993). Further, successful results could have been obtained by using DNA markers and molecular techniques determine genetic traits for pepper improvement in recent years (Geleta et al. 2005). *Capsicum* species have been studied using morphological descriptors, cytogenetic data, and molecular markers by many researchers (Conicella et al. 1990; Lefebvre et al. 1993; Zewdie and Zeven 1997; Lefebvre et al. 2001, Geleta et al. 2005; Moscone et al. 2007; Ince et al. 2009; Karaağaç and Balkaya, 2010; Villota-Cerón et al. 2012; Ramchiary et al. 2014;

Barboza et al. 2019). According to the literature, there are similarities and differences regarding morphological variations and molecular markers in pepper (mostly of *C. annuum*) genetic resources. To date, characterization and the determination of morphological variation in *C. chinense* populations are less than other *Capsicum* species. Therefore, this research aimed to define plant characteristics of C. *chinense* genotypes and determine similarities and differences in the morphological variation of *C. chinense* genetic resources collected from the different eco-geographical regions of the world.

Materials and Methods

The study was carried out in the experimental field of Ondokuz Mayıs University Faculty of Agriculture in the year 2018. Seventy-five genotypes belonging to the *Capsicum chinense* obtained from the USDA-ARS National Germplasm Bank; these genetic materials were collected from different parts of the world (Table 1).

The seeds of all genotypes were sown into plug trays containing peat and perlite (in the ratio 2:1) on March 05, 2018. Seedlings were grown in a controlled greenhouse unit at 25°C ± 2 temperature until they reached four true leaves. It was planted on April 25, 2018. The distance between rows of *C. chinense* plants was 0.5 m and with 0.5 m between plants in the row. Soil tests were done before and after planting. After the seedling planting, all cultural processes were applied regularly. The harvest period started at the end of July and lasted until the end of October because the investigated populations have different harvest periods.

Morphological analyses were carried out on 20 plants harvested from each genotype. The morphological characters measured and their scales are presented in Table 2. All characters were measured in the field and at the normal harvest time. The characters are included in the description form developed for *Capsicum* spp. by UPOV with reference TG/76/8 (UPOV 2006). Fruit characteristic analyses were carried out on 10 fruits from each of the accessions. These characters are expressed according to the principles of numerical taxonomy (Sneath and Sokal 1973), so that similarity or dissimilarity coefficients between cultivars can be estimated. The diversity present in a group of populations can be displayed by means of Cluster analysis (Balkaya et al. 2005). Statistical analysis of the data was conducted using the statistical programme SPSS (15.0 for Windows). Principal Component Analysis (PCA) was used for revealing the general differences between genotypes as numerical values, which indicate the traits that could be used to differentiate between genotypes (Balkaya et al. 2010). In the Principal Component Analysis (PCA) and the load coefficient values which relate the values, those principal components with eigenvalues >1.0 were selected, and those characters with load coefficient values >0.3 were considered highly relevant characters cores for principal components (Brown 1991). For a better overview of diversity in the *C. chinense* genotypes, Cluster analysis was also used according to Ward's method. The results of cluster analysis are presented in the form of a dendrogram. The dendrogram obtained in the study represents "similarities among the groups" (Rohlf 1993; Balkaya et al. 2005; Balkaya and Ergün 2008; Balkaya et al. 2010).

Results and Discussion

The results of the plant characteristics examined in genotypes belonging to the *C. chinense* species are given in Table 3. In terms of plant growth types of genotypes, it was determined that 29.3% had vertical, 53.4% semi-upright, and 17.3% horizontal. It was determined that the majority of *C. chinense* genotypes developed in semi-upright growth form. The longest plant height was measured respectively in CC40-3 (106.0 cm), CC40-4 (93.0 cm), CC40-2 (88.0 cm) genotypes and the shortest plant height were found in CC29-1 (34.0 cm), CC11 (36.0 cm), and CC72 (37.5 cm) genotypes (Table 3). It was determined that there is approximately a 3-fold difference between *C. chinense* genotypes in terms of plant height. Cherian and Indira (2003) reported that the average plant height ranged 29.0-52.0 cm in 25 genotypes belonging to the *C. chinense* species. Deonton and Vakinde (1993) determined that the average plant height varied 35.0-95.0 cm in the local pepper genotypes from Nigeria. Otulaj and Makine (1994) measured the average plant height as 30.9 cm-47.8 cm in bell pepper and long pepper genotypes. In another study, Alegbejo and Orakwue (2002) reported that the average plant height ranged from 42.2 cm to 83.62 cm in different pepper varieties. The thickest stem diameter was measured in the CC52 (26.3 mm) genotype, and the thinnest stem diameter was found in the CC61 (8.4 mm) genotype (Table 4). Karaağaç (2006) reported that the stem thickness showed a distribution between 7.6-15.5 mm in red pepper genotypes in Samsun location. The differences between the mentioned literatures may be due to the effect of the species and genotype. This study determined that 85.3% of the *C. chinense* genotypes did not have anthocyanin coloration in the plant stem (Table 4).

Leaf characteristics of *C. chinense* genotypes are given in Table 5. It has been determined that there are significant differences between genotypes in terms of

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leaf length values. The highest leaf height was measured as 9.3 cm in the CC5 genotype. The CC11 (2.2 cm) was determined as the shortest genotype in terms of leaf length. The widest leaf width was determined respectively, CC5 (17.0 cm), CC22 (13.1 cm) and CC3 (12.9 cm) genotypes. The narrowest leaf width (3.7 cm) was measured in the CC11 genotype. The leaf colours are visually identified as light green, green, and dark green in *C. chinense* populations (Table 5). It was determined that 18.6% of the leaves of the detailed genotypes were light green, 49.4% green, and 32.0% dark green tonnes.

When the genotypes of *C. chinense* species were examined in terms of flower colour, it was determined that they had white (21.4% of the genotypes) and yellowish flower colours 78.6% of the genotypes). Vasconcelos et al. (2012) reported a high level of variation and genetic diversity in terms of flower characteristics in *C. chinense* genotypes. Ortiz et al. (2010) mentioned that the flower colour is mostly white in genotypes belonging to the *C. chinense* species. The difference with the mentioned literature has arisen from the different genotypes within the species.

Average fruit length values varied between 14.5-123.3 mm in Table 6. The longest fruit length was measured in the CC40-3 genotype with 123.3 mm, and the shortest fruit length was 14.5 mm in the CC13 genotype. It was determined that there is an 8.5-fold difference between genotypes in terms of fruit lengths. This result shows that the population is very heterogeneous in terms of fruit length. It was determined that the average fruit width values varied between 8.4 mm and 49.7 mm (Table 6). The widest fruit width was measured at 49.7 mm in CC76 genotype, and the narrowest fruit width was determined as the CC61 genotype with a width of 8.4 mm. There was a significant difference of approximately 6.0 times between *C. chinense* genotypes in terms of fruit width values. Deonton and Vakinde (1993) reported that the average fruit length was 2.5-14.0 cm and the fruit width was 2.0-10.5 cm in the local pepper genotypes from Nigeria. Otulaj and Makine (1994) measured the average fruit length as 4.0- 9.2 cm and the fruit width as 2.0-4.5 cm in pepper genotypes. Hallidri and Tome (2000) reported that the average fruit length ranged from 7.6 cm to 12.5 cm in sweet pepper genotypes. Alegbejo and Orakwue (2002) found that the fruit length in pepper genotypes is between 1.93-12.03 cm and the fruit width is between 0.81-2.33 cm. Cherian and Indira (2003) determined that the average fruit length in genotypes belonging to the *C. chinense* species is between 3.0-7.7 cm and the fruit width is between 0.9-6.2 cm. Akıncı and Akıncı (2004) reported that the average fruit length varied between 10.4-13.6 cm and the fruit diameter varied between 1.8-2.6 cm in 22 pepper varieties from different countries. It was determined that the CC40-3 genotype has the highest fruit shape index (7.2) (Table 6). The lowest fruit shape index was found to be the CC47 genotype (0.6). The significant difference in fruit sizes caused the high variation in the *C. chinense* genetic resources.

The genotypes in terms of fruit shape; have been determined as flat, round, heart-shaped, square, isosceles trapezoid, triangular, narrow triangle, and horn-shaped. Of the investigated genotypes, 10.7% had flat, 5.4% had round, 14.6% had heart-shaped, 6.6% had square, 8% had isosceles trapezoid triangle, 32% had triangular, 10.7% had a narrow triangle, and 6.6% had horn-shaped fruits. The fruit colours of the *C. chinense* genotypes were determined visually. In the visual examination, it was determined that there were significant differences in terms of colour tones. The fruits were detected to be in dark green, green, light green, yellow, and light-yellow colour tones (Table 7; Figure 1). In this work, of the genotypes belonging to the *C. chinense* species, 25.4% were determined to have dark green, 40.0% green, 24.0% light green, 8.0% yellow, and 2.6% light yellow fruit colour. The fruit stalk lengths varied between 19.9-61.9 mm in *C. chinense* genotypes (Table 7). The shortest fruit stalk length value was measured in the genotype CC11 (19.9 mm). The longest fruit stalk length was determined in the CC5 genotype with 61.9 mm. It was found that there is approximately a 3-fold difference between genotypes in terms of fruit stalk lengths.

The study determined that *C. chinense* populations show a rich genetic variability in terms of fruit yield components (Table 8). The average number of fruits in *C. chinense* genotypes ranged between 54-2100. The highest fruit number was found as 2100 in the CC52 genotype. This was followed, respectively, the CC50 genotype (1913) and the CC61 genotype (1555). The lowest number of fruits was determined to be in the CC40-4 genotype as 54 units. Deonton and Vakinde (1993) reported that the number of fruits per plant in local pepper genotypes ranged between 16-273 units. In another study, Otulaj and Makine (1994) mentioned that there were between 60-123 unit/plants in bell pepper and long pepper genotypes. Cherian and Indira (2003) stated that the average number of fruits per plant in the *C. chinense* genotypes changed between 4.0 and 63.5. The results of the present study were higher than Cherian and Indira's (2003) findings. This difference occurred due to genotypes and environmental factors. The average fruit weight varied between 0.5 g and 14.1 gin *C. chinense* genotypes (Table 8). The highest

average fruit weight values were determined in the CC40-4 (14.1 g), CC37 (13.0 g), and CC55 (11.6 g) genotypes, respectively. Otherwise, the lowest fruit weights were found in the genotypes CC34 (0.4 g), CC11 (0.5 g) and CC52 (0.5 g). Cherian and Indira (2003) stated that the average fruit weight in *C. chinense* genotypes changed varied between 0.9-7.2 g. The results of this research showed the average fruit weights to be higher compared to the mentioned literature. The highest total yield per plant values were found in the CC56 (6548.6 g), CC60 (5374.7 g), and CC79 (4955.3 g) genotypes (Table 8). The lowest yield value was determined respectively, CC25 (216.0 g) and CC39-2 (217.0 g) genotypes. Cherian and Indira (2003) reported that the yield value per plant in *C. chinense* genotypes was between 12.0 g and 185.0 g. The results of this study in respect to the fruit yield values were very high compared to the mentioned literature.

Determination of variation shown by available genetic resources for quantitative and qualitative traits is important for vegetable breeding programmes (Escribano et al. 1998). The number of studies revealing the level of variation in existing populations in *C. chinense* species is quite low (Cherian and Indira 2003; Manju and Sreelathakumary 2004; Fonseca et al. 2008). The existence of morphological variation in *C. chinense* populations collected from different parts of the world has been demonstrated with this study. Principal Component Analysis (PCA) was used for revealing the general differences between genotypes as numerical values, which indicate the traits that could be used to differentiate between genotypes (Balkaya et al. 2010). In this study, the principal components of *C. chinense* populations were performed in Table 9. The total variance ratios and cumulative variance values of the principal axes were also determined in detail. The fact that eigenvalues are greater than 1 in the principal component analysis indicates that the principal component axes values considered are quite reliable (Mohammadi and Prasanna 2003; Balkaya et al. 2010). This study found that the eigenvalues of the first six principal axes ranged from 1.02 to 4.18. The principal component analysis showed that the first six principal component axes explained 70.99% of the total multivariate variation. The first principal component axis accounted for 26.18% of the variation, whereas the second and third axes accounted for 12.45% and 10.49%, respectively (Table 9). The first three principal component axes explained 49.13% of the total variation. Mohammadi and Prasanna (2003) reported that the total variation of the first three axes should be over 25%. In this study, traits with high coefficients in the first, second, and third principal components should be considered more important since these axes explain the biggest share of the total variation. Though clear guidelines do not exist to determine the significance of a character coefficient, one rule of thumb is to treat coefficients>0.3 as having a large enough effect of being considered important (Brown 1991). Characteristics with high coefficients are: leaf width (0.38), leaf length (0.37), fruit stalk length (0.34) and plant height (0.32) for principal component 1; fruit length 0.40), average fruit weight (0.37), and anthocyanin coloration on the stem (0.31) for the second principal component, and fruit width (-0.45), leaf colour (0.41) and the number of fruits per plant (0.37) for the third principal component. On the PC4 axis, which represents 8.65% of the total variation, the characteristics of stem diameter (0.41), fruit attitude (0.38), and plant attitude (-0.32) were found to be important. Characters such as flower colour (-0.60) and pre-maturity fruit colour (0.35) were found to be important in the PC5 axis. Finally, principal component 6 was mainly related to fruit shape (0.61). Obtained results indicated that the *C. chinense* populations could be distinguished by leaf length, fruit stalk length, and plant height, which had the highest coefficients on the first principal component axis.

Duman and Düzyaman (2004) reported that the total variation was 81.77% as a result of the principal component analysis among 25 pepper genotypes. Karaağaç and Balkaya (2010) determined that the total variation was 74.3% according to the PCA results in 56 red pepper genotypes. Binbir and Baş (2010) reported that according to the results of the PCA performed nine principal component axes representing 85.35% of the total multiple variations in 29 pepper genotypes. Villota-Cerón et al. (2012) determined that the total variation was 70.8% as a result of the principal component analysis among 68 pepper genotypes. It has been found that the results of this study are generally compatible with the mentioned literatures.

To better understand the overall diversity of the *C. chinense* populations, the data were analysed by Cluster analysis that revealed the distribution of genetic diversity. The resultant groups and their subgroups are shown in Table 10, and the related dendrogram is shown in Figure 2. *C. chinense* genotypes clustered within 7 groups and 16 subgroups in the dendrogram. The seven groups and sixteen subgroups can be considered to be distinct germplasm pools in this study. General plant and fruit characteristics of the investigated *C. chinense* populations are as follows:

Group A: There were a total of 12 genotypes in group A. This group consisted of five subgroups (Table 10; Figure 2). It was determined that they varied as horizontal and semi-vertical forms in terms of plant

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growth type of genotypes. The average stem diameter in this group was 23.4 mm, higher than all the other groups.

Group B: This group consisted of 12 genotypes. Genotypes in this group were clustered into four subgroups. The average fruit width was 30.5 mm. The fruit width of this group was the greatest of all the groups.

Group C: This group, which consists of twelve genotypes in the dendrogram, was classified into four subgroups. It was found that the average leaf length (6.2 cm) had the longest among all groups. The flower colour was yellowish tonnes. The average plant height was 70.1 cm. This value was the second rank after Group F among all groups.

Group D: There were a total of 15 genotypes in group D. This group had the biggest cluster of genetic groups (Table 10). The average fruit length in these populations was 38.2 mm. Fruit shapes changed according to the genotypes. Fruit shapes; rectangular, isosceles trapezoid, square, heart shape, narrow triangle, and triangle are defined in this group.

Group E: This group consists of 10 *C. chinense* genotypes. The average leaf length was 2.4 cm. This value was the shortest among all groups. The average fruit weight was 4.8 g. The average fruit stalk length was measured as 19.4 mm. The formation of anthocyanin in the stem of the plants was determined in this group.

Group F: There were a total of seven genotypes in this group. This group was clustered into two subgroups. It was determined that the genotypes in group F had the longest average plant height (81.6 cm) among all groups. The average leaf width was 11.1 cm. The leaf width of this group was the greatest of all the groups. Group F has the longest fruits (93.5 mm) in terms of fruit length. The fruits were horn-shaped or narrow triangular-shaped. The average fruit weight was 9.2 g. The fruit weight of this group was determined to rank firstly among all groups.

Group G: This group consisted of seven *C. chinense* genotypes and clustered into two subgroups (Table 10). Group G had the narrowest fruits in terms of average fruit width (11.5 mm). Genotypes in this group ranked first among all groups in terms of the number of fruits per plant (1570 units). The average fruit weight was 1.1 g. Its fruits were the smallest of all groups. It was ranked last among all groups in terms of fruit weight. This finding showed that the fruits were maximum in number but very small size than the other groups.

This study shows that there is considerable genetic diversity between *C. chinense* populations in terms of all morphological characteristics. Cluster groups were not associated with the geographical origins of *C. chinense* genotypes collected from different countries. The clustering of *C. chinense* genetic resources on the dendrogram in seven separate groups resulted from their different morphological structure and special fruit characteristics. Morphological differences between genotypes may have resulted from the influence of the origin from which they were collected and the environmental conditions.

Conclusions

C. chinense is one of the most important cultivated species in the genus *Capsicum*. Today, there are wild and transitional forms along with the forms that are cultivated. *C. chinense* species is an important genetic resource in terms of resistance to biotic and abiotic stress conditions. The genotypes in *C. chinense* show a high level of genetic diversity in terms of fruit shape, fruit colour, fruit size, and bitterness levels. In this study, the components of the plant characteristics of *C. chinense* were demonstrated by applying multivariate techniques to the morphological data sets. At the end of this study, we have found that genetic diversity within populations of *C. chinense* is high, including variations in leaf length, fruit stalk length, and plant height. Reliable information on morphological variability within *C. chinense* germplasm collections is very useful for breeders in planning variety improvement programs.

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Figure 1. The view of the diversity fruit size, shape and colour for detailed *C. chinense* populations. (Original)

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Table 1. Genotype code, accession number and geographical origins of 75 *C. chinense* genotypes studied.

Genotype Code	Accession Number	Origin	Genotype Code	Accession Number	Origin
CC1	PI 159223 01	USA	CC39-2	PI 281430 01	Bolivia
CC2	PI 213916 01	Bolivia	CC39-3	PI 281430 01	Bolivia
CC3	PI 215736 01	Peru	CC39-4	PI 281430 01	Bolivia
CC4	PI 244667 01	India	CC40-1	PI 315013 01	Peru
CC5	PI 257085 01	Colombia	CC40-2	PI 315013 01	Peru
CC6	PI 257129 01	Colombia	CC40-3	PI 315013 01	Peru
CC7	PI 257145 01	Peru	CC40-4	PI 315013 01	Peru
CC8	PI 260470 01	Peru	CC47	PI 238053 01	Mexica
CC9	PI 260485 02	Bolivia	CC50	PI 497976 01	Philippines
CC10	PI 260486 01	Bolivia	CC51	PI 241669 01	USA
CC11	PI 260508 01	Peru	CC51-3	PI 241669 01	USA
CC13	PI 281393 01	Mexica	CC52	PI 653747 01	Venezuela
CC14	PI 281417 01	Philippines	CC54	PI 653677 02	Peru
CC16	PI 281435 01	USA	CC55	PI 653676 02	Peru
CC17	PI 281440 01	Venezuela	CC56	PI 645487 03	India
CC18	PI 315019 01	Peru	CC57	PI 257068 01	Costa Rica
CC19	PI 315023 02	Peru	CC59	PI 639655 02	Costa Rica
CC20	PI 322721 01	India	CC60	PI 645555 01	Mexica
CC21	PI 406725 01	Costa Rica	CC61	PI 593925 02	Bolivia
CC22	PI 438532 01	Belize	CC62	PI 585253 04	South Korea
CC23	PI 438636 02	Mexica	CC63	PI 241668 01	Equator
CC24	PI 439416 01	Bolivia	CC65	PI 257064 01	Spain
CC25	PI 439432 01	South Korea	CC66	Grif 9261 01	Costa Rica
CC26	PI 585278 02	Equator	CC68	PI 439419 01	Mexica
CC27	PI 257158 01	Peru	CC69-1	PI 257126 01	Colombia
CC28	PI 666562 01	Mexica	CC69-2	PI 257126 01	Colombia
CC-29	PI 260491 01	USA	CC69-3	PI 257126 01	Colombia
CC29-1	PI 260491 01	USA	CC69-4	PI 257126 01	Colombia
CC-30	PI 666561 01	Bolivia	CC72	PI 441635 01	Brazil
CC31	PI 438635 01	Peru	CC72-4	PI 441635 01	Brazil
CC33	PI 439467 01	India	CC76	PI 260465 02	Argentina
CC34	PI 653746 02	Colombia	CC78	Grif 9193 02	Colombia
CC35	Grif 9308 01	Colombia	CC79	PI 666547 01	Guatemala
CC36	PI 639657 04	Peru	CC82-1	PI 260477 01	Peru
CC37	PI 485593 01	Peru	CC82-2	PI 260477 01	Peru
CC38	PI 209028 01	Bolivia	CC82-3	PI 260477 01	Peru
CC38-2	PI 209028 01	Bolivia	CC82-4	PI 260477 01	Peru
CC39-1	PI 281430 01	Bolivia			

Table 2. List of morphological characters used in the characterisation of *C. chinense* populations.

1.	Plant attitude (1.prostrate, 2. semi-upright, 3. upright)
2.	Plant height (cm)
3.	Anthocyanin coloration (1. absent, 2. present)
4.	Stem diameter (mm)
5.	Leaf length (cm)
6.	Leaf width (cm)
7.	Leaf colour (1. light green, 2. green, 3.dark green)
8.	Leaf shape (1. ovate, 2 lanceolate, 3. deltoid)
9.	Flower colour (1.white, 2. yellow)
10.	Fruit attitude
11.	Fruit length (mm)
12.	Fruit width (mm)
13.	Fruit shape index (fruit length/fruit width)
14.	Fruit stalk length (mm)
15.	Fruit shape (1. flat, 2. round, 3. heart shape, 4. square, 5. isosceles, 6. trapezoid, 7. triangle)
16.	Fruit colour (before maturity) (1. dark green, 2. green, 3. light green, 4. yellow)
17.	Fruit number/plant
18.	Total fruit weight (g / plant)
19.	Average fruit weight (g)

Table 3. Distribution of *C. chinense* genotypes in terms of plant height values.

Genotype Code	Plant Height (cm)	Genotype Code	Plant Height (cm)	Genotype Code	Plant Height (cm)	Genotype Code	Plant Height (cm)
CC1	61.0	CC22	65.4	CC39-2	34.0	CC62	50.0
CC2	58.7	CC23	51.0	CC39-3	65.0	CC63	77.5
CC3	48.3	CC24	48.5	CC39-4	57.0	CC65	84.5
CC4	63.5	CC25	40.0	CC40-1	87.0	CC66	63.0
CC5	67.0	CC26	60.0	CC40-2	88.0	CC68	62.0
CC6	71.0	CC27	71.5	CC40-3	106.0	CC69-1	60.0
CC7	85.5	CC28	31.0	CC40-4	93.0	CC69-2	73.0
CC8	68.5	CC29	30.5	CC47	55.0	CC69-3	48.0
CC9	50.0	CC29-1	34.0	CC50	63.0	CC69-4	52.0
CC10	58.3	CC30	52.4	CC51	58.6	CC72	37.5
CC11	36.0	CC31	47.3	CC51-3	38.0	CC72-4	56.0
CC13	63.5	CC33	47.0	CC52	59.0	CC76	63.0
CC14	43.0	CC34	45.7	CC54	48.4	CC78	71.3
CC16	61.5	CC35	44.5	CC55	51.0	CC79	56.8
CC17	61.0	CC36	46.5	CC56	78.8	CC82-1	51.0
CC18	54.5	CC37	56.5	CC57	55.8	CC82-2	42.0
CC19	57.0	CC38	49.5	CC59	73.5	CC82-3	63.0
CC20	63.0	CC38-2	58.0	CC60	49.6	CC82-4	59.0
CC21	83.4	CC39-1	76.0	CC61	44.0		

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Table 4. Distribution of *C. chinense* genotypes in terms of stem diameter and anthocyanin coloration characters.

Genotype Code	Stem Diameter (mm)	Anthocyanin Coloration	Genotype Code	Stem Diameter (mm)	Anthocyanin Coloration
CC1	21.8	Absent	CC39-2	13.0	Absent
CC2	20.6	Absent	CC39-3	25.9	Absent
CC3	21.5	Present	CC39-4	14.1	Absent
CC4	24.4	Absent	CC40-1	16.3	Absent
CC5	20.9	Absent	CC40-2	11.9	Absent
CC6	23.9	Absent	CC40-3	19.9	Absent
CC7	24.9	Absent	CC40-4	15.2	Absent
CC8	27.5	Absent	CC47	20.3	Absent
CC9	25.6	Absent	CC50	21.1	Absent
CC10	23.5	Absent	CC51	16.8	Absent
CC11	11.2	Absent	CC51-3	12.8	Absent
CC13	21.5	Absent	CC52	26.3	Absent
CC14	16.8	Absent	CC54	19.9	Present
CC16	27.3	Absent	CC55	24.1	Present
CC17	22.2	Absent	CC56	25.8	Absent
CC18	29.5	Absent	CC57	16.0	Present
CC19	19.0	Present	CC59	19.0	Absent
CC20	20.4	Absent	CC60	23.0	Absent
CC21	22.9	Absent	CC61	8.4	Present
CC22	25.5	Absent	CC62	13.7	Absent
CC23	19.6	Absent	CC63	16.7	Absent
CC24	18.1	Absent	CC65	22.0	Present
CC25	18.2	Absent	CC66	13.5	Absent
CC26	18.1	Absent	CC68	22.2	Present
CC27	20.8	Absent	CC69-1	19.5	Absent
CC28	10.4	Absent	CC69-2	21.3	Present
CC29	13.5	Absent	CC69-3	13.8	Absent
CC29-1	17.5	Absent	CC69-4	15.1	Absent
CC30	20.3	Absent	CC72	13.3	Present
CC31	20.2	Absent	CC72-4	15.9	Present
CC33	23.2	Absent	CC76	17.3	Absent
CC34	18.9	Absent	CC78	14.1	Absent
CC35	13.4	Absent	CC79	23.5	Absent
CC36	21.9	Absent	CC82-1	17.1	Absent
CC37	13.0	Absent	CC82-2	16.6	Absent
CC38	17.5	Absent	CC82-3	20.1	Absent
CC38-2	18.9	Absent	CC82-4	14.5	Absent
CC39-1	21.3	Absent			

Table 5. Leaf characteristics of genotypes belonging to the *C. chinense* species.

