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Genotypic basis response of fenugreek genotype grown under different levels of salinity stress

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