Genotype Code	Leaf Length (cm)	Leaf Width (cm)	Leaf Colour	Leaf Shape
CC1	6.0±1.7	8.9±2.5	Dark green	Ovate
CC2	5.3±2.6	11.2±2.1	Green	Ovate
CC3	6.7±1.3	12.9±0.4	Green	Ovate
CC4	5.7±0.8	11.0±0.5	Dark green	Lanceolate
CC5	9.3±2.1	17.0±1.1	Dark green	Deltoid
CC6	6.3±1.1	11.5±1.5	Green	Deltoid
CC7	5.8±1.4	12.1±0.6	Green	Ovate
CC8	6.0±1.0	10.6±0.7	Dark green	Deltoid
CC9	6.0±1.3	10.6±0.6	Light green	Deltoid
CC10	6.2±1.6	11.5±0.7	Dark green	Ovate
CC11	2.2±0.7	3.7±2.2	Dark green	Deltoid
CC13	5.0±0.9	9.7±0.6	Dark green	Ovate
CC14	4.2±1.1	5.6±0.7	Green	Ovate
CC16	6.3±1.1	11.8±0.6	Green	Ovate
CC17	8.4±1.3	12.0±0.8	Light green	Deltoid
CC18	7.3±1.7	13.0±0.8	Green	Deltoid
CC19	4.7±0.7	9.2±0.4	Green	Ovate
CC20	6.7±1.1	11.5±0.8	Light green	Ovate
CC21	8.2±1.3	10.0±1.3	Light green	Lanceolate
CC22	7.9±1.8	13.1±0.9	Dark green	Deltoid
CC23	6.9±1.4	11.4±0.9	Dark green	Deltoid
CC24	6.1±1.7	11.7±0.6	Dark green	Deltoid
CC25	6.4±0.9	10.2±0.8	Green	Deltoid
CC26	5.8±1.0	12.4±0.9	Green	Deltoid
CC27	6.1±2.1	9.6±1.1	Green	Deltoid
CC28	2.6±0.5	4.9±0.2	Dark green	Ovate
CC29	2.7±0.8	6.2±0.4	Green	Lanceolate
CC29-1	4.7±0.8	8.7±0.7	Green	Lanceolate
CC-30	5.7±1.1	9.8±0.7	Light green	Ovate
CC31	4.1±0.7	7.9±0.4	Light green	Lanceolate
CC33	4.8±0.8	8.8±0.5	Green	Deltoid
CC34	3.6±0.5	6.2±0.4	Green	Lanceolate
CC35	6.2±1.2	11.4±0.7	Light green	Ovate
CC36	6.2±1.3	10.8±0.6	Light green	Lanceolate
CC37	4.1±0.8	8.1±0.9	Green	Lanceolate
CC38	5.5±0.9	9.7±0.9	Green	Ovate
CC38-2	5.5±0.4	9.8±0.4	Green	Ovate

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Continuing Table 5

Genotype Code	Leaf Length (cm)	Leaf Width (cm)	Leaf Colour	Leaf Shape
CC39-1	5.8±0.7	10.9±0.2	Light green	Lanceolate
CC39-2	3.9±0.5	8.0±0.2	Green	Lanceolate
CC39-3	4.1±1.1	7.4±0.2	Light green	Lanceolate
CC39-4	4.1±1.0	8.6±0.8	Light green	Lanceolate
CC40-1	6.7±0.8	10.8±0.4	Dark green	Ovate
CC40-2	4.9±2.4	8.8±1.2	Dark green	Ovate
CC40-3	6.9±0.5	12.8±0.4	Dark green	Ovate
CC40-4	5.8±1.1	10.1±0.6	Dark green	Ovate
CC47	6.2±0.4	10.2±0.3	Green	Deltoid
CC50	3.8±0.4	6.6±0.6	Dark green	Deltoid
CC51	4.3±0.6	8.6±0.5	Green	Lanceolate
CC51-3	4.5±0.6	8.0±0.5	Green	Lanceolate
CC52	3.2±0.8	7.1±0.6	Dark green	Lanceolate
CC54	5.7±1.0	14.7±0.6	Dark green	Deltoid
CC55	4.1±1.0	8.9±0.5	Dark green	Ovate
CC56	4.7±0.9	8.3±0.5	Green	Ovate
CC57	3.5±1.2	8.0±0.5	Dark green	Lanceolate
CC59	5.3±1.2	10.1±0.8	Dark green	Deltoid
CC60	3.0±0.7	6.2±0.4	Green	Ovate
CC61	2.3±0.9	4.8±0.4	Dark green	Lanceolate
CC62	3.4±0.9	6.7±0.4	Light green	Lanceolate
CC63	4.4±1.0	7.9±0.6	Light green	Ovate
CC65	4.8±1.3	10.9±0.5	Green	Ovate
CC66	4.9±1.3	9.9±0.6	Light green	Ovate
CC68	4.5±2.0	9.9±0.7	Dark green	Lanceolate
CC69-1	3.0±0.4	6.5±0.2	Green	Ovate
CC69-2	4.5±1.4	8.2±0.8	Green	Ovate
CC69-3	4.3±1.4	9.1±0.4	Green	Ovate
CC69-4	3.8±0.7	8.0±0.5	Green	Ovate
CC72	3.6±0.9	7.2±0.3	Green	Ovate
CC72-4	4.1±0.4	8.2±0.2	Green	Ovate
CC76	3.9±1.0	10.9±0.5	Green	Lanceolate
CC78	6.7±0.9	8.9±0.6	Green	Ovate
CC79	5.7±1.9	9.4±0.8	Dark green	Ovate
CC82-1	3.9±1.0	7.2±0.7	Green	Ovate
CC82-2	3.9±0.4	6.8±0.8	Green	Ovate
CC82-3	4.7±1.0	7.6±0.8	Green	Ovate
CC82-4	4.2±0.6	7.4±0.5	Green	Ovate

Table 6. Fruit dimensions results of *C. chinense* genotypes.

Genotype Code	Fruit Length (mm)	Fruit Width (mm)	Fruit Shape Index	Genotype Code	Fruit Length (mm)	Fruit Width (mm)	Fruit Shape Index
CC1	74.3±6.6	23.6±4.7	3.1	CC39-2	46.7±6.3	10.7±1.9	4.3
CC2	45.6±6.1	18.8±2.9	2.4	CC39-3	41.1±8.9	19.6±3.1	2.0
CC3	52.8±6.7	22.2±4.0	2.3	CC39-4	28.6±5.7	24.8±8.1	1.1
CC4	46.9±9.8	18.0±5.4	2.6	CC40-1	90.5±12.7	21.6±1.7	4.1
CC5	71.7±11.7	18.8±4.0	3.8	CC40-2	67.0±13.3	12.1±1.8	5.5
CC6	39.8±8.2	17.6±3.0	2.2	CC40-3	123.3±18.5	17.0±2.2	7.2
CC7	26.1±3.4	22.4±2.6	1.1	CC40-4	113.2±14.9	18.3±2.3	6.1
CC8	40.1±5.6	23.8±3.5	1.6	CC47	21.5±3.6	33.3±4.3	0.6
CC9	51.5±7.5	21.3±4.3	2.4	CC50	31.7±6.0	14.1±4.1	2.2
CC10	36.2±8.0	26.5±9.3	1.3	CC51	63.0±11.9	19.3±3.3	3.2
CC11	21.3±6.1	10.2±2.1	2.0	CC51-3	48.8±5.0	19.4±1.7	2.5
CC13	14.5±2.3	18.0±3.6	0.8	CC52	16.9±12.3	13.2±4.6	1.2
CC14	43.8±5.2	19.8±2.1	2.2	CC54	49.5±7.0	25.8±3.3	1.9
CC16	41.3±4.2	14.6±1.4	2.8	CC55	49.8±9.4	23.7±3.8	2.1
CC17	28.1±3.5	24.3±3.7	1.1	CC56	41.7±5.3	35.2±4.1	1.1
CC18	28.2±5.4	23.1±2.7	1.2	CC57	47.9±6.9	17.9±2.5	2.6
CC19	28.1±5.6	21.3±1.9	1.3	CC59	86.6±16.2	19.3±2.6	4.4
CC20	22.6±2.0	20.7±1.6	1.0	CC60	36.0±7.6	22.5±2.5	1.6
CC21	27.4±2.3	22.5±2.5	1.2	CC61	16.9±1.9	8.4±0.7	2.0
CC22	28.4±4.6	27.9±0.8	1.0	CC62	55.1±7.8	21.6±2.8	2.5
CC23	38.3±4.0	27.1±4.7	1.4	CC63	55.7±10.9	15.8±2.0	3.5
CC24	26.5±3.1	28.1±3.4	0.9	CC65	46.1±8.1	18.1±2.5	2.5
CC25	15.3±2.9	17.9±1.2	0.8	CC66	52.4±6.1	14.3±2.4	3.6
CC26	42.3±5.6	13.4±2.3	3.1	CC68	63.8±8.8	10.1±2.1	6.3
CC27	77.3±12.2	17.1±3.7	4.5	CC69-1	40.1±5.1	15.3±1.5	2.6
CC28	19.4±2.5	10.3±1.5	1.8	CC69-2	65.5±8.7	13.2±4.9	4.9
CC29	32.1±5.2	24.8±2.5	1.2	CC69-3	28.7±3.5	18.0±1.6	1.5
CC29-1	49.5±8.0	25.3±3.2	1.9	CC69-4	22.1±3.5	16.8±1.4	1.3
CC-30	29.3±5.3	31.6±3.8	0.9	CC72	37.6±9.5	21.3±1.9	1.7
CC31	42.2±7.5	26.7±3.9	1.5	CC72-4	24.3±2.4	20.2±1.3	1.2
CC33	39.7±5.1	26.6±5.0	1.5	CC76	54.5±8.5	49.7±2.5	1.0
CC34	10.3±1.4	9.3±0.8	1.1	CC78	47.2±4.2	21.3±2.9	2.2
CC35	50.2±7.5	18.5±2.1	2.7	CC79	32.4±4.4	34.6±3.2	0.9
CC36	42.1±6.5	26.7±5.4	1.5	CC82-1	60.8±7.9	21.3±1.8	2.8
CC37	102.3±18.4	39.7±3.7	2.5	CC82-2	40.3±5.7	25.5±2.4	1.5
CC38	26.1±6.3	31.4±5.3	0.8	CC82-3	44.3±4.1	24.2±6.0	1.8
CC38-2	41.7±5.9	28.7±3.8	1.4	CC82-4	50.8±4.1	24.0±2.7	2.1
CC39-1	50.1±8.7	17.3±1.5	2.8				

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Table 7. Results of fruit colour and fruit stalk length traits of *C. chinense* genotypes.

Genotype Code	Fruit Colour	Fruit Stalk Length (mm)	Genotype Code	Fruit Colour	Fruit Stalk Length (mm)
CC1	Green	37.1±7.4	CC39-2	Green	32.1±3.1
CC2	Green	30.5±5.3	CC39-3	Green	28.1±5.1
CC3	Dark green	34.4±5.0	CC39-4	Green	34.1±4.6
CC4	Light green	40.7±7.5	CC40-1	Green	49.1±4.4
CC5	Yellow	61.9±8.2	CC40-2	Dark green	34.9±2.6
CC6	Green	37.3±6.4	CC40-3	Dark green	48.6±3.9
CC7	Light green	44.8±13.7	CC40-4	Green	42.8±6.1
CC8	Green	26.9±4.2	CC47	Light green	26.3±3.2
CC9	Dark green	33.7±4.9	CC50	Yellow	25.4±4.6
CC10	Green	29.3±5.0	CC51	Light green	35.8±5.9
CC11	Light yellow	19.9±3.2	CC51-3	Yellow	32.0±4.1
CC13	Dark green	26.8±5.5	CC52	Light green	23.5±5.8
CC14	Green	32.6±5.6	CC54	Light green	39.8±4.8
CC16	Dark green	30.3±5.9	CC55	Dark green	35.6±4.8
CC17	Light green	29.9±3.4	CC56	Green	34.2±5.2
CC18	Dark green	27.4±4.1	CC57	Green	34.3±4.6
CC19	Dark green	28.1±3.3	CC59	Dark green	41.5±7.0
CC20	Green	27.2±4.2	CC60	Yellow	26.4±5.3
CC21	Light green	32.4±6.5	CC61	Dark green	24.7±4.6
CC22	Dark green	27.9±4.8	CC62	Green	35.1±6.7
CC23	Green	31.3±3.8	CC63	Light green	38.9±7.1
CC24	Green	25.7±3.7	CC65	Green	35.3±5.0
CC25	Light green	23.0±2.5	CC66	Yellow	35.3±54
CC26	Green	34.0±5.4	CC68	Dark green	35.0±6.8
CC27	Green	35.0±6.2	CC69-1	Dark green	44.5±6.6
CC28	Light green	21.6±3.5	CC69-2	Green	39.7±6.0
CC29	Green	25.6±3.1	CC69-3	Yellow	34.0±4.5
CC29-1	Light green	28.9±3.5	CC69-4	Light green	30.0±4.2
CC-30	Light green	32.9±5.6	CC72	Dark green	31.6±4.9
CC31	Dark green	30.6±5.0	CC72-4	Green	27.1±3.3
CC33	Light yellow	35.2±5.3	CC76	Dark green	34.5±5.1
CC34	Dark green	22.2±3.5	CC78	Green	38.6±6.0
CC35	Green	32.9±4.6	CC79	Green	33.5±4.5
CC36	Green	35.4±7.1	CC82-1	Green	23.7±4.9
CC37	Green	28.2±5.0	CC82-2	Light green	29.3±5.7
CC38	Light green	30.1±5.5	CC82-3	Dark green	30.3±3.3
CC38-2	Light green	30.5±5.5	CC82-4	Light green	28.8±4.0
CC39-1	Green	31.9±3.8			

Table 8. Results of fruit yield components of *C. chinense* genotypes.

Genotype Code	Fruit Number/Plant	Average Fruit Weight (g)	Total Fruit Weight/Plant (g)	Genotype Code	Fruit Number/Plant	Average Fruit Weight (g)	Total Fruit Weight/Plant (g)
CC1	217	6.0	1321.5	CC39-2	128	1.6	217.0
CC2	120	2.2	270.2	CC39-3	310	3.7	256.0
CC3	335	3.9	1333.3	CC39-4	184	3.0	564.5
CC4	440	3.1	1372.8	CC40-1	81	8.5	747.9
CC5	550	6.3	3514.5	CC40-2	95	3.8	380.2
CC6	120	2.5	300.0	CC40-3	160	13.2	1781.9
CC7	298	2.5	736.6	CC40-4	54	14.1	560.3
CC8	692	4.2	2920.2	CC47	917	3.6	4250.4
CC9	426	8.0	3433.5	CC50	1913	1.9	3740.0
CC10	110	7.5	834.9	CC51	479	3.5	2499.4
CC11	1280	0.5	640.0	CC51-3	231	2.6	918.9
CC13	63	3.0	192.1	CC52	2100	0.5	1570.2
CC14	626	4.3	2691.8	CC54	556	9.9	4737.8
CC16	216	2.2	483.8	CC55	551	11.6	4427.1
CC17	302	2.7	830.5	CC56	975	6.4	6548.6
CC18	481	2.8	1351.6	CC57	679	6.6	2281.7
CC19	190	2.3	446.5	CC59	148	5.4	1392.1
CC20	128	2.7	352.0	CC60	1382	3.4	5374.7
CC21	1469	2.8	4171.9	CC61	1555	0.7	1010.5
CC22	592	3.5	2107.5	CC62	246	5.3	1444.0
CC23	228	3.4	793.4	CC63	892	3.1	3156.7
CC24	126	4.3	544.3	CC65	658	2.8	2407.4
CC25	100	2.1	216.0	CC66	663	2.5	1547.8
CC26	856	3.3	2824.8	CC68	1235	3.6	2368.2
CC27	397	4.8	1944.4	CC69-1	1469	1.6	327.6
CC28	1239	1.0	1264.6	CC69-2	592	1.5	1111.3
CC29	355	4.8	1715.6	CC69-3	227	2.2	636.6
CC29-1	128	7.1	910.2	CC69-4	692	1.7	972.4
CC30	294	5.3	1576.4	CC72	708	3.6	2904.6
CC31	441	4.5	1992.5	CC72-4	355	1.8	1957.4
CC33	377	5.4	2057.5	CC76	544	3.5	2458.8
CC34	1434	0.4	600.0	CC78	558	4.1	2458.8
CC35	433	3.7	1634.7	CC79	956	4.3	4955.3
CC36	207	5.3	1098.6	CC82-1	394	3.0	1603.1
CC37	262	13.0	3395.8	CC82-2	166	4.0	843.1
CC38	617	4.0	2514.9	CC82-3	231	4.9	1776.1
CC38-2	165	4.7	783.1	CC82-4	222	3.9	1039.5
CC39-1	190	3.5	680.2				

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Table 9. Principal component (PC) analysis of characters associated with 75 *C. chinense* populations. Proportions of variations are associated with first six PC axes, which correspond to Eigenvalues greater than 1.

	PC Axis					
Eigenvalues	4.18	1.99	1.67	1.38	1.15	1.02
Variation, %	26.18	12.45	10.49	8.65	7.19	6.00
Cumulative variation, %	26.18	38.64	49.13	57.79	64.99	70.99
	Eigen Vectors					
Trait	**PC 1**	**PC 2**	**PC 3**	**PC 4**	**PC 5**	**PC 6**
Stem diameter (mm)	0.19	-0.27	0.13	0.41	0.23	-0.32
Plant height (cm)	0.32	-0.02	0.34	-0.22	0.06	-0.09
Plant attitude	0.29	-0.19	0.26	-0.32	0.03	0.14
Leaf length (cm)	0.37	-0.30	0.04	0.15	-0.07	-0.09
Leaf width (cm)	0.38	-0.20	0.07	0.28	-0.10	-0.08
Leaf colour	0.02	0.24	0.41	0.22	0.26	0.41
Flower colour	-0.15	0.08	0.17	0.19	-0.60	0.12
Fruit attitude	0.21	0.19	-0.14	0.38	-0.29	0.27
Fruit stalk length (mm)	0.34	0.17	0.18	-0.11	-0.28	-0.04
Fruit width (mm)	0.15	-0.07	-0.45	0.26	0.27	0.30
Fruit length (mm)	0.28	0.40	0.01	-0.24	-0.01	0.14
Fruit colour (before maturity)	-0.11	0.25	0.24	0.20	0.35	-0.08
Fruit shape	-0.10	-0.37	0.20	0.06	-0.03	0.61
Anthocyanin coloration	-0.08	0.31	0.21	0.37	-0.12	-0.27
Number of fruits per plant	-0.25	-0.07	0.37	0.03	0.17	0.02
Average fruit weight (g)	0.30	0.37	-0.16	0.00	0.26	0.10

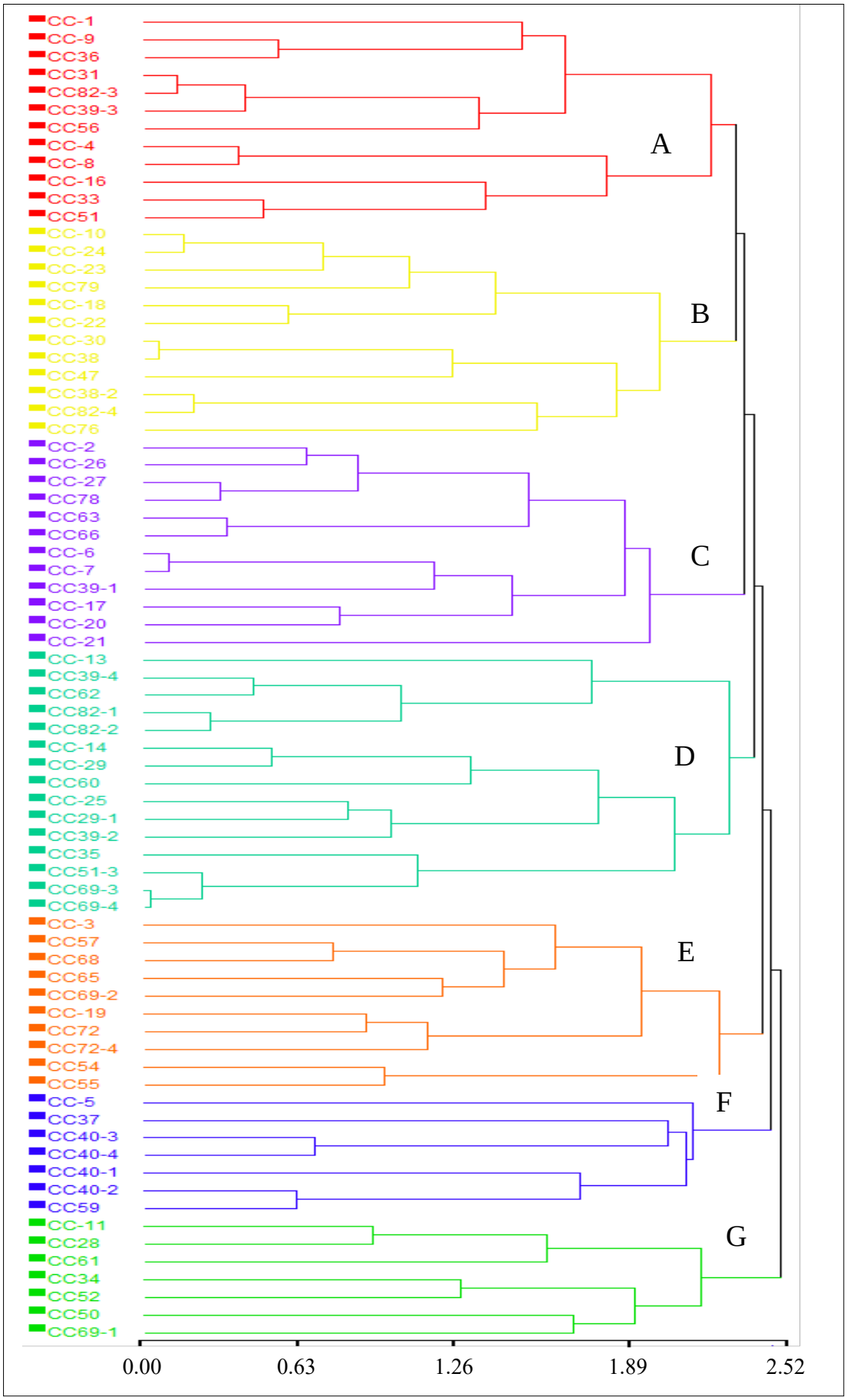

Figure 2. Genetic groupings of *C. chinense* genotypes according to cluster analysis.

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Table 10. *C. chinense* genotype groups and subgroups obtained by Cluster analysis.

Groups	Subgroups	Genotypes	Total Genotype Number
A	5	CC1, CC9, CC36, CC31, CC82-3, CC56, CC39-3, CC4, CC8, CC16, CC33, CC51	12
B	4	CC10, CC24, CC23, CC79, CC18, CC22, CC30, CC38, CC47, CC38-2, CC82-4, CC76	12
C	4	CC2, CC26, CC27, CC78, CC63, CC66, CC6, CC7, CC39-1, CC17, CC20, CC21	12
D	5	CC13, CC39-4, CC62, CC82-1, CC14, CC82-2, CC29, CC60, CC25, CC29-1, CC39-2, CC35, CC51-3, CC69-3 CC69-4	15
E	4	CC3, CC57, CC68, CC65, CC69-2, CC19, CC72, CC72-4, CC54, CC55	10
F	2	CC5, CC37, CC40-3, CC40-4, CC40-1, CC40-2, CC59	7
G	2	CC11, CC28, CC61, CC34, CC52, CC50, CC69-1	7
Total	**16**		**75**

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Transgenics for Improving Salt Stress Tolerance in Legume Crops Chickpea and Pigeon Pea

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ABSTRACT

Legumes, being rich in proteins, are an important part of human diet and account for about 27 per cent of crop production around the globe. Chickpea and Pigeon pea are the two most important legume crops of India. However, production in legume crops is adversely affected due to salinity in arid and semi-arid regions of world. Salt stress reduces water potential, creates imbalance in ion concentration and causes toxicity. Helicases (RuvB & p68) have been shown to play an important role in plants against salt stress. p68 which is a DEAD-box helicase interacts with Ca^{2+} -CaM. LecRLK is another important gene involved in regulating diverse signalling pathways under salt stress condition in plants. The present review highlights the role of salinity stress tolerance by these helicases and lectin receptor kinases genes by developing transgenic chickpea and pigeon pea lines.

Keywords: Chickpea, helicases, LecRLK, legume, pigeon pea, salinity, transgenics

Introduction

Abiotic stress is the major cause of decreasing the yield of important food crops by more than 50%, leading to the losses worth of million dollars every year (Rasool et al. 2013; Lamaoui et al. 2018). Among abiotic stresses, high salinity stress is the most severe environmental stress, which impairs crop production on at least 20% of irrigated land worldwide. Out of the 1500 million hectares agricultural land, 32 million (2%) is affected by secondary salinity of varying degrees. Further, problems will be worsened as nearly 50% of the arable land will hit salinity by 2050 (Machado and Serralheiro, 2017). Extensive economic losses due to salinity include costs of $27 billion-plus loss of crop value per year (Kumar et al. 2017).

Excess of salt in soil is one of the major devastating abiotic stresses for global agriculture as it may cause degradation of arable soils, particularly those that are heavily irrigated via adverse impacts on seed germination, plant growth and development, plant vigour and crop yields and hence drastically reducing agricultural productivity (Cheeseman 2015; Akram et al. 2017; Kumar et al. 2017). A saline soil is defined as one in which the electrical conductivity (EC) of the saturation extract (EC_e) in the root zone exceeds 4 dS/m (approximately 40 mM NaCl) at 25°C and has an exchangeable sodium of 15%. The yield of most crop plants is reduced at this EC_e, though many crops exhibit yield reduction at lower EC_{es} (Munns, 2005; Jamil et al. 2011). The repercussions of salinity stress on crop productivity and concerns regarding its management have been the focus of several prior comprehensive reviews (Hoffman et al. 2007; Grattan et al. 2011; Pereira et al. 2014). The direct effects of excess of soluble salts in soil causes imbalance or accumulation of specific ions (Cl, Na) in plants which results in osmotic stress because of reduced soil water availability and ion imbalance and ion toxicity (Munns 2005) which lead to plant demise ultimately (Maas and Hoffman 1977; Zorb et al. 2014).

Recent estimates show an increase in global salt-affected area with an area of 1,128 million ha

(Mandal et al. 2018). According to Shrivasata and Kumar (2015) approx. 20% of total cultivated and 33% of irrigated agricultural lands worldwide are affected by high salinity. Moreover, the salt affected areas are increasing at a rate of 10% annually for several reasons, including high surface evaporation, low precipitation, irrigation with saline water, weathering of native rocks, and poor agricultural practices. In India, nearly 5% of the net cultivated area is having salt affected soils, spreading from Jammu & Kashmir (Ladakh region) in north to Kanyakumari in south, and Andaman & Nicobar Islands in the east to Gujarat in the west. Increasing trend in the salt-affected soils is becoming a major threat to economic development and national food security in India.

Salinity stress affects plant health in two ways, first is decrease in soil porosity that leads to decrease in oxygen and water movement around the roots and secondly increased Na^+ concentration is toxic for essential enzymes which in turn alter the physiology of plants (Munns and Tester, 2008). It has been reported that when salinity rises to 100 mM NaCl in a field, most of the legume species die before maturity (Munns et al. 2002).

Legumes belong to the important plant family Leguminosae or Fabaceae and provide the prime single source of vegetable protein in human diets and livestock feed (Dita et al. 2006). Legumes can serve as resource-conserving alternative as these plants can fix atmospheric nitrogen, thus plummeting the requirement for chemical fertilizers and hence playing a role in improving soil health and increasing overall crop productivity. Reduction in pests, diseases and weed populations has been observed in farming systems, when legumes are used as an inter-crop. Legumes occupy 12-15% of worldwide arable land to provide 33% of dietary protein and 27% of major crop production (Flexas et al. 2004). In legumes, seedling and developmental stages are more sensitive to salinity stress than the germination stage (Al-Mutawa et al. 2003).

Salinity also has an adverse effect on shoot biomass, pod set and pod filling in chickpea (*Cicer arietinum*), causing reduced yields (Flowers et al. 2010; Atieno et al. 2017). High salt concentration reduces the NO_3 supply from the soil which leads to lower protein content in chickpea, faba bean and mung bean (Cordovilla et al. 1995; Ghassemi-Golezani et al. 2010; Qados et al. 2011).

Conventional breeding approach has been widely used to develop stress tolerant and high yielding crop plants but this procedure is lengthy, labour intensive and costly and dependent on access to germplasm with enough genetic variability (Ashraf, 2010; Yu et al. 2016., Wani et al. 2016). To resolve these barriers associated with conventional breeding, biotechnological approaches such as genetic engineering provide a viable alternative and are now becoming more widely used throughout the world to obtain better results in shorter time. Transgenic approach is effectively used by plant scientists to impart salinity tolerance in various crops which mainly includes integration of genes that encode compatible organic solutes, ion transport proteins and transcriptional factors for gene regulation (Ashraf et al. 2010). These genetic processes demand the arbitration of several types of crucial enzymes including helicases. Helicases are the proteins which play a role in unwinding of nucleic acids and can be categorized into three groups- RNA helicases, DNA helicases, and Chromatin Remodelers. Other group of signal perception and signaling related genes (Passricha et al. 2019a). The constitutive expression of such genes can be used to construct stress tolerant plants. Studies reported that these genes provide stress tolerance when overexpressed are PDH45 (Shivakumara et al. 2017), p68 (Tuteja et al. 2014) and more (Passricha et al. 2019b). LecRLK homolog from *Pisum sativum* has been reported to provide salinity stress tolerance in overexpressed tobacco and rice plants (Passricha et al. 2019b; Vaid et al. 2013). In this review, we have summarized the functional validation of signal perception gene *Os*LecRLK, helicase gene and p68 gene in providing salinity stress tolerance in legume crops through transgenic approach.

Role of helicases in salt stress tolerance

DNA helicases are involved in replication, transcription, recombination, and repair so can also be called as 'genome caretakers' (Chu and Hickson, 2009; Brosh et al. 2013). On the other hand, RNA helicases play diverse roles in almost all processes of RNA metabolism like transcription, translation, pre-RNA splicing and export, removal of secondary structure of RNA ribosome biogenesis, miRNA processing and RNA metabolism which are crucial to cell survival (Putnam and Jankowsky, 2013; Jarmoskaite and Russell, 2014; Bourgeois et al. 2016; Sloan and Bohnsack, 2018). Chromatin remodelers perform ATP hydrolysis alter the interaction between DNA and histone proteins in a non-covalent fashion (Clapier and cairns, 2009). Out of the six helicase SFs, the monomeric SF1 and SF2 contain DNA helicases which are involved in the transcription, repair and recombination. Whereas SF6 contains replicative eukaryotic DNA helicases. Different abiotic stresses such as heavy metals, drought, salt, temperature, UV, etc. increase the amount of endogenous ROS in the cell

which cause oxidative damage to the plant (Manova and Gruszka, 2015). These damages may end up in double-stranded breaks (DSBs), base modifications by insertion or deletions, inter - or - intra strand cross-linking or and formation of pyrimidine dimers. As plant cannot readily escape from the harsh climatic changes, they rely heavily on DNA damage detection and repair pathways for the timely and accurate removal of DNA lesions and preservation of genomic stability (Manova and Gruszka, 2015).

RuvB is a DNA helicase, which belongs to the AAA+ family of proteins and is very well characterized in bacteria. Almost all the members of this family are ATPases, but some members of this family contain helicase activity also. In prokaryotes, it plays a role in DNA damage repair mechanism by the formation of Holliday junction with RuvA and RuvC (Donaldson et al. 2004), branch migration and resolution of Holliday junction. A mutation study in *Saccharomyces cerevisiae* has revealed that RuvB is essential for growth of cells (Ahmad et al. 2012). It is an important component of various multiprotein complexes and is involved in multicellular pathways such as cell cycle progression, replication fork reversal, nonsense-mediated mRNA decay, apoptosis, mitosis, and development (Ahmad et al. 2012). *RuvB* stands as a potential candidate gene which can be involved in abiotic stress tolerance. Till date there are only two reports on characterization of RuvB in plants (Wang et al. 2011; Saifi et al. 2018). However, there are reports on other helicases like pea DNA helicase 45 (PDH45) which was found to be induced in pea seedlings in response to high salt (NaCl), dehydration, wounding, and low temperature. Transfer of its gene to tobacco provided a high salinity tolerance without affecting yield (Sanan-Mishra et al. 2005). Another helicase from pea (PDH47, pea DNA helicase 47) was reported to be induced in response to cold and salinity stress in shoots and roots, and heat and abscisic acid (ABA) treatment in roots (Vashisht et al. 2005). These reports suggest that helicases play an important role in stress tolerance. Though the exact mechanism of helicase-mediated tolerance of stress has not yet been understood. Saifi et al. (2018) highlights the role of rice homologue of RuvB gene (*OsRuv*BL1a) under various abiotic stresses. The *OsRuv*BL1a protein was characterized using *in silico* and biochemical approaches. The studies confirmed the presence of all the four characteristic motifs of AAA+ superfamily in this protein. It was also shown that *OsRuv*BL1a exhibits unique DNA-independent ATPase activity and unwinds the duplex DNA in the 3' to 5' direction. Moreover, the upregulation of its transcript under abiotic stress conditions suggested its involvement in multiple cellular pathways. Singh et al. (2020) developed transgenic pigeon pea lines having *Os*RuvB gene (Kharb et al. 2018; patent application number: 201811012099) and subjected six T_1 generation transgenic lines to 75mM salt stress. Observations were recorded for different physio-biochemical parameters viz. chlorophyll content, relative water content, MDA content, membrane injury index, total soluble sugar content, proline content, peroxidase activity, and catalase activity at 4 and 8 DAT with 3 replications for each treatment. The results showed that in addition to more chlorophyll and relative water content under salinity, the transgenic plants also showed higher activity of peroxidase and catalase. Level of proline and total soluble sugar was increased in T_1 transgenic plants, but the increase was lower than in wild type plants under salt stress. The transgenic lines didn't have significant increase in osmolytes proline and total soluble sugar, which indicates that the tolerance is being imparted either by some other osmolytes or some entirely different mechanism yet to be uncovered might be working in these plants.

*OsRuv*B gene was integrated in chickpea (cv. HC-1) plants using tissue culture independent patented protocol (Kharb et al. 2012) by Preeti and Kharb (2020) and obtained transformation efficiency of 17% when screening was done using gene specific primers. Transgene copy number in each event was detected by Southern hybridization which was later confirmed by real time PCR. After 20 days of germination plants were subjected to 100mM salt stress and it was observed that all the transgenic chickpea plants performed far better in comparison to wild type chickpea plants in terms of having high chlorophyll content, relative water content, proline content, total soluble sugar content, peroxidase and catalase activity but reduced MDA content and membrane injury index.

Role of p68 gene (DEAD-box family protein) in salt stress tolerance

DEAD-box helicases are required mostly in all aspects of RNA and DNA metabolism and play a significant role in various abiotic stresses, including salinity. The p68 is member of DEAD-box family and plays a very important role in cell/organ development (Stevenson et al. 1998). It also participates in various biological processes including pre-rRNA processing (Liu, 2002; Bates et al. 2005; Fuller-Pace, 2006), RNA-induced gene silencing (Ishizuka et al. 2002), transcription initiation (Fuller-Pace 2006) and alternative splicing processes (Kar et al. 2011). It was also reported that ATPase activity of recombinant p68 in yeast was stimulated by double-stranded RNA and it unwinds RNA in both 3' to 5'

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and 5' to 3' directions (Huang and Liu 2002). It has been reported that p68 RNA helicase activities are stimulated after phosphorylation with protein kinase C (Pradhan et al. 2005) which is a general cascade to cope with stresses in plants. Wang et al. (2013) reported that p68 also interacts with Ca^{2+}-CaM which regulates various signaling pathways leading to tolerance in plants under stress.

Psp68 DEAD-box protein exhibits ATPase activity in the presence of both DNA and RNA, binds to DNA as well as RNA and shows unique bipolar DNA helicase activity which suggest that it could be a multifunctional protein (Tuteja et al. 2014). *Psp68* provided salinity stress tolerance in transgenic tobacco and transgenic rice by reducing oxidative stress and improving photosynthesis machinery (Banu et al. 2015). Karthik et al. (2019) evidenced the role of the p68 gene against salinity, by enhancing the tolerance towards salinity stress in soybean plants. The transgenic soybean (T_1) plants showed a higher accumulation of chlorophyll, proline, CAT, APX, SOD, RWC, DHAR and MDHAR than the NT plants under salinity stress conditions. The transformed (T_1) soybean plants also retained a higher net photosynthetic rate, stomatal conductance and CO_2 assimilation as compared to NT plants. Further analysis revealed that (T_1) soybean plants accumulated higher K^+ and lower Na^+ than NT plants. Yield performance of transformed soybean plants was estimated in the transgenic greenhouse under salinity stress conditions. The transformed (T_1) soybean plants expressing the p68 gene were morphologically similar to non-transformed plants and produced 22–24 soybean pods/plant containing 8–9 g (dry weight) of seeds at 200 mM NaCl concentration.

Moreover, Banu et al. (2015) suggested that *Psp68* interacts with pea argonaute (AGO1), a catalytic component of the RNA-induced silencing complex (RISC) responsible for the gene silencing. The microarray analysis showed that *Psp68* regulates many transcripts involved in the abiotic and oxidative stress responses as well as gene-silencing mechanisms in rice. Thus, the *Psp68* functions as a molecular switch in different signaling path-ways leading to stress tolerance. Overall, *P*sp68 may serve as a useful biotechnological tool for the improvement of stress tolerance crop.

Neha and Kharb (2019) obtained 16% transformation efficiency when transformed pigeon pea (cv. Manak) with *Psp68* gene (Fig.1). Selected PCR positive transgenic plants were subjected to 75mM NaCl salt stress 15 days after germination and observance were recorded 4 days and 8 days after treatment. Analysis of various physio-biochemical parameters showed that transgenic plants performed well with respect to all the parameters with higher chlorophyll content, relative water content, total soluble sugar content, proline content, catalase and peroxidase activity and reduced lipid peroxidation, electrolyte leakage.

Role of *OsLecRLK* in salt stress tolerance

Lectin receptor-like kinase (LecRLK) is an important family that plays a major role in stress sensing through lectin receptor and further activates downstream signaling by kinase domain.

Plant perceives stress by various sensors (Wall-associated kinase, G-protein couple receptors-like protein(s) or receptor like kinases [RLKs]) present on the cell membrane, which leads to activation of downstream signaling (Tuteja and Sopory, 2008). Plant lectin receptor-like kinases (LecRLKs) are membrane-embedded RLK proteins. Extracellular lectin domain has a role in stress perception through recognition of different ligands (such as hormones and complex saccharides) generated in response to environmental challenges (Barre et al. 2002; Passricha et al. 2019b). RLKs participate in various processes, including regulation of development, disease resistance, and hormone perception. RLK is a vast family of proteins that have 610 genes in *Arabidopsis* and 1100 genes in rice (Morillo and Tax 2006). Members of this gene family are not well characterized but some reports provide their role in stress such as *Arabidopsis*, L-VI.2 (At5g01540) provide resistance against *Pseudomonas syringae* and *Pectobacterium carotovorum* (Singh et al. 2012). LecRLK-1 in *Nicotiana tabacum* which is responsive to herbivorous signaling mediated through elicitors released by larvae of *Medunca sexta* (Bonaventure, 2011). NbLRK1 (LecRLK in *Nicotiana benthamiana*) directly associate with elicitor protein IFN1 released *by Phytophthora infestans* through its kinase domain (Kanzaki et al. 2008). Similar studies on LecRLK in different plant systems such as *Arabidopsis* (Deng et al. 2009*), Pisum sativu*m (Vaid et al. 2012), Glycine soja (Sun et al. 2013) and rice (Saifi et al. 2017) showed the importance of LecRLKs in alleviating stress condition. Among the 610 RLKs in *Arabidopsis thaliana* and 1100 RLKs in rice (Shiu et al. 2004), some have been characterized as receptors for polypeptides, phytohormones and pathogens. Each of these RLKs can rapidly initiate signalling through the formation of oligomers and cross-phosphorylation of the intracellular serine/threonine kinase domain upon binding to ligand (Dievart and Clark 2004) and together they play diverse roles in plant development and resistance (Antolín-Llovera et al. 2012; Osakabe et al. 2013). Some RLKs are also reported to play role

in drought and salt responses (Ouyang et al. 2010; Marshall et al. 2012; Vaid et al. 2013). Rice SIK1 (Os06g03970), that is expressed most strongly in stem and panicle but which is not expressed in root, was found to be salt-inducible and a positive regulator of salt tolerance (Ouyang et al. 2010).

The *LecRLKs* acting as membrane receptors is well-known, however related evidences of downstream and upstream components and how they interact with various signalling components is still not known.

Vaid et al. (2015) reported that *PsLecRLK* transcripts are upregulated in salinity stress response and overexpression of the gene showed enhanced water uptake in plants through the activation of water channel. In 2014, *SIT1* a salt tolerance gene reported mainly expressing in root epidermal cells in rice. The gene was found rapidly activated by NaCl and phosphorylated MPK3/6 then further facilitates ethylene accumulation & ROS production and accumulation in plants ultimately leads to inhibition of plant death under stress. Zhang et al. (2019) reported *PnRLK-1* (a type of cytoplasmic RLK) in an Antarctic moss (*Pohlia nutans*) upturn ABA sensitivity and also upregulates ROS scavenger machinery that suppress ROS accumulation that ultimately results in reduction of salt stress. Table 1 depicts impact of various transgenes inserted in different plants.

Pratibha (2019) transformed pigeon pea (cv. Manak) plants with *OsLecRLK* gene and obtained 16 plants out of 86 showing amplification for the gene of interest representing a transformation efficiency of 18.6%. Transgenic copy no. and integration was confirmed through Southern hybridization and Real-time PCR analysis in T_0 generation and found that 5 Transgenic lines (L-9, L-17, L-18, L-19 and L-48) carried single copy insertion of gene whereas, one transgenic line (L-89) with two copies of the transgene. Physio-biochemical analysis was done to assess the efficacy of transgene via subjecting wild type and selected T_1 transgenic plants to 75 mM salt stress. The results showed that transgenic line performed better in terms of maintaining higher relative water content, chlorophyll content, total soluble sugar content, proline content, peroxidase and catalase activity in comparison to the wild type plants. Moreover, membrane injury index and MDA content were significantly reduced in transgenic lines then wild type plants indicating that the transgenic lines were less affected by salt stress (Figure 1)

Chickpea (cv. HC-1) plants were transformed by Singh (2018) with *OsLecRLK* gene and obtained 17.82% transformation efficiency. Transgene copy number was confirmed using Real time PCR & Southern hybridization. Transgenic chickpea plants were subjected to 100 mM salinity stress 15 days after germination. The transgenic chickpea plants showed & better growth than non-transformed chickpea plants and synthesized more compatible solute such as proline, high sugar level, increased MDA content and decreased membrane injury and significant maintenance of chlorophyll content under salt stress conditions. (Figure 1). Table 2 shows comparative performance of various physio-biochemical parameters in different transgenic lines.

Conclusions

The present review highlights the helicases (*OsRuv*B and p68) and kinases (*OsLecRLK*) mediated salt stress tolerance in two legume crops i.e. chickpea and pigeon pea. It was also interesting to observe that genes isolated from rice, a monocot, induced salt tolerance in chickpea and pigeon pea, both being dicot plants. Although more research is required to identify the exact molecular mechanism and the underlying signalling pathway of all these above mentioned genes. Till date, no information on ligands, downstream targets or factors governing activation or inactivation of *OsRuv*B and *OsLecRLK* is available. Therefore, further research is being undertaken in our laboratory to understand the role of these genes in providing salinity tolerance in plants.

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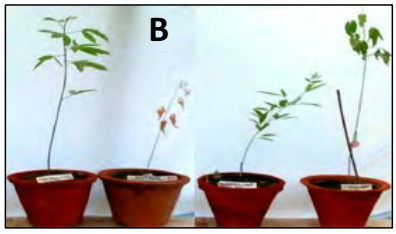
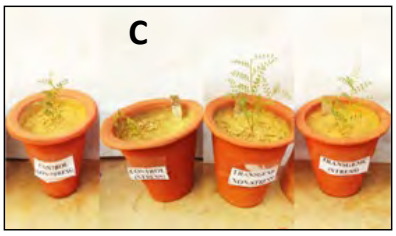
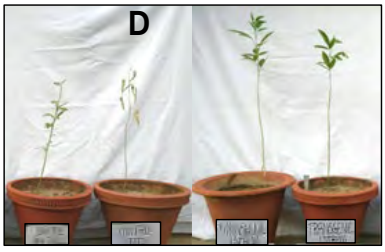
Effect of 75 mM NaCl salt stress on wild type (control) and *OsRuv*B carrying transgenic pigeon pea plants. (Original)



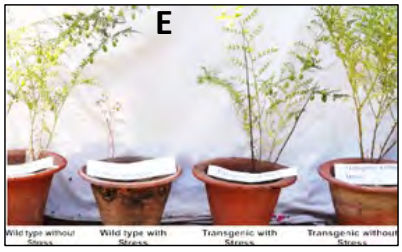
Effect of 75 mM NaCl salt stress on wild-type and *p68* gene containing transgenic pigeon pea plants. (Original)



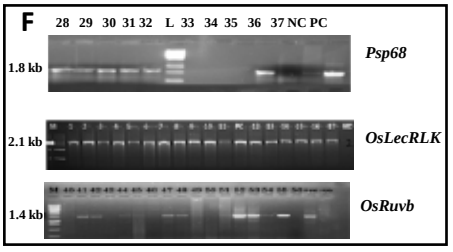
Effect of 100 mM NaCl salt stress on wild-type *OsRuv*B containing transgenic chickpea plants. (Original)



Effect of 75 mM NaCl salt stress on wild type (control) and *OsLec-RLK* carrying transgenic pigeon pea plants. (Original)



Effect of 100 mM NaCl salt stress on wild-type and transgenic carrying *OsLec-RLK* gene chickpea plants. (Original)



PCR amplifiction of *OsRuv*B, *p68* and *LecRLK* gene using gene specific primers.

Figure 1. Effect of salt stress on transgenic chickpea and pigeon pea carrying *Os*RuvB, *Psp68* and *Os*LecRLK gene (A-E) and PCR amplification of *Os*RuvB, *Psp68* and *Os*LecRLK genes in transgenic pigeon pea and chickpea plants.

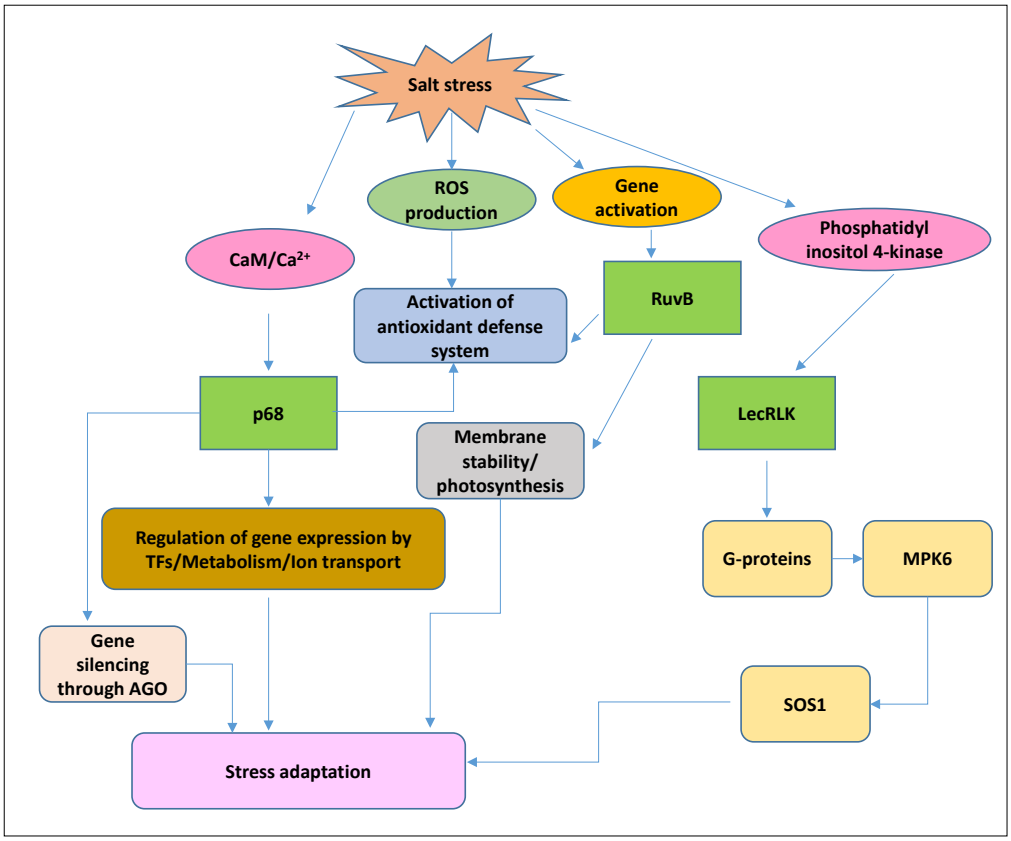


Figure 2. Proposed action of helicases (*RuvB* and *p68*) and lectin receptor kinases (*Lec-RLK*) in legume for providing salinity tolerance.

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Evaluation of Morphological, Quality and Yield Characteristics of Some Registered Chickpea (*Cicer arietinum* L.) Varieties in The Eastern-Mediterranean Region

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ABSTRACT

This research was conducted to evaluate regional adaptation of registered chickpea varieties, their yield and some yield related characteristics observed at trial fields under winter growth conditions in Eastern Mediterranean region of Turkey in Adana location during 2014 and 2015. Trials were conducted in fields of Eastern Mediterranean Agricultural Research Institute. In this study, 17 registered varieties and 3 control varieties in total 20 varieties were tested in trials. During this study, the varieties were evaluated in Adana location for their fitness to winter growth conditions.
The highest and the lowest yield resulted in 2014 for Adana location were 3.94 t/ha and 1.76 t/ha for Trial, and respectively. In 2015, the highest and the lowest yield resulted for Adana location were 5.08 t/ha and 0.17 t/ha for Trial, respectively. In terms of quality values for both growing seasons of 2014 and 2015, the average protein analysis values of the Trial were 21.90% for the Hasanbey variety as the highest and 10.26% for the Hisar variety as the lowest values.

Keywords: Chickpea, registered varieties, adaptation, sowing date

Introduction

The edible grain legumes are an important source of plant-derived protein which is widely consumed in Turkey. It is an important basic nutrient in human and animal nutrition in terms of its average protein richness of 22-26%. Chickpeas are rich in nutritional value and have positive contributions to the soil due to their symbiotic lifestyle with rhizobia. In Turkey, the chickpea production was 630.000 tonnes with a sowing area of 517.785 ha while the grain yield was 122.00 kg/da (FAO, 2021). The legume industry in Turkey gains importance every day. Legume processing, packaging industry, and the production of various chickpea-based nuts (roasted chickpea) are also developing industries that increase the importance of chickpeas.

Although the most important problem in chickpea cultivation is Ascochyta blight, it is aimed to breed for varieties that are tolerant against Ascochyta blight, suitable for mechanized cultivation and harvest, and also offer them to the farmers as promising varieties. Since the purpose of chickpea production is to obtain

grain products of high yield and quality, developing suitable varieties for target regions where they will be grown is an important factor that needs to be considered. This study aimed to develop a list of recommended chickpea varieties for different regions and will stimulate an increase in cultivation area. Studies were performed during 2013-2014 and 2014-2015 growing seasons under winter growing conditions. Yield, quality, disease, and pest tolerance parameters were examined.

Materials and Methods

Adaptation studies were carried out using 17 registered varieties in the location of Adana during the 2014 and 2015 winter growing season. In the 2014 and the 2015 growing seasons, in the field with 17 varieties and 3 control varieties registered varieties were conducted in Adana location. In. this study, plantings were made in 4 rows (9 m^2 parcels) of 5 m length with 45 cm between rows and 8 cm above rows. Before planting, fertilization was applied at a rate of 2-3 kg N, 5-6 kg P_2O_5 per da, and disease scorings (1-9) were made to determine tolerance to Ascochyta blight disease (Şehirali, 1988). Samples for quality analysis in chickpea genotypes in both growing seasons of 2014 and 2015, were taken from the combined and thoroughly blended repetitions in the post-harvest trials.

Precipitation level in Adana location during December and January 2014 was below the average of previous years for the same period and germinated plants became susceptible to abiotic stress factors. Despite the uneven distribution of precipitation in the November-July period and the drought stress after planting, the incidence of Ascochyta blight disease was low due to rainfall and the appropriate temperature and humidity rates in March and April, which are the flowering and pod tying period. After planting in 2015, although the amount of rainfall was low compared to last years in November, December and January, there was sufficient rainfall and a decrease in germination was not observed. In this growing season, the intensity of Ascochyta blight disease has increased due to the intensity of rainfall in March (115.81 mm; flowering period). Due to the heavy rains in May (81.02 mm; the beginning of the pod tying period), disease incidence in parcels of varieties susceptible to Ascochyta blight disease increased and ended with a high plant death rate.

The uneven distribution of rainfall across the months were challenged the plants, though the temperature and the humidity values showed coherence to the previous year's average (Figure 1).

The study was designed according to randomized block trials and One Way ANOVA together with Tukey's B analyses was applied on all data at the significance level of 0.05.

Results and Discussion

The average values and groups formed from the registered varieties trial conducted in the Adana location in 2014 are given in Table 1. Although there was no statistical difference between the varieties in terms of flowering days, first pod height, plant height, and grain yield, it varied between 57-67 days, 23.3-32.7 cm, 66.6-95.5 cm, and 176-394 kg/da, respectively. Statistically significant differences between the varieties in terms of the number of days until pod tying were observed, and it varied between 72.0-76.6 days, and the highest value in terms of the mentioned feature was observed for Seçkin variety and the lowest for İzmir-92 variety. Statistically significant difference between all varieties in terms of 100 grain weight was observed, with values varying between 28.5-51.9 g, with the highest mean for Çağatay, Sezenbey, Sarı 98 and Cevdetbey 98 varieties. Yield parameters of 2014 growing season were not affected by Ascochyta blight disease. Erdemci et al. (2016), have determined negative and significant ($p<0.05$) relationship between grain yield and 100-seed weight in different chickpea genotypes grown for winter in Diyarbakır ecological conditions in 2011 and 2012; positive and significant ($p<0.01$) relationships between plant height, number of main branches in the plant, number of full pods per plant and the number of seeds per plant (Slim et al. 1993), (Şehirali, 1988). The average values obtained from the yield experiment registered varieties in Adana location in 2015 and the groups formed are given in Table 1. There is a significant difference between the cultivars in terms of the number of days until the flowering and the number of days for the pods tying, and the lowest and the highest values varied between 108.7-113.3 days and 112.9- 133.9 days for 2014 and 2015 respectively. The highest and the lowest number of days until flowering was observed for TAEK-Sağel and Eser varieties, respectively, and days until pod tying was the highest for Inci and Cevdetbey 98 varieties and the lowest for TAEK-Sağel variety. First pod height values varied between 24.01-64.4 cm and plant height values varied between 47.47-93.3 cm, however, there was no statistically significant difference between the cultivars in terms of first pod height and plant height. Statistically significant differences were observed for the 100/grain weight and the yield values. The lowest and the highest values of the examined properties were obtained from Menemen-92 and Aksu varieties with 28.0 g and 42.3

g respectively, and Seçkin and Cevdetbey 98 varieties with 17.1 kg/da and 508.5 kg/da respectively. Gül et al. (2006) conducted a study to investigate the possibilities of growing chickpea plants under winter conditions, and reported that the resistance/tolerance to them rated as 55.42% in standard varieties and varied between 70.91 and 78.75% in other lines. In addition, they stated that many features related to the winter - grown chickpea, especially grain yield, are more advantageous than summer plantings and that winter sowing may be more advantageous in terms of its characteristics and suitability for machine harvesting.

The two-year average values were obtained from the registered varieties yield trial and the groups formed are given in Table 1. Although there is no statistically significant difference between the varieties in terms of the two-year average for flowering days, first pod height, and plant height values, they vary between 84.33-88.67 days, 26.17-48.03 cm, 63.12-93.32 cm, respectively. While Aksu, İnci-K are the varieties with the longest time until flowering, Damla and İzmir-92 varieties reached the flowering period faster than other cultivars. In terms of days until the pod tying phase, statistical differences between the varieties were found to be significant and the values according to the varieties varied between 93.42-103.67 days. While it took longer to tie pods for İnci and Cevdetbey 98 varieties, TAEK-Sağel variety tied the pods for the shortest duration. The statistically significant differences were observed in terms of 100/grain weight and the yield values. It was reported that as the number of pods increases, the pod weight decreases and both the hundred-seed weight and the yield per plant decrease (Amini et al. 2002).

The lowest and highest values of the investigated traits were observed for Eser and Aksu varieties with 28.28 g and 42.74 g, respectively, and TAEK-Sağel and İnci varieties with 118.48 and 426.96 kg/da, respectively. According to two-year average data of registered varieties yield test, varieties İnci, Seçkin, Hasanbey, Damla, Güler, Menemen-92, Aydın-92 and Aksu showed better performance in terms of grain yield, disease tolerance and other parameters. Regional varieties (İnci, Seçkin, Hasanbey) had higher grain yield values in both years compared to other varieties. Mart et al. (2015) performed a study in order to evaluate the national and ICARDA originating chickpea lines under Çukurova region climatic conditions in terms of yield and 100/grain weight parameters. Their study was performed during 2012-2014 years and yield parameters for 2012-2013 season were 353.93 kg/da for İnci variety, 278.07 kg/da for Seçkin variety and 275.41 kg/da for FLIP 06-59C line. One hundred grain weight varied between 42.87-31.77 gr. In 2013-2014 growing season yield parameters were 362.6 kg/da for Hasanbey variety, 360.8 kg/da for İnci variety, 347.8 kg/da for EN 1820 line and 197 kg/da for EN 1685 line (Babagil, 2011; Bakoğlu, 2009; Sozen et al. 2018).

In Adana Location, no negative effect was observed since Ascocyhta blight disease incidence was low in the first year. However, in the second year, negative effects were observed on 100 grains and yields. Anlarsal et al. (1999) studied the agricultural parameters of the chickpea population consisting of 23 lines that they cultivated for two years for winter under Çukurova (Eastern Mediterranean) regions' climatic conditions. Plant height (67.9-84.2 cm), number of pods per plant (15.8-27.3), number of seeds per plant (17.0-28.8), 100-grain weight (26.7-37.5 g), the harvest index (28.37-34.93%), the plant grain yield (5.3-8.6 g) and yield (178.6-271.9 kg/da) exhibited variation between varieties. In chickpea Ascochyta blight appears due to a combination of three factors i.e. susceptible host, virulence of pathogen and favourable environmental factors such as temperature and humidity. In the disease triangle, host tolerance is the most important element in the struggle against pathogens. Moderate resistance chickpea varieties under disease friendly environments produced potential yield to a certain extent. But sensitive cultivars in disease friendly environment were affected largely (Kaiser et al. 1997; Mart, 2006; Bayraktar et al. 2007; Kahraman et al. 2015).

Quality studies on registered varieties

The quality values of the seeds obtained from the registered varieties yield trial performed in Adana Location during the 2014 period were analyzed. The highest and the lowest values for all parameters analyzed were 54,51-34,21 g for dry weight, 108,8-68,57 g for wet weight, 0,54-0,34 g/grain for water intake capacity, 1.11-0,92% for water intake index, 91-76 ml for dry volume, 196-158 ml for wet volume, 0.55-0,25 ml/grain for swelling capacity and 2,44-1,76% for swelling index. Amir et al. (2006), In the years with a high amount of rainfall chickpea, lentil, and bean products grown under agro-climatic conditions of Algeria, the protein ratio and total sugar amount were higher and other parameters were higher in years when rainfall was less.

The quality values of the seeds obtained from the registered varieties yield trial performed in the Adana location during the 2015 period were analyzed. The highest and the lowest values for all parameters analyzed were 48.9-33.20 g for dry weight, 99.65-66.35 g for wet weight, 0.51-0.32 g/grain for water intake capacity, 1,11-0,94% for water intake index, 87-75 ml for dry volume, 190-160 ml for wet volume, 0.53-0.35 ml/grain for swelling capacity and 2.56-2.00% for

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swelling index. Among the varieties included in the registered varieties yield trial in the Adana location, the Sezenbey variety came to the fore with the highest values in terms of dry weight, wet weight, water intake capacity, dry volume, wet volume, swelling capacity. Toğay et al. (2001), They determined that the water intake capacity of chickpea varieties registered in Turkey varied between 0.979-1.223 g/grain and the difference between varieties was significant (Table 2).

Two-years Average for quality properties from the registered varieties trial was calculated. The highest and lowest values for all parameters analyzed were 49.84-33.71 g for dry weight, 101.23-67.95 g for wet weight, 0.52-0.34 g/grain for water intake capacity, 1.08-0.94% for water intake index, 87.5-75.5 ml for dry volume, 191-160 ml for wet volume, 0.54-0.03 ml/grain for swelling capacity and2.48-2.06% for swelling index. The highest and lowest average protein values were obtained for the Aksu variety (22.88%) and Cevdet Bey 98 variety (11.24%), respectively (Table 2). Atmaca (2008), In the doctoral study, determined that as the planting date is delayed, the average volume decreases. In addition, the dry volume values of other varieties with coarse grains are high in other varieties, and the dry volume values of small-grained species are low and which causes a decrease in wet volume values. It was observed that as the spacing between rows narrowed, the grain size increased and the grains removed more water in the future, which increased in wet volume (Mart, 2010; Özer et al. 2010; Srivastava et al. 2020; Sinem et al.2021).

Conclusions

In this study, the regional adaptations of registered chickpea (*Cicer arietinum* L.) varieties under different climatic conditions and their tolerance/resistance to Ascochyta blight were investigated. In the Adana location, negative effects of Ascochyta blight disease on the 100/grains and the yields were observed. Among the registered varieties, regional varieties İnci, Hasanbey and Seçkin exhibited the highest performance.

In terms of grain yield, disease tolerance, and other traits according to two-year averages, yield values were found to vary between 426.96-118.48 kg/da; İnci, Seçkin, Hasanbey, Damla, Gülümser, Menemen-92, Aydın-92, and Aksu varieties come to the fore in the registered varieties yield test. Regional varieties had higher grain yield values in both years compared to other varieties.

In both growing seasons, the average protein values were the highest for the Aksu variety (22.88%) and the lowest for the Cevdetbey 98 cultivar (11.24%). İnci variety had higher grain yield values in both years compared to other varieties. In this trial, in terms of quality values, the Sezenbey variety came to the fore with higher values compared to other varieties in terms of dry weight, wet weight, water intake capacity, wet volume, and swelling capacity.

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Table 1. Results of registered varieties trial performed during 2014-2015 period performed in Adana location.

No	Varieties	Days Until Flowering (day)			Ascochyta Blight (1-9)		Days Until Pod Tying (day)			Height of First Pod (cm)			Plant Height (cm)			100 Grain Weight (gr)			Yield (kg/da)		
		2014	2015	Ave.	2014	2015	2014	2015	Ave.	2014	2015	Ave.	2014	2015	Ave.	2014	2015	Ave.	2014	2015	Ave.
1	İnci	60,67	113,0A	86,83	1-1	3	75,3 AB	132,0A	103,6A	27,77	45,53	36,65	67,22	81,63	74,43	32,6 F-H	31,9AB	32,29E-H	394	459,8A	426,96A
2	Seçkin	61,33	110,7A-C	86,00	1-2	3	76,0 AB	130,0A-C	103,0A	26,11	41,13	33,62	66,66	71,10	68,88	37,4 D-G	40,1A	38,76A-E	285	508,5A	396,59AB
3	Hasanbey	57,33	112,0A-C	84,67	1-2	3	74,0 AB	131,0AB	102,5A	31,11	61,07	43,86	76,11	74,4	75,27	41,5 B-E	40,5A	41,01AB	344	289,7A-F	317,04A-F
4	Damla	57,67	111,0A-C	84,33	1-3	4	75,6 AB	130,0A-C	102,8A	26,66	37,77	30,55	75,55	77,1	76,36	32,5 F-H	28,2B	30,36G-H	354	313,4A-E	333,52A-E
5	Gülümser	58,67	111,7A-C	85,17	1-3	6	73,3 AB	130,7A-C	102,0A	23,33	36,67	31,67	74,44	83,3	78,87	35,9 D-H	36,9AB	36,47A-G	369	208,3B-G	288,67A-H
6	Çağatay	60,33	111,7A-C	86,00	1-3	7	74,6 AB	131,3A	103,0A	26,66	54,97	40,54	72,22	80,5	76,38	45,5 A-C	35,9AB	40,73AB	211	89,6F-G	150,22E-H
7	Sezenbey	58,67	111,3A-C	85,00	1-3	7	73,3 AB	130,7A	102,00A	26,11	36,10	33,33	82,22	72,7	77,48	46,2 AB	38,0AB	42,13A	272	156,3D-G	213,93B-H
8	Zuhal	59,0	112,3AB	85,67	1-2	6	74,0 AB	131,3A	102,67A	30,55	48,87	38,60	73,33	78,8	76,10	42,6 B-E	37,7A	40,17A-C	273	126,2E-G	199,70C-H
9	İzmir-92	58,0	111,0A	84,50	2-3	6	72,0 B	131,0A	101,50	28,33	34,97	32,48	73,33	74,9	74,15	40,2 B-F	38,5A	39,34A-D	297	166,1C-G	231,74B-H
10	Menemen-92	59,67	112,0A-C	85,83	1-2	6	74,0 AB	131,0AB	102,50A	30,00	40,77	36,77	85,00	78,7	81,87	38,7 B-G	28,0B	33,39D-H	369	161,2C-G	265,22A-H
11	Aydın-92	59,33	112,3AB	85,83	1-2	4	75,3 AB	131,3AB	103,33A	32,77	47,20	39,16	92,78	71,07	81,92	34,7 E-H	32,6AB	33,69C-H	377	362,4A-D	369,85A-D
12	Sarı 98	59,0	112,7AB	85,88	1-2	8	72,6 AB	130,0A-C	101,3A	31,11	24,01	26,17	78,78	47,47	63,12	51,9 A	---	---	176	17,8G	---
13	Cevdetbey 98	60,0	112,7AB	86,33	1-2	8	73,3 AB	133,9A	103,6A	28,33	25,83	27,36	86,11	63,03	74,57	44,8 A-C	30,6AB	37,7A-E	260	17,1G	138,63F-H
14	Aziziye	58,33	111,7A-C	85,00	1-2	7	73,3 AB	131,3AB	102,36A	28,89	27,47	26,23	81,11	69,60	75,36	38,9 B-G	34,8AB	38,07A-F	213	116,5E-G	164,67E-H
15	TAEK-Sağel	59,0	113,3A	86,17	1-3	9	74,0 AB	112,9D	93,42 B	25,00	48,60	38,47	88,77	86,93	87,85	38,3 B-G	28,8AB	33,91B-H	198	38,6G	118,48GH
16	Aksu	66,67	110,7A-C	88,67	1-2	5	72,6 AB	130,0A-C	101,33A	28,33	64,40	48,03	91,66	83,20	87,43	43,2 B-D	42,3A	42,74A	328	311,1A-E	319,41A-F
17	Eser	61,33	108,7C	85,00	1-2	6	75,3 AB	127,3C	101,33A	31,66	32,20	28,32	83,88	70,5	77,21	28,5 H	28,0B	28,28H	179	198,7B-G	188,67D-H
18	HasanBey-K	61,33	110,3A-C	85,83	1-2	4	73,3 AB	130,0A-C	101,67A	24,44	38,83	34,97	95,55	84,73	90,14	36,3 D-H	40,5A	38,4A-E	239	378,4A-C	308,63A-G
19	Seçkin-K	62,33	109,7B-C	86,00	1-2	4	76,6 A	128,3BC	102,50A	31,66	48,30	39,98	93,33	93,30	93,32	38,0 C-G	40,6A	39,3A-D	212	398,1AB	305,07A-H
20	İnci-K	61,33	112,7AB	87,00	1-2	4	76,0 AB	131,3AB	103,67A	24,44	45,00	34,72	83,33	81,07	82,20	31,4 GH	31,4AB	31,41F-H	324	440,2A	382,26A-C
F		---	**	---			**	**	**	---	---	---	---	---	---	**	**	**	---	**	**
CV (%)		5,82	0,9	2,21			1,96	0,8	1,30	16,89	43,9	4,79	17,14	18,8	11,08	6,93	10,3	1,18	35,54	29,6	1,30

Ave=Average, The F values were obtained based on the Tukey test, CV=Variation of coefficient, **=Significant level

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Table 2. Results of quality traits analysis from registered variety trial performed during 2014-2015 period

No	Varieties	Dry Weight (100 grain) (g)			Wet Weight (g)			Water Intake Capacity (g/grain)			Water Intake Index (%)		
		2014	2015	Ave.	2014	2015	Ave.	2014	2015	Ave.	2014	215	Ave.
1	İnci	39,13	38,14	38,64	75,99	74,05	75,02	0,37	0,36	0,37	0,94	0,94	0,94
2	Seçkin	42,10	40	41,05	87,33	81,69	84,51	0,45	0,42	0,44	1,07	1,04	1,06
3	Hasanbey	44,48	42,77	43,63	90,49	84,53	87,51	0,46	0,42	0,44	1,03	0,98	1,01
4	Damla	35,52	35,11	35,32	70,03	70,22	70,13	0,35	0,35	0,35	0,97	1,00	0,99
5	Gülümser	39,67	39,86	39,77	76,72	80,65	78,69	0,37	0,41	0,39	0,93	1,02	0,98
6	Çağatay	50,68	42,84	46,76	102,3	90,38	96,34	0,52	0,48	0,50	1,02	1,11	1,07
7	Sezenbey	50,69	48,99	49,84	102,8	99,65	101,23	0,52	0,51	0,52	1,03	1,03	1,03
8	Zuhal	48,24	43,25	45,75	96,93	91,35	94,14	0,49	0,48	0,49	1,01	1,11	1,06
9	İzmir-92	45,37	40,18	42,78	87,07	79,19	83,13	0,42	0,39	0,41	0,92	0,97	0,95
10	Menemen-92	43,84	38,32	41,08	86,32	80,04	83,18	0,42	0,42	0,42	0,97	1,09	1,03
11	Aydın-92	39,64	37,32	38,48	77,10	73,53	75,32	0,37	0,36	0,37	0,95	0,97	0,96
12	Sarı 98	54,51	---	---	108,8	---	----	0,54	---	----	1,00	----	---
13	Cevdetbey 98	48,43	---	---	96,16	---	---	0,48	----	---	0,99	---	----
14	Aziziye	49,4	46,79	48,10	96,62	95,06	95,84	0,47	0,48	0,48	0,96	1,03	1,00
15	TAEK-Sağel	41,16	---	41,16	82,77	---	82,77	0,42	---	0,42	1,01	---	1,01
16	Aksu	47,35	44	45,68	95,74	89,96	92,85	0,48	0,46	0,47	1,02	1,04	1,03
17	Eser	34,21	33,21	33,71	68,57	67,33	67,95	0,34	0,34	0,34	1,00	1,03	1,02
18	Hasan Bey-K	43,44	40,42	41,93	88,99	81,85	85,42	0,46	0,41	0,44	1,05	1,02	1,04
19	Seçkin-K	41,91	39,79	40,85	88,23	81,21	84,72	0,46	0,41	0,44	1,11	1,04	1,08
20	İnci-K	38,17	33,97	36,07	74,84	66,35	70,60	0,37	0,32	0,35	0,96	0,95	0,96

performed in Adana location.

Continuing Table 2

Dry Volume (ml)			Wet Volume (ml)			Swelling Capacity (ml/tane)			Swelling Index (%)			Protein (%)		
2014	**2015**	**Ave.**	**2014**	**2015**	**Ave.**	**2014**	**2015**	**Ave.**	**2014**	**2015**	**Ave.**	**2014**	**2015**	**Ave.**
79	79	79,0	166	166	166	0,37	0,37	0,37	2,28	2,28	2,28	22,40	19,33	20,87
82	80	81,0	178	172	175	0,46	0,42	0,44	2,44	2,40	2,42	25,19	18,55	21,87
84	83	83,5	180	176	178	0,46	0,43	0,45	2,35	2,30	2,33	23,79	19,06	21,43
76	77	76,5	162	164	163	0,36	0,37	0,37	2,38	2,37	2,38	23,70	19,70	21,70
79	81	80,0	168	174	171	0,39	0,43	0,41	2,34	2,39	2,37	22,62	18,54	20,58
89	83	86,0	192	182	187	0,53	0,49	0,51	2,36	2,48	2,42	22,74	19,73	21,24
88	87	87,5	192	190	191	0,54	0,53	0,54	2,42	2,43	2,43	21,98	20,22	21,10
86	82	84,0	186	182	184	0,5	0,50	0,50	2,39	2,56	2,48	22,80	18,10	20,45
84	81	82,5	176	170	173	0,42	0,39	0,41	2,24	2,26	2,25	22,13	18,95	20,54
83	80	81,5	176	170	173	0,43	0,40	0,42	2,30	2,33	2,32	22,91	19,24	21,08
80	79	79,5	168	166	167	0,38	0,37	0,38	2,27	2,28	2,28	21,63	19,58	20,61
91	---	---	196	---	---	0,55	-0,50	0,03	2,34	2,00	2,17	24,13	0,00	12,07
86	---	---	186	---	---	0,5	-0,50	0,00	2,39	2,00	2,20	22,47	0,00	11,24
88	85	86,5	186	184	185	0,48	0,49	0,49	2,26	2,40	2,33	21,60	17,68	19,64
82	---	82,0	172	---	172	0,4	-0,50	-0,05	2,25	2,00	2,13	24,62	0,00	12,31
86	83	84,5	184	180	182	0,48	0,47	0,48	2,33	2,42	2,38	26,67	19,09	22,88
76	75	75,5	160	160	160	0,34	0,35	0,35	2,31	2,40	2,36	22,34	18,49	20,42
83	81	82,0	158	173	165	0,25	0,42	0,34	1,76	2,35	2,06	24,73	18,93	21,83
82	80	81,0	178	172	175	0,46	0,42	0,44	2,44	2,40	2,42	23,14	18,68	20,91
79	75	77,0	166	160	163	0,37	0,35	0,36	2,28	2,40	2,34	25,74	17,85	21,80

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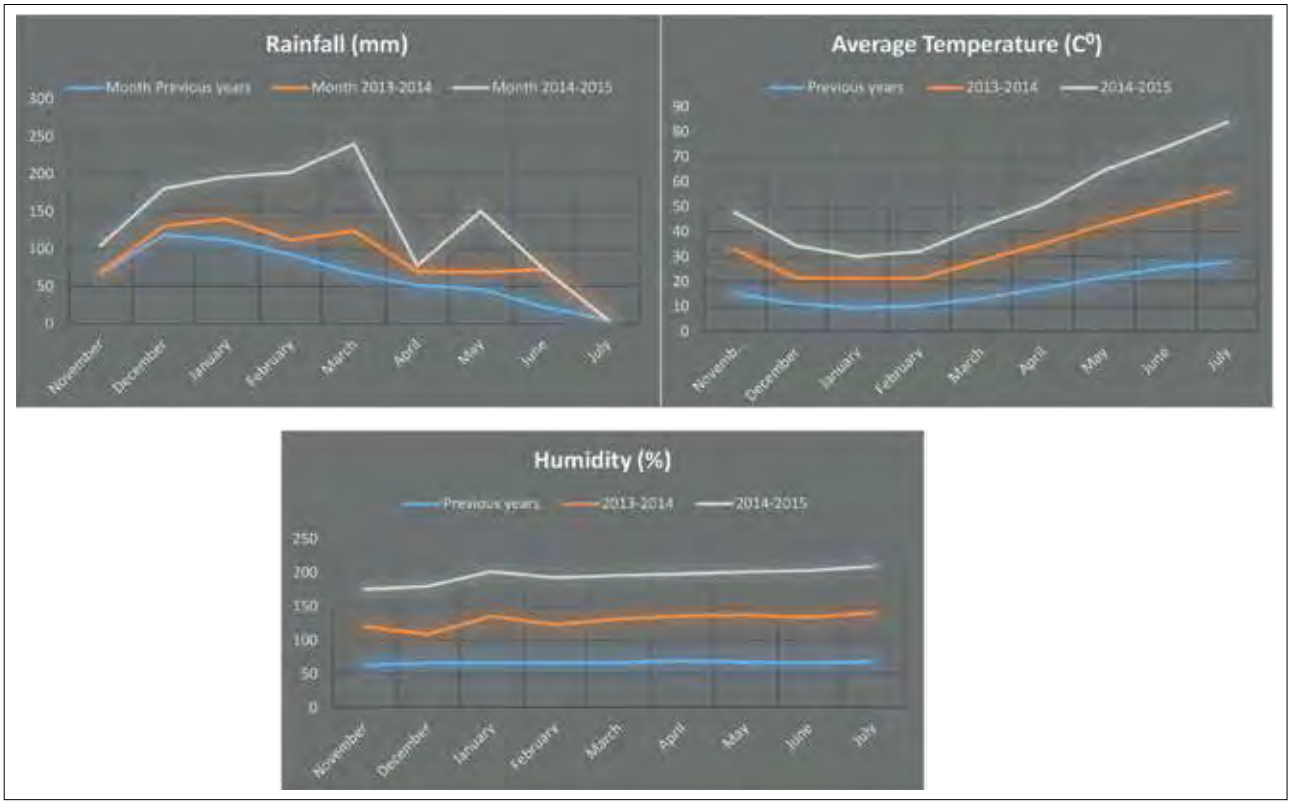

Figure 1. Environmental conditions of Adana location during 2013-2014 and 2014-2015 periods together with previous years average.

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Research Article

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Studies on Variability and Character Association for Yield and Yield Related Traits in Faba Bean (*Vicia faba*)

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ABSTRACT

One hundred and forty-five faba bean genotypes were assessed for two years for 13 agronomic traits against three elite varieties PRT-7, PRT-12 and Vikrant in Augmented Design. There was significant difference among the blocks for leaf length, leaf width and 100 seed weight but no difference was observed for days to flowering, days to maturity, plant height, number of branches, number of pods per plant, number of grains per pod, number of pods per cluster, pod length, yield per plant and seed yield. Among the checks, PRT-12 registered highest seed yield (kg/ha). Three germplasm lines viz. EC243770, EC117792, EC329725 showed higher seed yield (kg/ha) than the best check variety PRT-12 (1565 kg/ha).

Keywords: Genetic resources, germplasm, variability, faba bean

Introduction

Today, entire world is concerned about the impact of climate alteration on crop plants. In the last two centuries, climate change was so fast that certain plant species have found it hard to adapt. The climate change will have dramatic consequences for crops (Arya et al. 2020). The earth's average surface temperature has increased by 1 degree F in just over the last century. Consequently, agriculture researchers consider any assessment has to be individually considering each location. But in order to meet the challenges of temperature ahead of global warming, concerted efforts are need to evaluate, identify and develop genotypes suitable for terminal heat stressed environment (Arya et al. 2016).

Faba bean (*Vicia faba* L.) also known as broad bean, is an annual crop. It is a partially allogamous crop. The per cent mean cross pollination in this crop has been reported to range from 32 and 40 per cent, however, it belongs to family Fabaceae. The rate of outcrossing depends on the genotype, environmental factors, row space and the number of pollinating insects (Bishnoi et al. 2015). It is mainly grown in hills and northern plains for its protein rich pulse and green pods which are used as vegetable. Faba bean is grown in over 3 million hectares in the world with a total production is over 4.5 million tons. Average productivity of faba bean is 2800 to 4800 kg/ha. It is mainly used as animal feed in advanced countries and food for human consumption in developing countries. Its value as a feed and food specially is due to availability its high lysine-rich protein, vitamins, minerals, and carbohydrates (Kumar et al. 2019), which make it one of the best solutions to the malnutrition, mainly in developing countries.

It fixes atmospheric nitrogen and used as an important component in crop rotation, which is almost neglected in modern cropping system. Today, there is an urgent need to minimize the impact of chemical fertilizers on the environment, reduce emissions of undesirable grasses and to economize of the following crops (Arya, 2018). It is good for sustainable agriculture in marginal areas (Arya et al. 2019). Efforts have been made to evaluate, characterize, conserve and catalogue

the genetic resources of faba bean. Improvement for the seed and protein yields are receiving foremost attention in this crop. Hence there is a need to intensify efforts to search for appropriate donors for utilization in the locations specific breeding programmes. In the present paper an attempt has been made to evaluate the genetic resources of a faba bean augmented recently to assess their potential use in varietal development programme for faba bean.

Materials and Methods

One hundred and forty-five accessions faba bean along with three standard checks were evaluated in Augmented Block Design (Federer, 1956 and 1961) during the *rabi* 2015-16 and 2016-17 at New Area IARI, New Delhi. The accessions were grown in two rows of 3 m length with 30x15 cm spacing. Standard agronomic practices were followed and plant protection measures were adopted as and when required. Observations were recorded on five competitive randomly selected plants for 13 yield attributes. The data was analysed according to MS-Office Excel program. The one hundred and forty-five test entries were equally distributed in ten block containing 15 entries per block for first nine block and ten entries for last 10th block. The three different checks, namely, PRT-7, PRT-12 and Vikrant were randomly distributed in each block. The total plots per block were 18 and in 10th block was 13. The total number of plots in ten blocks were 175. Correlation and direct and indirect effects were computed by using standard statistical methods (Dewey and Lu, 1959).

Results and Discussion

Genotypes performance

Results have been calculated on the basis of 13 attributes because significant difference among the test entries was observed for all the characters. Therefore, 13 characters were studied for selecting the promising lines. No significant difference was observed among the blocks for days to flowering, days to maturity, plant height, number of branches, number of pods per plant, number of grains per pod, number of pods per cluster, pod length, yield per plant and seed yield. Since there is no block effect on the test entries, the observed value of test entries will be the actual performance of particular genotypes while the significant difference was observed among the blocks for leaf length, leaf width and 100 seed weight. The adjusted values of these characters were calculated. The observed value of 145 test entries for different 10 agronomic traits and adjusted value for three characters were consider for identify the promising line and mean, range and phenotypic coefficient of variation (PCV) for different characters were given in Table 1. The highest check mean value along with the standard error for different characters have been obtained here as a criteria for selecting the better performing genotypes on the basis of observed values for ten characters and adjusted values for three characters. The list of promising genotypes for different yield attributes (better than check values) is given in Table 2. Three germplasm lines viz. EC243770, EC117792, EC329725 showed higher seed yield (kg/ha) than the best check variety PRT-12 (1565 kg/ha). Similar results for one or more characters were reported by Bakhiet et al. 2015; Arya 2018 and Arya et al. 2020.

Characters inter-relationship

Correlation coefficients for thirteen matrix traits in faba bean are presented in Table 3. Seed yield (kg/ha) was positively correlated with all the characters except days to maturity. However the highly positive significant correlation of seed yield were observed with plant height (0.4229), number of pods per plant (0.5239), No. of pods per cluster (0.1715), pod length (0.2769), leaf width (0.2158), 100 seed weight (0.5058) and seed yield/plant (0.6586). Therefore, selection of high value for these characters will ultimately increase the seed yield. The days to flowering, days to maturity, No. of branches, No. of grains per pod and leaf length have the nonsignificant association with seed yield.

The contribution of these characters was further analyzed by computing their direct and indirect effects on seed yield (kg/ha) and is presented in Table 4. The days to flowering, plant height, pods per plant, no. of seed per pod, no. of pods per cluster, leaf width, 100 seed weight and seed yield per plant had direct positive effect. The direct effect of remaining characters was negative and small in magnitude. The characters showing high positive direct effect and indirect effect via each other. The seed yield per plant showed the highest indirect effect on seed yield (kg/ha) through pods per plant, pod length, leaf width and 100 seed weight. 100 seed weight also showed the indirect effects on the seed yield through the days to maturity, plant height, leaf width and pod length. On the other hand, days to maturity showed negative indirect effect of seed yield through all the characters except no. of branches, pod per plant, no. of seeds per pod and no. of pods per cluster. Plant height had the positive indirect effect on seed yield except no. of pods and no. of grains per cluster. Similar results for one or more characters were reported by Bakhiet et al. 2015; Tofiq et al. 2016; Arya et al. 2019 and Dewangan et al. 2019.

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Table 1. Mean, range and coefficient of variation (CV) for different characters in faba bean germplasm based on 2 years data.

No.	Characters	Mean	Range	SD	CV (%)
1.	Days to 50% flowering	92.26	67.0-120.0	6.12	6.63
2.	Days to maturity	159.78	150-172	4.89	3.06
3.	Plant height (cm)	72.46	49.0-95.0	9.58	13.23
4.	No. of branches	6.11	2.0-17.0	1.84	30.04
5.	Pods per plant	30.09	2.38-81.40	12.06	40.09
6.	No. of grains per pod	2.88	1.40-4.00	0.37	12.71
7.	No. of pods per cluster	1.27	1.00-2.80	0.31	24.61
8.	Pod length (cm)	4.11	2.50-7.20	0.63	15.33
9.	Leaf length (cm)	6.32	4.62-7.70	0.52	8.27
10.	Leaf width (cm)	2.86	2.24-3.60	0.29	10.26
11.	100 seed weight (g)	24.00	2.00-36.50	6.24	26.00
12.	Yield per plant (g)	17.53	1.00-100.0	10.52	60.04
13.	Yield (kg/ha)	1141	37-3389	6.64	58.26

Table 2. Performance of Promising genotypes of faba bean based on 2 years data.

No.	Characters	Genotypes	Best Check Value
1.	Days to 50% flowering	IC361496, EC329691, EC550179, EC117724 (< 75.0 days)	PRT-12 (89.10 days)
2.	Days to maturity	VKG29/64, IC361499 (< 152.0 days)	PRT-12 (158.10 days)
3.	Branches per plant (No.)	JBT30/78, JBT42/RP-3/31, VKS18/46, BGR-82, VKG29/91 (> 10.0)	PRT-12 (5.72)
4.	Pods per plant (No.)	JBT42/RP-3/31, EC329725, VKG29/53 (> 58.0)	Vikrant (37.05)
5.	Grains per pod (No.)	JBT30/78 (> 3.85)	Vikrant (2.99)
6.	Pods per cluster (No.)	EC267641, IC346272, JBT42/RP-3/28, EC267648, JBT41/80, JBT42/RP-3/31, IC332102, VKG29/53 (> 1.50)	Vikrant (1.37)
7.	Pod length (cm)	VKS18/46, JBT30/78 (> 6.0 cm)	PRT-12 (4.12 cm)
8.	Leaf width (cm)	EC25192 (>3.50 cm)	PRT-7 (2.93 cm)
9.	100 seed weight (g)	EC343808, EC329679 (> 34.50 g)	PRT-12 (25.15 g)
10.	Yield per plant (g)	EC243756 (> 40.0 g)	PRT-12 (22.80 g)
11.	Yield (kg/ha)	EC243770, EC117792, EC329725 (> 3000 kg/ha)	PRT-12 (1565 kg/ha)

Table 3. Correlations among different agro-morphological traits in Faba bean germplasm.

Characters	Days to 50% Flowering	Days to Maturity	Plant Height (cm)	No. of Branches	Pods/Plant	No. of Grains/Pod.	No. of Pods/Cluster	Pod Length (cm)	Leaf Length (cm)	Leaf Width (cm)	100 Seed Wt. (g)	Yield/Plant (g)	Yield (q/ha)
Days to 50% flowering	1.0000												
Days to maturity	0.4132**	1.0000											
Plant height (cm)	0.1110	0.3080**	1.0000										
No. of Branches	0.1378	-0.1633*	0.1346	1.0000									
Pods/Plant	-0.1197	-0.2667**	0.2558*	0.2590*	1.0000								
No. of grains/pod.	-0.0248	-0.4173**	-0.1619	0.3679**	0.1684*	1.0000							
No. of pods/cluster	-0.0984	-0.3634**	-0.1659*	0.0594	0.3955**	0.2653**	1.0000						
Pod length (cm)	0.1196	0.2545**	0.2929**	0.1410	0.0633	0.0712	-0.1735*	1.0000					
Leaf length (cm)	0.0800	0.1719*	0.1851*	0.0753	-0.0453	0.0845	-0.0305	0.2200**	1.0000				
Leaf width (cm)	0.2706*	0.4728**	0.3402**	-0.0049	-0.0707	-0.1575	-0.1443	0.2613**	0.5475**	1.0000			
100 seed wt. (g)	0.0222	0.4041**	0.4701**	-0.0492	0.2834**	-0.2321**	-0.1190	0.6440**	0.2450**	0.4175**	1.0000		
Yield/plant (g)	-0.0462	0.0398	0.2911**	0.0162	0.4292**	-0.0695	0.0984	0.2534**	0.0737	0.2408**	0.4060**	1.0000	
Yield (kg/ha)	0.0162	-0.0421	0.4229**	0.0812	0.5239**	0.0045	0.1715*	0.2769**	0.0621	0.2158**	0.5058**	0.6586**	1.0000

*=Significant at 5% level, **=Significant at 1% level.

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Table 4. Direct and indirect effects of different agro-morphological traits in Faba bean germplasm.

Characters	Days to 50% Flowering	Days to Maturity	Plant Height (cm)	No. of Branches	Pods/Plant	No. of Grains/Pod	No. of Pods/Cluster	Pod Length (cm)	Leaf Length (cm)	Leaf Width (cm)	100 seed wt. (g)	Yield/Plant (g)	Correlation on With Yield (kg/ha)
Days to flowering	**0.1314**	-0.1029	0.0219	-0.0039	-0.0143	-0.0010	-0.006	-0.0076	-0.0059	0.0169	0.0078	-0.0197	0.0162
Days to maturity	0.0543	**-0.2492**	0.0607	0.0047	-0.0318	-0.0170	-0.0240	-0.0161	-0.0127	0.0296	0.1426	0.0170	-0.0421
Plant height (cm)	0.0146	-0.0768	**0.1969**	-0.0038	0.0305	-0.0066	-0.0110	-0.085	-0.0137	0.0213	0.1659	0.1240	0.4228**
No. of branches	0.0181	0.007	0.0265	**-0.0286**	0.0309	0.0149	0.0039	-0.0089	-0.0056	-0.0003	-0.0174	0.0069	0.0812
Pods per plant	-0.0157	0.0665	0.0504	-0.0074	**0.1194**	0.0068	0.0262	-0.0040	0.0034	-0.0044	0.1000	0.1829	0.5239**
No. of grains /pod	-0.0033	0.1040	-0.0319	-0.0105	0.0201	**0.0406**	0.0175	-0.0045	-0.0063	-0.0099	-0.0819	-0.0296	0.0045
No. of pods/cluster	-0.0129	0.0905	-0.0327	-0.0017	0.0472	0.0108	**0.0661**	0.0110	0.0023	-0.0090	-0.0420	0.0419	0.1715*
Pod length (cm)	0.0157	-0.0634	0.0577	-0.0040	0.0076	0.0029	-0.0115	**-0.0633**	-0.0163	0.0163	0.2273	0.1080	0.2769**
Leaf length (cm)	0.0105	-0.0428	0.0364	-0.0022	-0.0054	0.0034	-0.0020	-0.0139	**-0.0741**	0.0342	0.0865	0.0314	0.0620
Leaf width (cm)	0.0356	-0.1178	0.0670	0.0001	-0.0084	-0.0064	-0.0095	-0.0165	-0.0406	**0.0625**	0.1473	0.1026	0.2158**
100 seed weight (g)	0.0029	-0.1007	0.0926	0.0014	0.0338	-0.0094	-0.0079	-0.0408	-0.0182	0.0261	**0.3529**	0.1730	0.5058**
Yield per plant (g)	-0.0061	-0.0099	0.0573	-0.0005	0.0512	-0.0028	0.0065	-0.0160	-0.0055	0.0151	0.1433	**0.4261**	0.6587**

Residual effects=0.3819, Figures in bold indicate direct effects, *=Significant at 5% level, **=Significant at 1% level

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Research Article

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Stability Analysis of Fodder Cowpea Genotypes under Different Environments

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ABSTRACT

Stability of green fodder yield and its component characters was assessed for thirty genotypes over six environments (two seasons 2019 and 2020 × three environments) to determine the quantitative response of cowpea genotypes. The investigation was undertaken at Pusa Farm of Dr. Rajendra Prasad Agricultural University, Pusa, Samastipur, Bihar under open field and rain-out shelter conditions in randomized block design with three replications. The results green fodder revealed that five genotypes (RL-5, PL-4, EC 97738, FD-2262and FD-2258) were found stable for favourable environment and four genotypes (RL-6, EC 390252, FD-2230, FD-2272) were found suitable for poor environment. The genotype, Kashigauri and Bundel Lobia-1 for green fodder yield were found suitable for average environment and encompasses fair stability and wider adaptation. Therefore, the genotype Kashigauri and Bundel Lobia-1 may be recommended for green fodder production after testing over time and space.

Keywords: Fodder cowpea, rain-out shelter, green fodder yield, stability, regression coefficient

Introduction

Livestock sector of India is one of the largest in the world. In rural areas animals rearing are the backbone of rural farmers and their economy. Deficiency in feed and fodder has been identified as one of the major component in achieving the desired level of livestock production (Kumar et al. 2012). The green fodder production is declining year after year but the projected need of green fodder is increasing. During lean period there animal rearing farmers face fodder shortage which also direct production of better quality feed at cheap cost (Kumari et al. 2017). The animal feeds from straw of wheat, rice, barley, sorghum etc. are encompassing low protein with low energy whereas legume feeds contain high protein which fulfil animal nutrition demand and improves milk production (Praveena et al. 2019).

Cowpea [*Vigna unguiculata* L.Walp] (2n=22) is an important summer/rainy season legume crop. It is one of the most ancient crop and commonly known as Lobia in Hindi, Bora in Bihar and other names *viz*., black eye pea, southern pea, chowla, barbati (Gupta et al. 2017). Cowpea improves soil fertility due to its nitrogen fixing ability and part of major agricultural cropping system (Kyei-Boahen et al. 2017). It is an importance drought tolerant crop and also grow under water stagnation condition as well as summer and rainy season legume crop (Panchta et al. 2021). The cowpea green fodder contains 15-20% crude protein and 50% digestible carbohydrate at the first stage of formation of pod. The fodder-cum-grain cowpea varieties may eradicate nutritional status of farm animals by using cowpea seeds in the preparation of animal ration. Therefore, it is considered as good source of calories, vitamins and minerals and also provides a significant amount of dietary protein and lysine (Ngoc et al. 2019). Besides being used as pulse crop, cowpea's immature pod and green leaf and growing twig can be utilized as vegetable. However, it is more important as the

source of green as well as dry fodder. Among fodder legumes, cowpea is grown for both grain and fodder in all tropical and sub-tropical regions (Vu et al. 2017).

Our country is the largest producer of cowpea in Asia, accounts for about 0.5 m t production with 1.5 m ha area and average grain plus fodder yield of 3 q/ha and 25-45 t/ha (Ahmad et al. 2017). The green fodder production is declining year after year but the projected need of green and dry fodder is 16848 and 15042 thousand tonnes (Gupta and Kumar, 2007). In Bihar the prime forage sources is met through less nutritious grasses. Thus, a good fodder source is need of the hour. It is well known fact that the genetic diversity is the primary requirement for a flourishing breeding plan. But, the evaluation of genotypes is a pre-requisite for crop improvement (Arya et al. 2019). After this, the core responsibility of plant breeder is to screen out genotypes; those are suitable genotypes for wider range of adaptation. Genotypes sometimes fail to perform equally in variety of environments as phenotype is the ultimate outcome of interaction between genotype and environment.

The core responsibility of plant breeder is to screen out genotype those are suitable for wider range of adaptation. Genotype sometimes fails to perform equally in variety of environments as phenotype is the ultimate outcome of interaction between genotype and environment. The most widely used method to measure stability was previously proposed (Finlay and Wilkinson, 1963) and later on improved (Eberhart and Russell, 1966). The regression coefficient value (b_i=1) coupled with non-significant (S^2d_i=0) specifies average stability. The stability is denoted as adaptation of varieties to unpredictable and transient environmental conditions. Thus, evaluation of stability in fodder cowpea is important to identify better genotypes to meet the shortage of green fodder to improve health status of animal with higher animal products. This study was undertaken to study stability of plant height, number of branches per plant and green fodder yield in thirty cowpea genotypes.

Materials and Methods

Study site and experimental design

The field experiment was conducted during *Kharif* seasons of 2019 and 2020 at Pusa Farm of Dr. Rajendra Prasad Central Agricultural University, Pusa, Samastipur, Bihar. The latitude and longitude of the experiment location are 25.980N and 85.670E, respectively. The mean altitude is 52 m above mean sea level and average annual rainfall of 1234 mm. Weather prevailed during experimental period depicted in Figure 1.

Treatment details

The research was carried out as under open field (two date of sowing 15th July 2019 and 26th July 2019) as well as in rain shelter condition (single date of sowing 15th July 2019) in *kharif* 2019 and in *kharif* 2020 under open field (15th July 2020 and 26th July 2020) as well as in rain shelter condition (15th July 2020) installed at Pusa farm where six different environment conditions named E_1, E_2, E_3, E_4, E_5 and E_6, respectively, were used for stability study. Thirty cowpea genotypes viz., EC 390216, Kashigauri, EC 390268, Kashikanchan, RL-1, RL-2, RL-3, RL-4, RL-5, RL-6, PL-4, EC 97306, EC 390252, IVTC-8, IVTC-10, IVTC-1, EC 97738, EC 9736,PL-2, PL-5, PL-3, FD-2230, FD-2229, FD-2233, FD-2242, FD-2260, FD-2262, FD-2272, FD-2258 and including one check BundelLobia 1 were obtained from different research station of the country was used for the trial. The experiment was laid out in Randomized Block Design with three replications and 45x10 cm spacing.

Observations recorded

The observation was recorded on plant height (cm), number of branches per plant and green fodder yield (g/plant). The plant height (cm) was recorded on five tagged plants in each genotype from each replication at 50% flowering stage. The numbers of branches were also counted from five tagged plants in each replication in all genotype of cowpea at 50% flowering stage. The green fodder yield data were collected by using average of five plants from each plot harvested near ground at 50% flowering stage from 30 genotypes of cowpea. The average data was recorded as g/plant.

Statistical analysis

The stability model of Eberhart and Russell (1966) were followed for analysis of six environment data. It involves the estimation of three stability parameters like mean ($\bar{X}_i$), regression coefficient (b_i) and deviation from regression (S^2d_i), which are defined by the following mathematical model

$Y_{ij} = \mu_i + \beta_i I_j + \delta_{ij}$ (I= 1, 2,……..t and j = 1,2……..S)

Where, Y_{ij}= Mean of i^{th} genotype in j^{th} environment

μ_i=Mean of all genotype over all environment

β_i = The regression coefficient of i^{th}genotype on the environmental index, which measures response of genotype to varying environment

δ_{ij}= The environmental index which is defined as deviation of the mean of all the genotypes at a given environment from the overall mean.

The regression coefficients and the mean value for 30 cowpea genotypes were analysed by INDOSTAT software.

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Results and Discussion

Plant height (cm)

The data on mean performance of thirty cowpea genotypes are depicted in Table 1. The plant height data were ranged from 54.66 cm (FD-2229) to 98.89 cm (FD-2258). The early planting date (E_1 and E_4) increases the plant height in all seasons. Likewise, considerable variation in plant height was also reported by Shekara et al. (2012) in fodder cowpea genotypes. For plant height, environment E_4 (75.78cm) was most favourable, followed by E_1 (75.53cm), E_5 (73.51cm), E_2 (71.79cm), E_6 (53.99cm) and E_3 (53.64). The stability parameters ($\bar{x}$, b_i and S^2d_i) as proposed by Eberhart and Russell (1966) of the individual genotypes are illustrated in Table 2. The genotypes *viz*., Kashikanchan, RL-5, EC390252, IVTC-8, PL-5, FD-2242, FD-2260, FD-2258, Bundel Lobia-1 (check) mean were superior to population mean.The examined results shows that only one genotype (FD-2242) was found suitable for average environment ($\bar{x}>\mu$, $b_i=1$, NS S^2d_i) for plant height.Genotypes IVTC-8, PL-5, FD-2260 and FD-2258 were examined as stable in rich environment and three genotypes Kashikanchan, EC 390252, Bundel Lobia-1 (check) were stable in poor environment. El-Shaieny et al. (2015) evaluated cowpea for best planting season and found fall season as most suitable also suggested four cowpea genotypes as stable for total dry seed yield base on three parameter model.

Number of branches/plant

The mean performance of genotypes (Table 2) ranged from 4.40 (IVTC-10) to 8.17 (EC 9736). The early sowing date improves number of branches in both the seasons but under rain-out shelter due to water stress the trait mean reduced significantly. For number of branches/plant, environment E_4 (7.19) was most favourable, followed by E_5 (6.72), E_1 (6.14), E_2 (5.67), E_6 (4.60) and E_3 (4.00). The stability parameters ($\bar{x}$, b_i and S^2d_i) as proposed by Eberhart and Russell (1966) of the individual genotypes are illustrated in Table 2. The genotypes EC 97306 and FD-2272 were found with significant regression coefficient (b_i) value with non-significant S^2di value. Total nine genotypes were found with significant S^2di value. The genotypes RL-6 ($\bar{x}>\mu$, $b_i=1$, NS S^2di) was found as suitable for average environment. The studied results for number of branch also indicated two genotype *viz*., Kashikanchan, IVTC-1, PL-5, PL-3, FD-2260, FD-2258 and Bundel Lobia-1 (check) could consistently do better in favourable environments and the genotypes *viz*., Kashigauri, RL-2, EC 97738 and EC 9736 were found stable in poor environment. Kabir et al. (2009) studied wheat variety and recommended that verity which were sensitive to environmental changes can be incorporate in cultivation for favourable condition. The results of our study is also in parallel with results from cowpea (Singh et al. 2020).

Green fodder yield (g/plant)

The mean performance of thirty cowpea genotypes depicted in Table 3 and it is ranges from 117.38 7(FD-2260) to 217.06 (FD-2258). For green fodder yield/plant (g), environment E_4 (192.30g) was most favourable, followed by E_5 (187.27g), E_1 (185.72g), E_2 (180.00g), E_3 (128.41) and E_6 (123.09). The stability parameters ($\bar{x}$, b_i and S^2d_i) as proposed by Eberhart and Russell (1966) of the individual genotypes are illustrated in Table 4. Genotypes *viz*., Kashikanchan, RL-1, RL-5, RL-6, EC 97306, EC 97738, PL-5 and FD-2262 exhibited significant regression coefficient (b_i) with non-significant deviation from regression (S^2d_i). Total sixteen cowpea genotype were found with ($b_i \leq 1$), twelve genotypes with ($b_i \geq 1$) and two genotypes with ($b_i=1$). Therefore, based on three parameter model, two genotypes (Kashigauri and Bundel Lobia-1) were found stable for average environment ($\bar{x}>\mu$, bi=1, NS S^2di) for this trait. Five genotypes (RL-5, PL-4, EC 97738, FD-2262 and FD-2258) were evaluated as stable for favourable environment and five genotypes (EC 390268, RL-6, EC 390252, FD-2230, FD-2272) were low responsive found suitable for unfavourable environment. El-Shaieny et al. (2015) reported considerable degree of genotypic differences and average stability in cowpea for yield related characters under multiple planting date environments. The deviation for regression if deviated non-significantly from zero ($S^2d=0$) genotypes were reported as stable for seed yield over all the environments (Manivannan et al. 2019). Similar findings were also obtained by Santos et al. (2015).

Conclusions

Genotypes which have regression coefficient ($b_i=1$), trait mean more than population mean ($\bar{x}>\mu$), small deviation from regression (S^2d_i) are considered as stable which are Kashigauri and Bundel Lobia-1 for green fodder yield and Kashigauri for dry matter % was found suitable for average environment and encompasses fair stability and wide adaptation over different environment. Therefore, the genotype Kashigauri may be recommended for green fodder as well as dry fodder production after testing over time and space.

Table 1. Mean performance of plant height (cm) under six environments and stability parameters.

No.	Genotypes	Plant Height (cm)								
		E_1	E_2	E_3	E_4	E_5	E_6	$\bar{x}$	b_i	s^2d_i
1	EC 390216	63.63	60.56	44.94	70.26	66.43	45.38	**58.53**	0.99	-1.57
2	Kashigauri	70.16	70.23	54.24	72.48	70.86	53.87	**65.31**	0.82*	-7.47
3	EC 390268	71.56	73.15	58.78	72.39	71.19	56.84	**67.32**	0.68*	-5.70
4	Kashikanchan	75.26	76.89	60.85	70.91	73.22	56.11	**68.87**	0.73	4.33
5	RL-1	73.37	64.56	47.43	65.86	71.12	44.24	**61.10**	1.12	3.62
6	RL-2	67.21	60.20	46.31	69.54	69.48	45.64	**59.73**	1.02	-1.07
7	RL-3	69.15	64.20	47.57	66.10	64.29	46.88	**59.70**	0.92	-7.04
8	RL-4	67.90	66.50	47.96	64.82	63.62	45.51	**59.39**	0.91	-3.51
9	RL-5	110.73	103.44	70.73	107.64	99.36	81.01	**95.49**	1.45	12.87*
10	RL-6	67.53	68.78	54.09	72.94	69.57	51.23	**64.03**	0.83	-3.69
11	PL-4	71.42	68.02	53.46	74.69	68.66	48.81	**64.18**	0.96	-3.68
12	EC 97306	70.94	66.50	48.96	73.03	67.53	49.10	**62.68**	1.01	-7.47
13	EC 390252	82.97	81.54	62.01	79.79	82.29	60.84	**74.91**	0.97	-3.98
14	IVTC-8	84.53	75.05	54.73	77.97	77.20	57.99	**71.25**	1.11	-1.19
15	IVTC-10	66.52	63.28	44.09	63.76	62.25	42.18	**57.01**	1.01	-6.03
16	IVTC-1	70.00	67.21	46.35	73.58	68.67	50.49	**62.72**	1.06	-5.60
17	EC 97738	72.82	72.12	58.53	71.10	70.27	56.34	**66.86**	0.68*	-6.13
18	EC 9736	67.11	68.04	56.35	70.74	67.58	50.95	**63.46**	0.71	-2.79
19	PL-2	71.61	63.59	51.62	70.88	64.04	50.58	**62.06**	0.83	-2.27
20	PL-5	87.76	81.98	62.34	91.51	85.21	67.00	**79.30**	1.09	-2.94
21	PL-3	69.36	64.36	44.02	70.03	64.83	46.52	**59.85**	1.08	-7.21
22	FD-2230	74.28	67.26	48.21	80.86	66.18	53.11	**64.98**	1.09	14.22*
23	FD-2229	63.75	57.44	44.58	58.88	62.54	40.75	**54.66**	0.88	-1.45
24	FD-2233	76.13	74.63	47.38	72.61	72.08	50.60	**65.57**	1.20	-1.67
25	FD-2242	93.71	92.67	72.28	93.44	91.97	72.31	**86.06**	1.00	-7.32
26	FD-2260	78.25	69.18	49.36	77.31	79.04	51.91	**67.51**	1.25	-0.70
27	FD-2262	74.14	67.88	46.30	76.27	69.60	50.47	**64.11**	1.17	-4.51
28	FD-2272	75.98	68.13	47.55	79.03	80.58	52.20	**67.25**	1.29	7.47
29	FD-2258	105.80	104.78	81.52	109.02	108.86	83.36	**98.89**	1.20	-4.76
30	Bundel Lobia-1 (Check)	72.17	71.51	56.76	75.86	76.64	57.54	**68.42**	0.82	-4.01
Environmental Mean		**75.53**	**71.79**	**53.64**	**75.78**	**73.51**	**53.99**	**67.37**	**1.00**	-
CD (0.05)		8.41	8.89	6.03	9.24	8.35	8.90	-	-	-

E1=Environment 1 date of sowing 15 July 2019 in irrigated open field condition, E2=Environment 2 date of sowing 26 July 2019 in irrigated open field condition, E3=Environment 3 date of sowing 15 July 2019 in rainout shelter for drought condition, E4=Environment 4 date of sowing 15 July 2020 in irrigated open field condition, E5=Environment 5 date of sowing 26 July 2020 in irrigated open field condition, E6=Environment 6 date of sowing15 July 2020 in rainout shelter for drought condition, $\bar{x}$=Mean value, b_i=Regression coefficient, s^2d_i=Deviation from regression, *=Significant at 5% level, **=Significant at 0.01% level of significance, CD=Critical difference

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Table 2. Mean performance number of branches/plant under six environments and stability parameters.

No.	Genotypes	Number of Branches/Plant								
		E_1	E_2	E_3	E_4	E_5	E_6	$\bar{x}$	b_i	s^2d_i
1	EC 390216	5.60	5.07	3.49	6.61	6.13	5.01	**5.32**	0.84	0.00
2	Kashigauri	6.68	6.54	5.16	7.81	6.59	5.89	**6.45**	0.67	-0.03
3	EC 390268	5.99	5.82	4.51	6.85	6.34	4.00	**5.58**	0.85	0.01
4	Kashikanchan	7.56	7.35	5.91	8.80	8.10	5.13	**7.14**	1.05	0.13
5	RL-1	6.19	5.34	3.61	5.44	5.48	3.05	**4.85**	0.82	0.47**
6	RL-2	5.98	6.68	4.44	6.60	6.85	4.10	**5.77**	0.86	0.27
7	RL-3	4.97	4.37	3.00	5.99	5.99	3.60	**4.65**	0.99	-0.10
8	RL-4	5.85	5.26	3.74	7.37	6.63	4.76	**5.60**	1.04	-0.08
9	RL-5	4.33	3.63	2.68	6.35	6.17	4.53	**4.62**	0.99	0.56**
10	RL-6	6.88	6.81	5.34	8.66	8.11	6.22	**7.01**	0.96	-0.04
11	PL-4	5.03	4.68	3.48	7.15	6.89	4.32	**5.26**	1.12	0.15
12	EC 97306	5.85	5.11	3.30	8.03	7.23	4.11	**5.61**	1.45*	-0.03
13	EC 390252	5.62	5.32	3.90	6.89	6.03	5.11	**5.48**	0.77	-0.03
14	IVTC-8	5.79	4.91	3.30	6.93	5.98	4.31	**5.20**	1.04	-0.08
15	IVTC-10	5.68	4.72	3.16	5.15	4.54	3.16	**4.40**	0.70	0.27*
16	IVTC-1	6.06	5.21	3.34	8.88	8.37	5.04	**6.15**	1.63	0.42**
17	EC 97738	8.67	8.45	6.53	7.39	6.98	5.10	**7.19**	0.55	1.45**
18	EC 9736	8.76	8.43	6.79	9.83	8.27	6.95	**8.17**	0.86	0.09
19	PL-2	5.91	5.33	3.72	7.08	6.22	4.39	**5.44**	1.00	-0.13
20	PL-5	6.93	6.35	4.36	8.57	7.35	4.37	**6.32**	1.34	-0.03
21	PL-3	5.89	5.31	3.26	8.19	8.12	4.74	**5.92**	1.52	0.21
22	FD-2230	6.10	5.22	3.28	6.58	7.12	5.13	**5.57**	1.02	0.20
23	FD-2229	6.03	5.16	3.58	4.88	4.93	2.93	**4.59**	0.65	0.63**
24	FD-2233	4.92	4.57	2.84	6.16	5.21	3.83	**4.59**	0.92	-0.09
25	FD-2242	6.53	6.20	4.70	7.04	5.79	4.01	**5.71**	0.79	0.31*
26	FD-2260	6.91	6.44	3.92	6.67	7.60	4.55	**6.02**	1.08	0.26*
27	FD-2262	5.14	4.80	2.84	5.55	5.29	4.44	**4.68**	0.73	0.04
28	FD-2272	6.13	5.38	3.16	7.51	7.59	4.37	**5.69**	1.40*	-0.04
29	FD-2258	6.56	6.36	4.76	8.82	8.35	5.60	**6.74**	1.23	0.07
30	Bundel Lobia-1 (Check)	5.56	5.32	3.90	7.91	7.40	5.23	**5.89**	1.13	0.23*
Environmental Mean		**6.14**	**5.67**	**4.00**	**7.19**	**6.72**	**4.60**	5.72	**1.00**	-
	CD (0.05)	0.64	0.63	0.63	1.95	1.39	0.59	-	-	-

E1=Environment 1 date of sowing 15 July 2019 in irrigated open field condition, E2=Environment 2 date of sowing 26 July 2019 in irrigated open field condition, E3=Environment 3 date of sowing 15 July 2019 in rainout shelter for drought condition, E4=Environment 4 date of sowing 15 July 2020 in irrigated open field condition, E5=Environment 5 date of sowing 26 July 2020 in irrigated open field condition, E6=Environment 6 date of sowing15 July 2020 in rainout shelter for drought condition, $\bar{x}$=Mean value, b_i=Regression coefficient, s^2d_i=Deviation from regression, *=Significant at 5% level, **=Significant at 0.01% level of significance, CD=Critical difference

Table 3. Mean performance of green fodder yield/plant (g) under six environments and stability parameters.

No.	Genotypes	Green Fodder Yield/Plant (g)								
		E_1	E_2	E_3	E_4	E_5	E_6	$\bar{x}$	b_i	s^2d_i
1	EC 390216	145.49	138.85	102.14	164.39	145.56	106.72	**133.86**	0.74	15.00
2	Kashigauri	195.44	192.07	145.89	212.99	207.30	139.75	**182.24**	0.99	-14.42
3	EC 390268	198.51	195.20	169.64	224.53	227.74	181.88	**199.58**	0.61	154.19**
4	Kashikanchan	184.79	181.80	133.18	182.65	182.63	130.40	**165.91**	0.83*	-24.81
5	RL-1	186.56	178.41	124.55	191.69	187.44	111.47	**163.35**	1.13*	-31.15
6	RL-2	173.30	165.58	119.53	189.71	195.44	111.40	**159.16**	1.10	39.17
7	RL-3	182.69	175.36	119.43	200.39	191.75	114.60	**164.04**	1.18	-16.99
8	RL-4	162.06	156.29	104.94	169.12	149.95	99.16	**140.25**	0.95	-2.56
9	RL-5	208.86	198.56	134.99	207.19	200.32	118.97	**178.15**	1.26*	-7.21
10	RL-6	202.20	198.38	159.87	210.70	203.00	158.58	**188.79**	0.73**	-34.76
11	PL-4	181.92	176.63	122.95	191.82	200.02	126.90	**166.71**	1.04	17.94
12	EC 97306	139.53	131.84	93.36	150.54	143.17	93.98	**125.40**	0.79*	-24.48
13	EC 390252	202.47	191.82	157.31	211.60	201.71	144.71	**184.94**	0.86	-18.56
14	IVTC-8	174.38	165.37	113.40	171.65	153.14	111.31	**148.21**	0.88	35.53
15	IVTC-10	170.95	164.34	114.82	191.77	197.29	105.80	**157.49**	1.19	66.77*
16	IVTC-1	229.19	223.07	138.88	218.66	209.43	121.33	**190.09**	1.46	98.76**
17	EC 97738	234.76	232.05	151.00	238.61	225.06	136.82	**203.05**	1.45*	9.80
18	EC 9736	220.05	217.13	140.41	210.16	202.57	129.38	**186.62**	1.25	76.85*
19	PL-2	186.81	179.46	120.64	172.96	170.59	113.83	**157.38**	0.97	45.72
20	PL-5	146.28	139.92	95.90	149.28	140.46	90.57	**127.07**	0.84*	-31.06
21	PL-3	172.72	165.24	113.13	169.29	180.19	128.10	**154.78**	0.83	38.42
22	FD-2230	186.39	183.22	151.24	201.22	198.79	139.12	**176.66**	0.80	-6.08
23	FD-2229	154.70	148.09	102.33	160.92	177.87	111.44	**142.56**	0.88	78.37*
24	FD-2233	141.20	138.05	92.38	155.81	152.52	89.15	**128.18**	0.94	-20.64
25	FD-2242	64.50	54.57	68.82	67.64	53.05	128.28	**180.14**	1.09	109.43**
26	FD-2260	72.96	59.89	74.55	72.37	52.53	76.29	**117.38**	0.84	19.15
27	FD-2262	203.79	195.56	138.67	222.19	219.20	127.02	**184.41**	1.30*	2.97
28	FD-2272	181.97	175.69	126.57	191.06	198.54	132.35	**167.70**	0.95	17.42
29	FD-2258	241.75	238.79	172.47	244.27	236.09	168.97	**217.06**	1.13	-19.08
30	Bundel Lobia-1 (Check)	214.57	211.75	159.66	215.64	210.82	144.38	**192.80**	1.00	-12.89
Environmental Mean		**185.72**	**180.00**	**128.41**	**192.30**	**187.27**	**123.09**	**166.13**	**1.00**	-
	CD (0.05)	16.66	19.05	12.90	19.15	19.03	17.74	-	-	-

E1=Environment 1 date of sowing 15 July 2019 in irrigated open field condition, E2=Environment 2 date of sowing 26 July 2019 in irrigated open field condition, E3=Environment 3 date of sowing 15 July 2019 in rainout shelter for drought condition, E4=Environment 4 date of sowing 15 July 2020 in irrigated open field condition, E5=Environment 5 date of sowing 26 July 2020 in irrigated open field condition, E6=Environment 6 date of sowing15 July 2020 in rainout shelter for drought condition, $\bar{x}$=Mean value, b_i=Regression coefficient, s^2d_i=Deviation from regression, *=Significant at 5% level, **=Significant at 0.01% level of significance, CD=Critical difference

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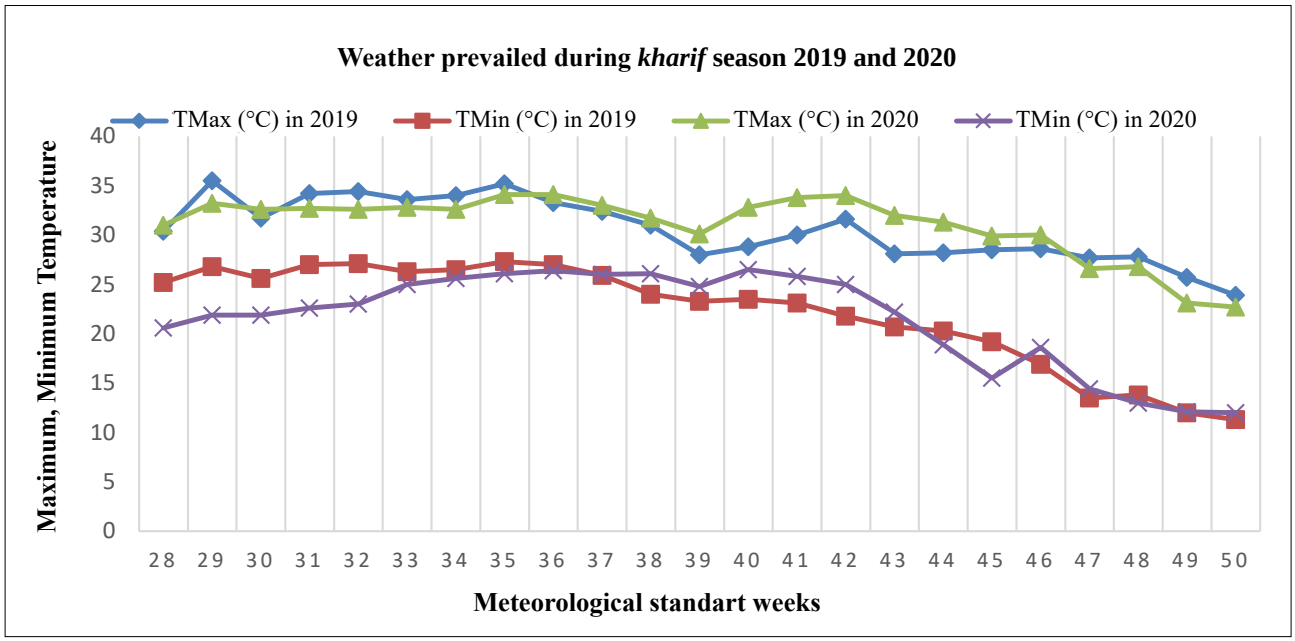

Figure 1.Weather prevailed during experimental period of *kharif* season 2019 and *kharif* 2020.

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Evaluation of Aonla Varieties Under Semi-Arid Conditions of Haryana

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ABSTRACT

The farmers or orchardist are trying different varieties/germplasm for growing as a commercial orchard without having knowledge about the performance of these varieties/germplasm. The experiment on varietal evaluation of on aonla comprising of nine promising cultivars (NA 6, NA 7, NA 10, NA 20, Krishna, BSR 1, Gujarat 1, Chakaiya and CHES 1) released from the different parts of the country was carried out to study the variation among different varieties on qualitative as well as quantitative basis and observed the performance of growth, physicochemical characters and yield during 2017-18, 2018-19, 2019-20 under semi-arid conditions to recommend the suitable variety. Plant shape was observed as spreading (CHES 1, Chakaiya, Krishna, NA 6, NA 7, NA 10, BSR 1); drooping (NA 20) and upright (G1) in different cultivars of aonla. The range of variability among different parameters such as plant height (4.90-6.70 m), plant spread-EW (4.47-7.15 m), plant spread-NS (4.44-7.53 m) , stem girth (46.45-95.37 cm), plant volume (86.8-283.9 m^3), plant canopy area (15.59-42.35 m^2), total soluble solids,TSS (9.17-18.32 °B), acidity (1.92-2.63%), TSS : acidity ratio (4.09-7.71), ascorbic acid (323-567 mg/100 g pulp), fruit weight (5.89-55.43 g), fruit length (1.87-3.33 cm), fruit breadth (2.28-3.70 cm), yield (36-102 kg/plant and 10.00-28.34 MT/ha). Fruit shape was observed as flattened round (CHES 1, Chakaiya, NA 6, NA 10, G 1, BSR 1), triangular (Krishna), oval (NA 7) and round (NA 20). Free base (cavity at stem end) was observed as absent (CHES 1), shallow (Chakaiya, NA 6, NA 20, G 1), deep (Krishna), flat (NA 7, NA 10, BSR 1) and fruit apex was observed as flat (CHES 1, Chakaiya, Krishna, NA 7, NA 10, NA 20), papillate(NA 6, BSR 1), depressed (G 1).

Keywords: Aonla or Indian gooseberry (*Phyllanthus emblica*), varieties, growth, yield and quality, plant volume, fruit shape, variability

Introduction

The aonla or Indian gooseberry (*Phyllanthus emblica* Linn.) belongs to family Phyllanthaceae and subfamily Phyllanthoidae. It is a subtropical plant and prefers dry subtropical climate and can be grown with an annual rainfall of 350-500 mm. It is indigenous meditational and minor fruit crop grown in tropical South-East Asia, particularly central and southern India. It also has a tremendous export potential due to its medicinal and therapeutic and high nutritive value, it has been recognized as *Amrit Phal* (life-giving fruit). The fruit is highly nutritive and second richest source of vitamin C after barbados cherry. It is a fair source of thiamine (vitamin B_1), riboflavin (vitamin B_2), and a rich source of pectin and minerals (iron, calcium and phosphorus). The ascorbic acid and other constituents are well retained in dried/processed aonla fruits. The fruits are processed into chutney, candy, preserves (*murabba*), sauce, candy, dried chips, tablets, jellies, pickles, powder *etc.*(Kumar et al., 2013). It is also used in shampoos, hair dyes and ink industries. *Trifla* and *chavanprash* are well-known indigenous products of aonla. Besides fruits, leaves, bark and even seeds are being used for various purposes.

Aonla fruit due to its nutritional security, high medicinal value and high productivity (15-20 t/ha) has the immense possibility for commercial growing in the arid zone and marginal soils, where only a few fruits can be grown (Chadha, 2013). It is gaining popularity because of its high yield, good returns, hardy nature, drought tolerant, prolific bearer and being a hardy plant, it can be grown successfully in marginal soils, moderately alkaline soils and slightly acidic to saline/sodic (pH 6.5-9.5) conditions (Chadha, 2013). However, well-drained fertile loamy soils are best.

Deep root system, reduced foliage and dormancy of fruitlets during dry weather (April-June) make it an ideal plant for growing in arid and semi-arid conditions. However, heavy frost during winter is not conducive to young plants but a mature plant can tolerate freezing as well as the high temperature of 46ºC (Bose and Mitra, 2001). Warm temperature seems to be conducive for the initiation of floral buds and ample humidity is essential for initiation of growth of dormant fruitlets during July-August. Dry spells during this period result in heavy fruit drop and delay in initiation of fruit growth.

Aonla gene pool is spread over different parts of the country and has enormous variability with respect to qualitative as well as quantitative characters due to old age practice of seed propagation. A large number of varieties, mostly from selection have been released for commercial cultivation from different institutes, but their adaptability has not been studied for semi-arid region of Haryana. Farmers are experiencing the challenges of identifying the suitable cultivars, as they are unfamiliar with the characteristics of varieties with respect to adaptability and fruit characters. Identification of suitable genotype for the region is necessary for promoting its productivity, production and quality of the fruits under semi-arid conditions (Nagar et al. 2017). In order to identify distinct characters of various aonla cultivars, the morphological characters are also equally important to the fruit characters. On the basis of growth, yield and quality performance of different germplasm, the emphasis has been made to find out the suitable cultivar(s) for the semi-arid region of Haryana. This will also help the growers in the selection of suitable cultivar(s) of this underutilized crop for large-scale cultivation to get higher yield and good quality fruits suitable for processing as well as medicinal formulation preparations. Unproductive land of the arid and semi-arid region could be utilized properly by growing such a hardy fruit crop, which holds promise for nutritional security and also helpful in generating income.

Materials and Methods

The present study was carried out at experimental orchard at Regional Research Station, Bawal (Rewari), situated at an altitude of 266 m above mean sea level with coordinates of 28º10´N latitude and 76º50´E longitudes in South-West zone of Haryana having typical semi-arid climatic zone with hot and dry summer and extremely cold winter. It shows a wide range of fluctuations in temperature (maximum and minimum) and rainfall. During May to June, the temperature reaches to maximum of around 44°C, while during December and January it remains as low as freezing point accompanied by frost is also quite common. The rainfall is highly erratic with 20-30 per cent annual and 30-50 per cent seasonal variations. Large variations occur for total rainfall and its distribution, about 80-85 per cent received during monsoon season, while during winter and spring seasons some rains occurs due to the western disturbances. A long term field experiment was conducted on aonla plants planted during 2007 at 6 × 6 m spacing in a randomized block design with three replications and two plants per replications in a loamy sand soil having low level of organic carbon and available phosphorus. The observations on all the genotypes were recorded during 2017-18, 2018-19, 2019-20. Plants were selected randomly and maintained under uniform conditions during the study period, where, all the agronomic practices were carried out as per recommended package of practices.

Plant shape was observed visually at pea size fruit stage in the month of August every year as upright, spreading and drooping; and mature fruit shape mature fruit was observed visually as oval, round, oblong or flattened-round and triangular (slightly conical at apex) as recommended in the descriptor of NBPGR (Mahajan et al. 2002), and guidelines for DUS testing of PPV and FRA (Anonymous, 2016). Plant height was measured with the help of a graduated measuring pole from ground level to the tip of the highest shoot and expressed in meters. Observation for stem circumference (girth) was measured with the help of measuring tape at 15 cm above the bud union of the plants. The average stem girth was calculated and expressed in centimeters. Plant spread was measured in both directions, *i.e.,* north to south and east to west, with the help of a graduated measuring tape. Average plant spread was calculated from both directions separately and expressed in meters. Plant volume was calculated using the formula $л\ r^2\ h$, where r = (plant spread NS, North-South + plant spread EW, East-West)/4); h = height of plant, it was expressed in m^3. Plant canopy cover area was calculated by using the formula $л\ r^2$.

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Physical characteristics of the fruits were estimated from the five randomly selected fruits plucked from each quarter of a plant, fruits were weighed on the digital electric balance and average fruit weight was expressed in grams, their length was measured from distal to proximal end with the help of digital vernier callipers and their average value was taken and expressed in cm, fruit breadth was measured with the help of digital vernier callipers and the average value was taken and expressed in cm.

Physiochemical characteristics were estimated from the five fruits selected randomly from tagged branch of each quarter of plant and their pulp was crushed to extract juice. Morphological characteristics such as fruit shape, fruit base (cavity at stem end) and fruit apex were observed by matching the fresh fruit with the shapes of the fruits available in the descriptor of NBPGR (Mahajan et al. 2002), and guidelines for DUS testing of PPV and FRA (Anonymous, 2016).

The TSS of fresh fruits were determined at room temperature using hand refractometer having a range of 0 to 32 °Brix (ERMA made) by putting a drop of fresh fruit juice on the screen and recorded the readings. The refractrometer was calibrated with distilled water after every use and the values were expressed in degree Brix (°B). The method suggested by A.O.A.C. (2000) was followed for estimation of titratable acidity. Diluted aonla extract was titrated against 0.1 N sodium hydroxide using phenolphathlein indicator. The TSS: acid ratio was calculated by dividing total soluble solids with percentage acidity. Fresh aonla juice was diluted with equal amount of meta-phosphoric acid and titrated rapidly with indo-phenol dye to estimate the ascorbic acid content. Similarly standard ascorbic acid solution and meta-phosphoric acid (blank) solution titrated against the indo-phenol dye (A.O.A.C., 2000). To calculate total fruit yield, the harvested fruits were weighed on the digital electric balance for each replication and the value was expressed in kilograms (kg/plant). Total yield per plant was divided by area or volume of the plant to calculate the yield per unit canopy area or volume.

The data presented in this manuscript are the average values of different parameters. The statistical method described by Panse and Sukhatme (1985) was followed for analysis and interpretation of the experimental results. In order to evaluate comparative performance of the various treatments, the data were analyzed by the technique of analysis of variance described by Fisher (1958). All the tests of significance were made at 5 per cent level of the significance. The data has been analysed using the statistical tool/ programme "*opstat*" developed by Sheoran et al. (1998), CCS HAU, Hisar. This tool is open for all and available on official website of CCS HAU, Hisar (www.hau.ac.in).

Results and Discussion

Varietal evaluation of aonla comprising of nine cultivars (NA 6, NA 7, NA 10, NA 20, Krishna, BSR 1, Gujarat 1, Chakaiya and CHES 1) was carried out for assessing the comparative performance of cultivar for growth and physicochemical characters under semi-arid conditions. Plant shape was observed as spreading (CHES 1, Chakaiya, Krishna, NA 6, NA 7, NA 10, BSR 1); drooping (NA 20) and upright (G1) in different cultivars of aonla. The maximum plant height (6.70 m), plant spread EW (7.15 m) and SW (7.53 m) and stem girth (95.37 cm) were recorded in Gujrat-1; followed by NA 6 with plant height (6.32 m) and Krishna with plant spread EW (6.58 m) and plant spread NS (6.46 m). Plant height was found minimum in Chakaiya (4.90 m). Minimum plant spread EW (4.47 m) and NS (4.44 m) was found in NA 7, whereas; stem girth (46.45 cm) in CHES 1. Maximum plant volume (283.9 m^3) was observed in G1, followed by Krishna (191.1 m^3) and minimum (86.8 kg/m^3) in NA 7. Plant canopy area was observes maximum (42.35 m^2) in G1 and minimum (15.98 m^2) in CHES 1. The variation in growth parameters such as plant shape, plant height, plant spread (EW &NS), stem girth, plant volume and plant canopy area might be due to the specific climatic requirement of the variety and the genetic makeup of the cultivar. Similar findings were recorded by Kumar et al. (2011).

Fruit shape was observed as flattened round (CHES 1, Chakaiya, NA 6, NA 10, G 1, BSR 1), triangular (Krishna), oval (NA 7) and round (NA 20). Free base (cavity at stem end) was observed as absent (CHES 1), shallow (Chakaiya, NA 6, NA 20, G 1), deep (Krishna), flat (NA 7, NA 10, BSR 1) and fruit apex was observed as flat (CHES 1, Chakaiya, Krishna, NA 7, NA 10, NA 20), papillate (NA 6, BSR 1), depressed (G 1). Maximum fruit weight (55.43 g) was recorded in NA 20 and minimum (5.89 g) in BSR 1. Maximum fruit length (3.33 cm) was recorded in NA 20 and fruit breadth (3.70 cm) in Chakaiya, whereas minimum fruit length (1.87 cm) and breadth (2.28 cm) were recorded in BSR 1. The results are in line with Singh et al. (2017) in their study on evaluation of aonla cultivars. The variability among the qualitative characters may be due to their different genetic makeup and it was also observed by Nagar et al. (2017) in bael. The variation among the growth parameters might be due to particular germplasm/ cultivar character. Increased fruit weight might be attributed to the character of genotype. The

weight and size of the fruits might be also related to the bearing habit and yield of that variety (Malshe et al. 2016). Similar kind of results in aonla was reported in past by Ghosh et al. (2013) in laterite soil of West Bengal.

The maximum TSS (18.32ºB) was recorded in BSR 1 being at par with G 1 (17.48ºB), whereas minimum TSS (9.17ºB) was recorded in NA 7. Maximum acidity (2.63%) was recorded in NA 10; which was at par with G 1 (2.48%) and minimum (1.92%) in NA 6. TSS: acid ratio was observed maximum (7.71) in BSR 1, followed by CHES 1 (7.34), however it was recorded minimum (4.09) in NA 7. Ascorbic acid was recorded maximum (567 mg/100g) in Chakaiya; followed by NA 7 (514 mg/100g) and minimum ascorbic acid (323 mg/100g) was recorded in BSR 1. The variation in the chemical constituent might be associated with the varietal characters and prevailing soil and climatic conditions in that locality (Malshe et al. 2016). Similar results were also observed by Singh et al. (2017) in aonla and Nagar et al. (2017) in bael.

Maximum yield per plant (102 kg) was recorded in NA 20; followed by NA 7 (90 kg) and minimum (36 kg) in BSR 1. Yield per unit plant volume was observed maximum (1.04 kg/m^3) in NA 7, however it was minimum (0.24 kg/m^3) in G1. Plant yield per unit canopy area was observes maximum (5.77 kg/ m^2) in NA 10 and minimum (1.56 kg/m^2) in BSR 1. The yield per unit volume was calculated to know the fruiting intensity on the plant and yield per unit canopy area was calculated to find out the variety suitable for increasing the yield with the increase the population pressure as well as adopting the variety suitable for more yields per unit area. The yield per plant and hectare was observed maximum (102 kg and 28.34 MT/ha) in NA 20, however, yield per unit canopy area (5.77 kg/m^2) as well as per unit plant volume (1.04 kg/m^3) was observed maximum in NA 7 because the planting was done at equal spacing but the plant spread EW and NS was observed less in NA 7. It means the plants of NA 7 can be recommended in high density planting.

Conclusions

The variety NA 7 can be recommended on the basis of yield per unit canopy area as well as yield per unit plant volume as it is the era of high density planting and land holding is also decreasing so this cultivar is having the capacity to produce more in reduced land holding. There is a more pressure of yields per unit area to meet out the demand of increasing population. However, fruit size and yield per ha was reported more in NA 20. Qualitative parameters such as TSS, acidity and ascorbic acids were found highest in BSR 1, NA 10 and Chakaiya, respectively. All the varieties were evaluated for different parameters so the breeder or grower can select as per their need.

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Table 1. Physiochemical properties of the soil of aonla orchard.

Soil Type:	Loamy Sand
Salt 1: 2 (dSm-1)	0.19
Organic carbon (%)	0.25
Available phosphorus (kg/ha)	13.6
Available potas (kg/ha)	192

Table 2. Plant growth parameters of aonla cultivars (average data 2017-18, 2018-19, 2019-20).

Cultivars	Plant Shape	Plant Height (m)	Plant Spread-EW (m)	Plant Spread-NS (m)	Stem Girth (cm)	Plant Volume (m^3)	Plant Canopy Area (m^2)
CHES 1	Spreading	5.69	4.58	4.44	46.45	90.9	15.98
Chakaiya	Spreading	4.90	5.57	5.88	59.76	126.1	25.74
Krishna	Spreading	5.72	6.58	6.46	62.91	191.1	33.40
NA 6	Spreading	6.32	5.56	5.85	67.06	161.5	25.56
NA 7	Spreading	5.56	4.47	4.44	54.56	86.8	15.59
NA 10	Spreading	5.95	5.40	5.53	59.23	139.8	23.48
NA 20	Drooping	6.30	5.81	6.07	78.62	174.6	27.72
G 1	Upright	6.70	7.15	7.53	95.37	283.9	42.35
BSR 1	Spreading	5.30	5.28	5.56	46.96	122.4	23.08
CD (P=0.05)	--	0.39	0.97	1.02	4.32	14.6	1.50
Range	--	4.90-6.70	4.47-7.15	4.44-7.53	46.45-95.37	86.8-283.9	15.59-42.35

EW=East-West, NS=North-South

Table 3. Morphological and physical characteristics of aonla germplasm under semi–arid conditions of Haryana (average data 2017-18, 2018-19, 2019-20).

Germplasm	Fruit Shape	Fruit Base (Cavity at stem end)	Fruit Apex	Fruit Weight (g)	Fruit Length (cm)	Fruit Breadth (cm)
CHES 1	Flattened round	Absent	Flat	15.36	2.43	2.94
Chakaiya	Flattened round	Shallow	Flat	35.47	3.28	3.70
Krishna	Triangular	Deep	Flat	27.82	3.18	3.47
NA 6	Flattened round	Shallow	Papillate	29.89	3.12	3.40
NA 7	Oval	Flat	Flat	28.06	3.31	3.43
NA 10	Flattened round	Flat	Flat	21.99	2.95	3.24
NA 20	Round	Shallow	Flat	55.43	3.33	3.51
G 1	Flattened round	Shallow	Depressed	13.80	2.46	2.84
BSR 1	Flattened round	Flat	Papillate	5.89	1.87	2.28
CD (P=0.05)	--	--	--	4.35	0.33	0.32
Range	--	--	--	5.89-55.43	1.87-3.33	2.28-3.70

Table 4. Physico-chemical parameters of aonla cultivars (average data 2017-18, 2018-19, 2019-20).

Cultivars	TSS (°B)	Acidity (%)	TSS: Acid Ratio	Ascorbic Acid (mg/100g)	Yield/Plant (kg/plant)	Yield (MT*/ha)	Yield (kg /m^3)	Yield (Kg/m^2)
CHES 1	15.05	2.05	7.34	443	48.67	13.52	0.54	3.05
Chakaiya	10.56	2.34	4.51	567	70.00	19.45	0.56	2.72
Krishna	10.62	2.19	4.85	494	65.33	18.15	0.34	1.96
NA 6	11.17	1.92	5.82	377	87.33	24.26	0.54	3.42
NA 7	9.17	2.24	4.09	514	90.00	25.00	1.04	5.77
NA 10	14.19	2.63	5.40	473	83.33	23.15	0.60	3.55
NA 20	13.04	2.24	5.82	453	102.00	28.34	0.58	3.68
G 1	17.48	2.48	7.04	427	68.67	19.08	0.24	1.62
BSR 1	18.32	2.38	7.71	323	36.00	10.00	0.29	1.56
CD (P=0.05)	0.92	0.28	0.55	14.2	9.0	2.0	0.85	0.52
Range	9.17-18.32	1.92-2.63	4.09-7.71	323-567	36-102	10.00-28.34	0.24-1.04	1.56-5.77

TSS=Total Soluble Solids, MT=Metric Tons

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Studies on the Seed Yield Performance of Isabgol (*Plantago ovata* Forsk) Elite Genotypes under Semi-Arid Conditions of Haryana

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ABSTRACT

A field experiment was conducted during the years 2016- 2017, 2017-18 and 2018-19 to evaluate the performance of 13 elite Isabgol genotypes for commercial cultivation under semi-arid conditions of Haryana at Research Farm of MAP Section, Department of Genetics and Plant Breeding CCS Haryana Agricultural University, Hisar. The results on the basis of mean performance over three years seed yield data of all 13 genotypes revealed that, the highest seed yield (kg/ha) was found in genotype HI-137 (307.89 kg/ha) and closely followed by HI-135 (307.86 kg/ha), which were significantly superior to all the genotypes. Some other genotypes like Niharika (290.82 kg/ha) and HI-133 (293.13 kg/ha) also produced good yield. Lowest seed yield was recorded in genotype HI-136 (189.94 kg/ha). On the basis of average of three years data, it is consolidated that the genotype, HI-135 had the longest spike (5.55 cm) followed by HI-131 (5.38 cm), HI-137 (5.26 cm) and HI-138 (5.16 cm). Likewise, HI-137 was also recorded the maximum number of florets/spike (47.71 florets/spike) closely followed by GI-2 (46.52 florets/spike), Niharika (46.11 florets/spike) and HI-135 (44.36 florets/spike). Under different environment conditions, the elite genotypes, HI-137 (307.89 kg/ha) and HI-135 (307.86 kg/ha) were able to perform better and were significantly superior to all other genotypes, therefore, these genotypes may be recommended for cultivation in semi-arid region of Haryana after further testing their preference over time and space.

Keywords: Isabgol, elite genotypes, and seed yield

Introduction

Allover the world, the demand and prices of different kind of medicinal plants have been increased several folds due to spread of COVID 19. The growing demand of medicinal plants makes them remunerative alternate crops to the traditional ones for marginal farmers. Suitable model for cultivation of medicinal plants need to be developed to optimize the production per unit area which help farmers in adopting commercial cultivation of medicinal and aromatic plants in a sustainable manner (Kirti and Arya**,** 2019).

Isabgol (*Plantago ovata* Forsk.) is one of the important and export potential medicinal plant of India, which is locally known as Isabgul, Issabagolu, Isakol, Isphagol, Ispaghol, Psyllium etc. Isabgol belongs to family Plantaginaceae. Isabgol is native to the Mediterranean region and West Asia extending up to Sutlaj and Sindh in West Pakistan. It is short stemmed plant which may grow upto 40 cm, highly cross pollinated winter season crop. It has alternative leaves having parallel venation. Its flowers are minute and white in colour. Its seeds are ovate and 1.8 to 3.8 mm long having brown grey colour and covered with two translucent membrane structures known as husk. The husk is the membranous covering of seeds, which may be white to brown grey light pink in colour. Isabgol husk has property of absorbing and retaining water (40-90%). The husk and seed are major products of Isabgol plant.

Isabgol seeds have 23.5% crude fibre, 8.7% protein, 50.65% carbohydrates and 6.85% ash, (Pendse et al. 1976). The outer seed coat contains hydrocolloidal polysaccharides i.e. mucilage, cellulose, fixedoil, tannin, aucubinglyvaside, sterols, starch, sugars and proteins etc. The mucilage of Isabgol is colloidal in nature which is composed ofxylose, galacturonic acid, arabinose, rhamnose and galactose (Salyers et al. 1978). In addition these, Isabgol seed contain amino acids i.e. valine, aniline, glutamic acid, glycine, cystine, lysine, leucine and tyrosine (Tyagi et al. 2016). Isabgol seeds husk is mild laxative, emmallient and demulcent, cooling, diuretic and used in inflammatory conditions of mucous membrane of gastro-intestinal and genital-urinary tract. It is also used in curing of chronic dysentery, diarrhea, duodenal ulcer, constipation and piles (Arya et al. 2021). It has hypoglycemic, anti-cancerous, antitoxic, hypotensive cardiac depressant,hypochloresteremic and cholinergic activities. In addition to these medicinal uses, it is also utilized in ice-cream/food industry, dyeing/ calico-printing as stabilizer. The dehusked seeds have nutritive value and are also used as birds/poultry and cattle feed (Tyagi, 2008).

It has ability to grow in a wide range of agro-climatic conditions, but it requires warm temperate regions cool and dry weather conditions for better growth and development of crop plants. The low rainfall areas with assured irrigation are best suited for its commercial cultivation. It needs 20°C temperatures for good seed germination. At flowering, the cloudy weather, mild dew or even light showers causes heavy shedding of flowers and seeds with intense losses in seed yield. Isabgol crop is generally able to grow in all type of soils, but the light and well drained sandy loam having pH 7-8 has been found more suitable for successful cultivation and seed production. Since, the crop is grown in the south-west region of Haryana and found successful to grow under sandy loam marginal lands and rained conditions; but, the identification of suitable elite genotypes, for these semi-arid conditions are major limiting factor for its cultivation. Keeping the above points in view, the present study was carried to evaluate the performance of Isabgol elite genotypes in order to identify superior genotypes for seed yield under semi-arid conditions of Haryana.

Materials and Methods

To conduct the field experiment, 13 newly developed elite genotypes of Isabgol (*Plantago ovata* Forsk.) were grown in RBD during winter 2016-17, 2017-18 and 2018-19 at Research Farm of MAP Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar located 29°10'N latitude and 75°46'E longitude with an elevation of 215.2 m above the mean sea level. The plot size was kept 4.0 x 1.2 m^2 with spacing 30x10 cm^2. The soil of experimental site was sandy loam, medium in available nitrogen (141.0 kg/ha), available phosphorus (14.0 kg/ha), available potassium (240.0 kg/ha)and organic carbon (0.46%). Weekly weather parameters data recorded from research area during winter 2016-17,2017-18 and 2018-19 given in Fig. 1, 2 and 3. Each elite genotype was planted in four rows of four meter length spacing 30 cm apart. All the recommended package of practices was followed to raise a good healthy crop. The observations on different morphological and yield attributing eight characters viz. plant height (cm), number of leaves, number of branches, length of spike, number of spikes, number of florets, days to maturity, seed yield (kg/ha) were recorded from five randomly selected plants from each replications. The data was subjected to statistical analysis as per standard procedure.

Results and Discussion

The mean performance of 13 elite genotypes of Isabgol for all the eight characters recorded during winter 2016-17, 2017-18 and 2018-19 presented in Tables 1-4. The analysis of variance showed significant variation among the different genotypes for all the characters during 2016-17 and 2017-18 except for length of spike (cm), and during 2018-19 except for plant height (cm), number of branches/plant, length of spike (cm), number of spikes/plant, number of florets/spike.

Plant height

The data (Table 1) revealed that amongst 13 elite genotypes under present investigation, for plant height, during 2016-17, Niharika was the tallest with 35.24 cm plant height followed by HI-138(34.80 cm), HI-131 (34.68 cm), GI-2 (33.79 cm) and HI-133 (33.78 cm). During 2017-18, HI-133 was the tallest with 37.00 cm followed by GI-2 (36.78 cm), Niharika (36.44 cm) HI-138(35.78 cm) and HI-2009 (35.78 cm). During 2018-19, HI-131 was the tallest with 38.33 cm followed by HI-133 (37.60 cm), GI-2 (37.60 cm), HI-138 (37.20 cm) and HI- 5(37.20 cm). On an average basis over the three years data revealed that the genotype, HI-133 was tallest (36.13 cm) and followed by GI-2 (36.06 cm), HI-131(36.04 cm) and Niharika (35.98 cm). The variable results might be due to genetic constituents of genotypes and variation in agro-climatic conditions during different years. The mean performances between various genotypes in Isabgol for different characters have also been reported earlier (Tyagi et al. 2016).

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Number of leaves per plant

For number of leaves per plant (Table 1), during 2016-17, the maximum number of leaves per plant (94.01) was exhibited in HI-2009 followed by HI-137 (91.58 leaves/plant), HI-133 (87.68 leaves/plant), and HI-134 (85.90 leaves/plant). However, during 2017-18, HI-134 revealed the maximum number of leaves per plant (85.11) followed by HI-133 (82.00 leaves/plant), JI-4 (80.56 leaves/plant) HI-131(74.44 leaves/plant) and Niharika (74.44 leaves/plant). Likewise, during 2018-19, HI-134 was having the maximum number of leaves per plant (84.80 leaves/plant) followed by HI-133(84.50 leaves/plant), JI-4 (78.95 leaves/plant) and HI-131(75.00 leaves/plant). On an average basis over the three years revealed that the genotype, HI-134 was found with maximum number of leaves per plant (85.27 leaves/plant) and closely followed by HI-133 (84.73 leaves/plant), and HI-2009 (80.89 leaves/plant).

Number of branches per plant

The results are presented in Table 2 for number of branches per plant during 2016-17, the maximum number of branches per plant (7.53) was exhibited in HI-133 followed by JI-4 (7.30 branches/plant), HI-132 (6.90 branches/plant), and HI-5 (6.88 branches/plant). However, during 2017-18, HI-5 revealed the maximum number of branches per plant (5.56) followed by HI-131 (5.33 branches/plant), HI-2009 (5.22 branches/plant) and HI-133 (5.11 branches/plant). Likewise, during 2018-19, Niharika was having the maximum number of branches per plant (6.87 branches/plant) followed by HI-135 (6.80 branches/plant) and JI-4 (6.80 branches/plant) and HI-134 (6.67 branches/plant). The average of data over the three years reflected that the genotype, HI-133 and HI-5 were found with maximum number of 6.32 branches per plant followed by JI-4 (6.26 branches/plant), and HI-2009 (6.06 branches/plant). In a similar study, Tyagi et al. (2016) reported the maximum seven numbers of branches per plant in Palampur-2 and HI-4.

Length of spike

The data of 2016-17 presented in Table 2 for length of spike revealed that, the genotype HI-134 exhibited longest spike with 5.30 cm followed by HI-135 (5.22 cm), HI-137 (5.18 cm) and HI-2009 (5.15 cm). However, during 2017-18, HI-135 revealed the longest spike (5.73 cm) followed by HI-131 (5.54 cm), HI-137 (5.31cm), HI-133 (5.26) and HI-138(5.26). Likewise, during 2018-19, HI-135 was having the longest spike with 5.70 cm followed by HI-131(5.50 cm), HI-137 (5.29 cm) and HI-138(5.27 cm). On the basis of average of three years data, it is consolidated that the genotype, HI-135 had the longest spike (5.55 cm) followed by HI-131 (5.38 cm), HI-137 (5.26 cm) and HI-138 (5.16 cm). The mean performances between various genotypes of Isabgol for different characters have also been supported by earlier findings (Hendry and Daulay, 1992).

Number of spikes/plant

For number of spikes/plant during 2016-17, the maximum number of spikes/plant (35.57) was exhibited in HI-2009 followed by HI-136 (35.34 spikes/plant), HI-133 (34.55 spikes/plant), and HI-137 (32.68 spikes/plant). Likewise, during 2017-18, HI-2009 revealed the maximum number of spikes/plant (42.22) followed by HI-138 (40.44 spikes/plant), HI-133 (38.56 spikes/plant) GI-2 (37.22 spikes/plant) and HI-131 (36.78 spikes/plant). However, during 2018-19, HI-138 was having the maximum number of spikes/plant (38.87 spikes/plant) followed by HI-131 (38.53 spikes/plant), HI-2009 (36.13 spikes/plant) and HI-133 (36.00 spikes/plant). The mean performance over the three years revealed that the genotype, HI-2009 was found with maximum number of spikes/plant (37.97) and closely followed by HI-133 (36.37 spikes/plant), HI-138 (35.70 spikes/plant) and HI-131 (35.00 spikes/plant). In another study, Tyagi et al. (2016) observed the maximum number of spike per plant was for Gummary (38.8) followed by HI-2009 (36.9) and Palampur-2 (36.0), respectively.

Number of florets/spike

It is evident from Table 3 for number of florets/spike during 2016-17, that the maximum number of florets/spike (52.62) was exhibited in GI-2 followed by Niharika (51.23 florets/spike), HI-138 (51.12 florets/spike), and HI-137 (50.35 florets/spike). However, during 2017-18, HI-137 revealed the maximum number of florets/spike (53.61) followed by GI-2 (49.94 florets/spike), Niharika (48.61 florets/spike) HI-2009 (47.22 florets/spike) and HI-135 (46.61 florets/spike). However, during 2018-19, HI-5 was having the maximum number of florets/spike (39.42 florets/spike) followed by HI-137 (39.17 florets/spike), HI-135 (38.67 florets/spike) and Niharika (38.50 florets/spike).The mean performance over the three years revealed that the genotype, HI-137 was found with maximum number of florets/spike (47.71 florets/spike) and closely followed by GI-2 (46.52 florets/spike), Niharika (46.11florets/spike) and HI-135 (44.36 florets/spike).

Days to maturity

In 2016-17, days taken to maturity were earliest (119.33) in the genotypes HI-131 and HI-132 followed by GI-2 (120.00 days), HI-138(120.00 days)and HI-5 (120.00 days). The genotypes HI-136 (129.33 days) and HI-137 (128.33 days) were late in maturity. In 2017-18, the earliest maturing genotype was HI-138

(121.67 days) followed by HI-137 (124.67 days) and GI-2 (125.33 days), while the genotypes HI-136 (129.33 days) and HI-133(129.00 days) were late in maturity. In 2018-19, the earliest maturing genotype was GI-2 with 119.00 maturity days, followed by HI-132 (120.33 days), HI-131(122.00 days) and HI-138 (122.33 days), while the genotypes HI-136 (128.33 days) and HI-135 (127.00 days) were late in maturity. The averages of the three years data on maturity revealed that the genotype, HI-138 was earliest in maturity and have average maturity 121.33 maturity days, closely followed by GI-2 (121.33 days), HI-132 (122.66 days) and HI-131(123.22 days). While the genotype HI-136 (129 days), HI-135 (126.44 days) and HI-137 (126.33 days) were late in maturity. The variation in maturity might be due to individual varietal characters and also influenced by environmental factors prevailing during cropping season. Tyagi et al. (2016) identified HI-32 (60.3 days) followed by HI-4 (60.6 days), HI-96 (60.6 days) as early maturing genotypes.

Seed yield (kg/ha)

It is revealed from Table 4 that the environment of year 2017-18 was most favourable for seed production followed by 2018-19 and 2016-17. During 2016-17, the seed yield (kg/ha) varied from 145.80 - 340.30 kg/ha. The highest seed yield (kg/ha) was found in genotype HI-5 (340.30 kg/ha), which was significantly superior to all the genotypes. Some other genotypes like HI-133 (304.20 kg/ha) and HI-2009 (286.10 kg/ha) also produced somewhat higher yield. But significantly lowest seed yield kg/ha was recorded in HI-137 (145.80 kg/ha). However, during 2017-18, the seed yield (kg/ha) varied from 194.44 -407.87 kg/ha. The highest seed yield (kg/ha) was found in genotype HI-137 (407.87 kg/ha), followed by HI-135(402.77 kg/ha) which were significantly superior to all the other genotypes. Some other genotypes like Niharika (312.26 kg/ha) and HI-133 (302.74 kg/ha) also produced somewhat higher yield, however, lowest seed yield was recorded in JI-4 (194.44 kg/ha). Similarly, during 2018-19, the seed yield (kg/ha) varied from 180.00 -370.00 kg/ha. On the basis of mean performance over three years data, the highest seed yield (kg/ha) was found in genotype HI-137 (307.89 kg/ha) and closely followed by HI-135 (307.86 kg/ha), which were significantly superior to all the genotypes. Some other genotypes like HI-133 (293.13 kg/ha) and Niharika (290.82 kg/ha) also produced somewhat higher yield. But, significantly lowest seed yield kg/ha was recorded in HI-136 (189.94 kg/ha). Tyagi et al. (2016) reported the seed yield/plant variation from 2.011 to 5.650 g/plant. They found highest seed yield/plant in Palampur-2 (5.650 g), MPI- 1 (5.141 g), Gummary (4.814 g), DM-11 (4.659 g), DM-10 (4.436 g) and GI-2 (4.413 g). The higher yield of elite genotypes might be due to higher number of branches, which leads to the production of more number of spike per plant that directly affect the production of higher seed yield. An addition this, number of florets/spike may also contributed to higher seed. The findings were also supported by Beniwal et al. (2007); Jadhav et al. (2008); Barfa et al. (2011) and Tyagi et al. (2016).

Today, entire world is concerned about the impact of climate change on plants. In the last two centuries, climate change has been taking place so rapidly that certain plant species have found it hard to adapt. The climate change will have dramatic consequences for crops. The effect of climate on agriculture is related to variability's in local weather parameters rather than in global climate patterns (Arya et al. 2020). Therefore, evaluation of promising genotypes over the year are required to know the consistency in their performance over the environments. Consistently good performance over a range of environments must be one of the important criteria while evaluating any genotype or variety, particularly in a country like India, where great variations occur in environmental conditions (Arya et al. 2010; Kant et al. 2014). The widespread cultivation of the crop all along the globe is largely due to high versatility of genome which enables its adaptation to different agro-climatic conditions (Preeti et al. 2016). Under different environment conditions, the elite genotypes, HI-137 (307.89 kg/ha) and HI-135 (307.86 kg/ha) were able to perform highest seed yield (kg/ha) and were significantly superior than all other genotypes, therefore, these genotypes may be recommended for cultivation in semi-arid reason of Haryana after further testing their preference over time and space.

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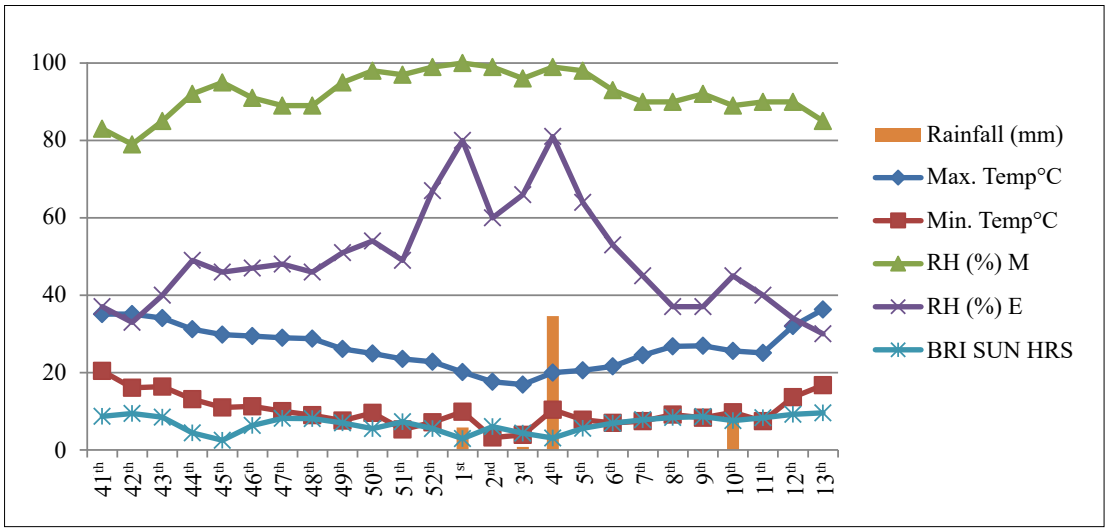

Figure 1.Weekly weather parameters data recorded at Hisar location during 2016-17.

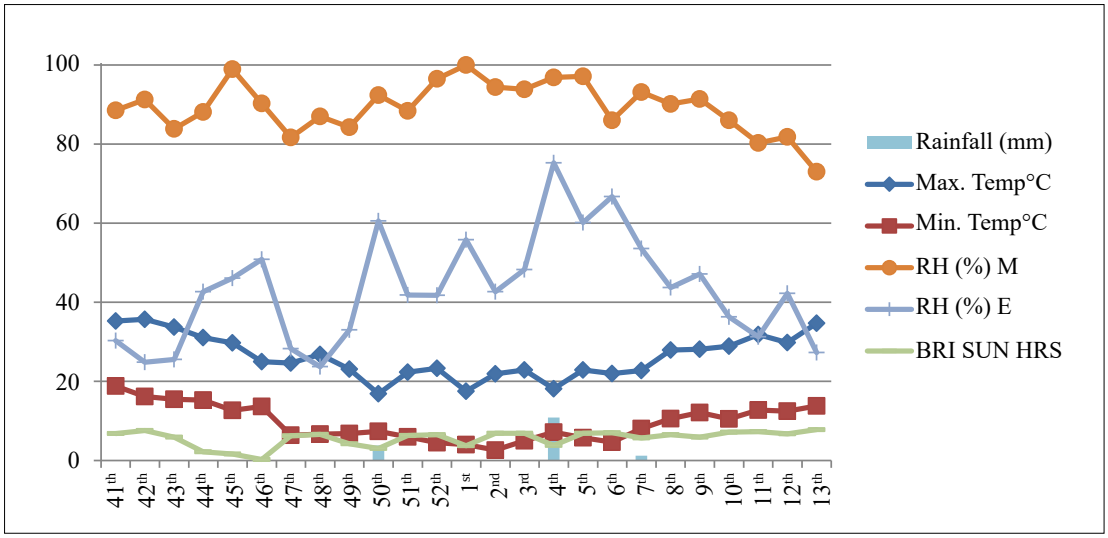

Figure 2. Weekly weather parameters data recorded at Hisar location during 2017-18.

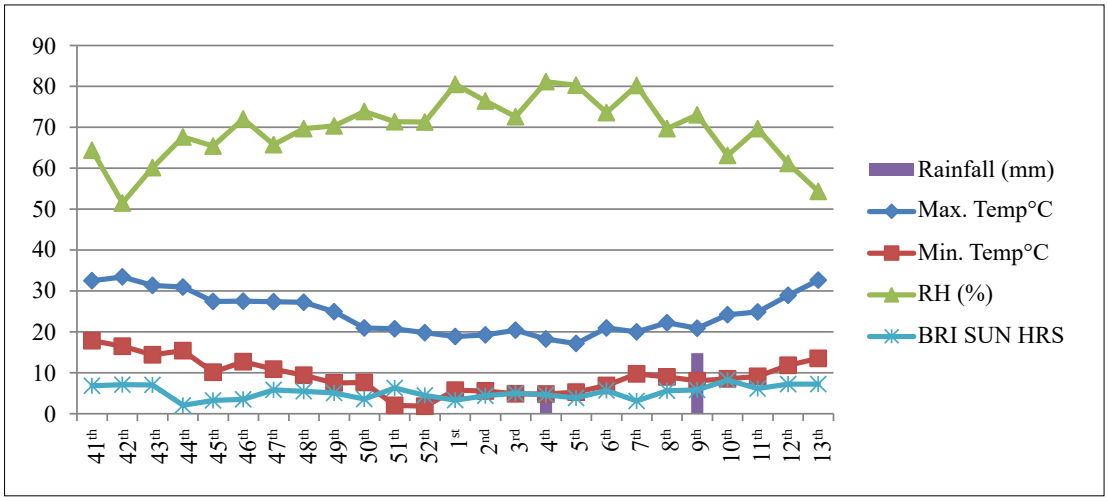

Figure 3. Weekly weather parameters data recorded at Hisar location during 2018-19.

Table 1. Mean performance of elite genotypes of Isabgol for plant height (cm) and number of leaves/plant.

No.	Genotypes	Plant Height (cm)				Number of Leaves/Plant			
		2016-17	2017-18	2018-19	Mean	2016-17	2017-18	2018-19	Mean
1	HI-131	34.68	35.11	38.33	36.04	71.11	74.44	75.00	73.52
2	HI-132	31.11	33.89	35.53	33.51	73.89	64.11	64.75	67.58
3	HI-133	33.78	37.00	37.60	36.13	87.68	82.00	84.50	84.73
4	HI-134	32.80	33.89	35.60	34.10	85.90	85.11	84.80	85.27
5	HI-135	32.91	34.89	36.33	34.71	72.44	68.44	70.33	70.40
6	HI-136	26.51	32.00	34.13	30.88	80.34	68.33	68.00	72.22
7	HI-137	27.03	35.44	35.87	32.78	91.58	70.11	74.33	78.67
8	HI-138	34.80	35.78	37.20	35.93	80.03	66.89	65.09	70.67
9	HI-2009	33.78	35.78	34.53	34.70	94.01	74.22	74.44	80.89
10	GI-2	33.79	36.78	37.60	36.06	72.45	71.33	70.00	71.26
11	JI-4	33.01	34.78	34.27	34.02	77.47	80.56	78.95	78.99
12	HI-5	33.45	35.56	37.20	35.40	80.45	66.94	70.25	72.55
13	Niharika	35.24	36.44	36.27	35.98	76.22	74.44	72.67	74.44
	Mean	**32.53**	**35.18**	**36.19**	**34.63**	**80.27**	**72.84**	**74.00**	**75.70**
	Range	26.51-35.24	32.00-37.00	34.13-38.33	30.88 -36.13	71.11-94.01	64.11-85.11	64.75-84.80	67.58-85.27
	CD (5%)	2.03	1.72	NS	-	4.24	6.04	6.77	-

Table 2. Mean performance of elite genotypes of Isabgol for number of branches/plant and length of spike (cm).

No.	Genotypes	Number of Branches/Plant				Length of Spike (cm)			
		2016-17	2017-18	2018-19	Mean	2016-17	2017-18	2018-19	Mean
1	HI-131	6.00	5.33	6.60	5.98	5.09	5.54	5.50	5.38
2	HI-132	6.90	4.89	6.27	6.02	4.43	4.96	5.00	4.80
3	HI-133	7.53	5.11	6.33	6.32	4.77	5.26	5.25	5.09
4	HI-134	6.43	4.56	6.67	5.89	5.30	4.90	4.89	5.03
5	HI-135	6.30	4.89	6.80	6.00	5.22	5.73	5.70	5.55
6	HI-136	5.33	4.11	6.00	5.15	5.06	4.98	5.00	5.01
7	HI-137	6.43	4.56	5.73	5.57	5.18	5.31	5.29	5.26
8	HI-138	5.63	4.89	6.27	5.60	4.95	5.26	5.27	5.16
9	HI-2009	6.57	5.22	6.40	6.06	5.15	4.82	4.85	4.94
10	GI-2	6.43	3.89	5.73	5.35	4.67	4.88	4.83	4.79
11	JI-4	7.30	4.67	6.80	6.26	4.05	4.81	4.80	4.55
12	HI-5	6.88	5.56	6.53	6.32	3.94	4.89	4.91	4.58
13	Niharika	6.00	5.00	6.87	5.96	4.95	4.79	4.79	4.84
	Mean	**6.44**	**4.82**	**6.38**	**5.88**	**4.83**	**5.09**	**5.08**	**5.00**
	Range	5.33- 7.53	4.11- 5.56	5.73-6.87	-	3.94-5.18	4.79 - 5.73	4.79 -5.70	4.55 -5.55
	CD (5%)	1.23	0.87	NS	-	1.54	NS	NS	-

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Table 3. Mean performance of elite genotypes of Isabgol for number of spikes/plant and number of florets/spike.

No.	Genotypes	Number of Spikes/Plant				Number of Florets/Spike			
		2016-17	2017-18	2018-19	Mean	2016-17	2017-18	2018-19	Mean
1	HI-131	29.68	36.78	38.53	35.00	43.72	43.89	33.58	40.40
2	HI-132	31.68	31.56	34.60	32.61	47.89	43.06	35.58	42.18
3	HI-133	34.55	38.56	36.00	36.37	46.63	45.61	38.00	43.41
4	HI-134	30.23	26.33	32.13	29.56	46.51	44.28	38.25	43.01
5	HI-135	32.01	30.56	31.00	31.19	47.79	46.61	38.67	44.36
6	HI-136	35.34	30.67	29.47	31.83	47.22	46.11	37.67	43.67
7	HI-137	32.68	30.22	30.67	31.19	50.35	53.61	39.17	47.71
8	HI-138	27.79	40.44	38.87	35.70	51.12	44.22	34.67	43.34
9	HI-2009	35.57	42.22	36.13	37.97	48.75	47.22	32.42	42.80
10	GI-2	29.55	37.22	34.00	33.59	52.62	49.94	37.00	46.52
11	JI-4	26.35	21.00	30.40	25.92	43.63	45.22	33.83	40.89
12	HI-5	29.33	32.89	35.00	32.41	46.23	44.83	39.42	43.49
13	Niharika	28.79	33.44	35.00	32.41	51.23	48.61	38.50	46.11
	Mean	**31.04**	**33.22**	**33.98**	**32.75**	**47.98**	**46.40**	**36.67**	**43.68**
	Range	26.35-35.57	21.00-42.22	29.47-38.87	29.56-37.97	43.63-52.62	44.22-53.61	32.42-39.42	40.89-47.71
	CD (5%)	2.86	3.26	NS	-	3.78	2.43	NS	-

Table 4. Mean performance of elite genotypes of Isabgol for days to maturity and seed yield (kg/ha).

No.	Genotypes	Days Tomaturity				Seed Yield (kg/ha)			
		2016-17	2017-18	2018-19	Mean	2016-17	2017-18	2018-19	Mean
1	HI-131	119.33	128.33	122.00	123.22	205.60	282.37	255.33	247.77
2	HI-132	119.33	128.33	120.33	122.66	205.60	233.79	210.50	216.63
3	HI-133	121.33	129.00	124.00	124.78	304.20	302.74	272.44	293.13
4	HI-134	122.33	126.33	125.00	124.55	183.30	223.15	200.80	202.42
5	HI-135	125.00	127.33	127.00	126.44	158.30	402.77	362.50	307.86
6	HI-136	129.33	129.33	128.33	129.00	188.90	200.92	180.00	189.94
7	HI-137	128.33	124.67	126.00	126.33	145.80	407.87	370.00	307.89
8	HI-138	120.00	121.67	122.33	121.33	219.40	282.40	254.00	251.93
9	HI-2009	120.67	128.67	123.00	124.11	286.10	281.94	253.75	273.93
10	GI-2	120.00	125.33	119.00	121.44	231.90	225.00	202.50	219.80
11	JI-4	121.33	126.33	124.00	123.89	213.90	194.44	250.45	219.60
12	HI-5	120.00	127.33	125.00	124.11	340.30	263.89	237.50	280.56
13	Niharika	124.00	127.00	125.33	125.44	279.20	312.26	281.00	290.82
	Mean	**122.38**	**126.90**	**123.95**	**124.41**	**227.90**	**277.96**	**250.47**	**252.11**
	Range	119.33-129.33	121.67-129.33	119.00-128.33	121.33-129.00	145.80-340.30	194.44-407.87	180.00-370.00	189.94-307.89
	CD (5%)	1.63	1.36	1.41	-	31.48	36.05	35.17	-

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Released Varieties

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Registration of "NKU Lider" Bread Wheat (*Triticum aestivum* L.) Variety

NKU Lider is a winter bread wheat (*Triticum aestivum* L.) variety, developed by Tekirdağ Namık Kemal University, Agricultural Faculty and registered in 2016. The spike of the NKU Lider variety is moderately long and dense, white, and awned. Grain is oval, semi hard and red color. NKU Lider is a medium-tall variety, similar to Flamura 85 and Tekirdağ bread wheat varieties. Plant height is between 85 and 90 cm depending on the growing conditions. NKU Lider variety is a winter type, medium-early, resistant to winter hardiness, good tolerant to drought, high ability of tillering and trashing, and since its wide adaptability, it can be grown safely not only in the Thrace-Marmara Region, but also in other wheat production areas of our country.

NKU Lider variety is tolerant to powdery mildew (*Erysiphe graminis* f. sp. *tritici*) and to stripe rust (*Puccinia striiformis* f. sp. *tritici*) and mild-sensitive to leaf rust (*Puccinia triticina*). It shows high yield stability ranging from 6.3-8.5 t ha^{-1} in Thrace Region, however if environmental conditions are appropriate and agronomic applications are apply well, it has the ability to increase grain yield even more. Suggested sowing rate is 500 seeds m^2. Depending on the soil type and structure and soil analysis results, it is recommended to apply phosphorus 60-70 kg ha^{-1} and nitrogen 150-160 kg ha^{-1}.

Bread-making quality of variety, NKU Lider is good. The mean values of some grain qualities of the official variety testing experiment are; test weight 76-79 kg hl^{-1}, thousand kernel weight 39-40 g, protein content 13-14%, water absorption 58-62%, Zeleny sedimentation 50-70 ml, alveograph energy value (W) 179-307 joule and flour yield 65-72%.

Pre-Basic and Basic seeds of the NKU Lider variety have been produced by Tekirdağ Namık Kemal University, Agricultural Faculty. Certified seed of the NKU Lider variety are produced by a private seed company.

Figure 1. (a) Spike and (b) grain of the NKU Lider variety. (Original)

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Registration of "MASS 1001" Tomato (*Solanum lycopersicum* L.) Variety

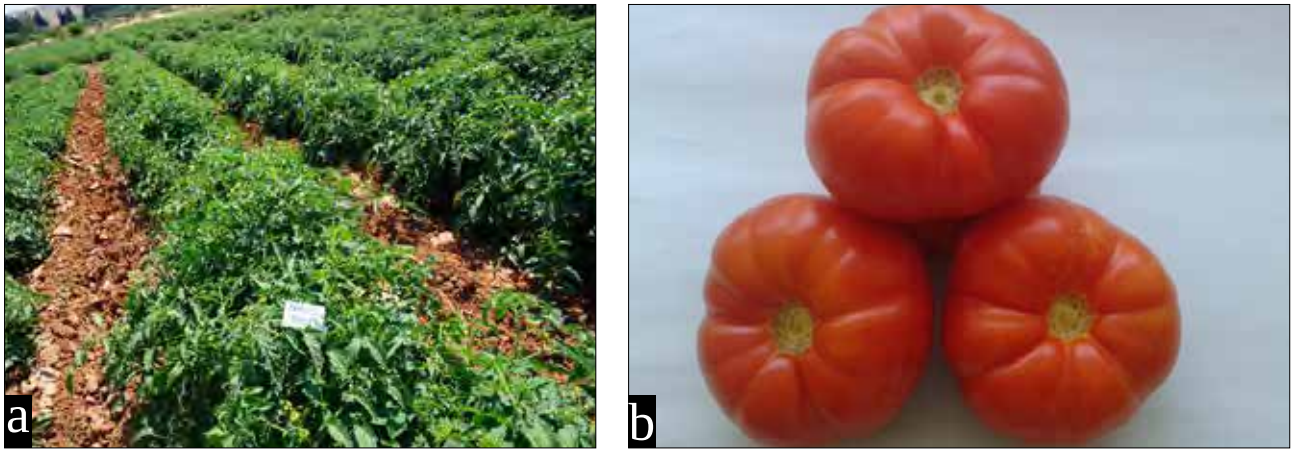
MASS 1001 is tomato (*Solanum lycopersicum* L.) variety developed by Aegean Agricultural Research Institute (AARI) and registered in 2018. It was obtained by crossing the pure tomato lines that selected from local populations in the gene pool of AARI. Tomato breeding program has been carried out in the institute for many years and lots of tomato varieties have been developed.

MASS 1001 is mid-season variety and recommended for commercial cultivation in open field areas. It has strong plants and high adaptability. Its plant growth type is determinate and its leaves properly cover the fruits.

MASS 1001 is a large sized red hybrid tomato variety, in other words a beef tomato or beef steak tomato is one of the largest varieties in Turkey. The average fruit weight of this variety is 400-500 g, and fruit shape in longitudinal section is flattened. The number of locules are also more than six. Because of very large fruit size, depression at peduncle end is strong, size of peduncle scar is broad, size of blossom scar is very large, shape at blossom end is intended to flat, and diameter of core in cross section in relation to total diameter is broad. In addition to this, abscission layer on peduncle is present and ribbing at peduncle end is medium.

MASS 1001, which stands out in terms of taste, and it will be a new flavor for beef type tomato lovers, also suitable for kitchen gardeners as well as market growers. Finally, it is recommended for all tomato growing areas, and the seeds of the hybrid MASS 1001 have been produced by AARI.

Figure 1. Picture showing (a) plants and (b) fruit shape of MASS 1001 variety. (Original)



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Registration of "Onur01" Chickpea (*Cicer arietinum* L.) Variety

Onur01 is a chickpea (*Cicer arietinum* L.) new variety, developed and registered in 2019 by Eastern Mediterranean Agricultural Research Institute (EMARI) of Turkey. The variety is well adopted to winter and early spring conditions of Mediterranean, Aegean and South East Anatolia Region of Turkey. "Selection Breeding Method" was used to develop this variety, in which a single plant was selected from local population as a source material.

Plant is well adopted to mechanised harvesting due to its erect growth habit, having 35-75 cm plant height and 9-34 cm first pod height. Time to flowering is 61-115 days and time to physiological maturity is 106-180 days. Grain is light-beige colored and round shaped which has 36-53g 100-grain weight. Water absorption capacity is 1.09-1.19 ml/grain; Water absorption index is 1.05-1.10%; Swelling index is 2.34-2.58%; Eight mm sieve value is 50.8-51.8%; Protein ratio is 23-24%. Time requirement for cooking is 45-57 minutes.

Onur01 yield potential is high however; high yield can be obtained, if environmental conditions are favorable and good agronomic practices are applied. Average grain yield of variety under field tests was recorded 2.5 t/ha with tolerance to Ascochyta blight.

Figure 1. Pictures showing (a) plant growth habit, (b) grain and (c) pod morphology of Onur01variety (Original).

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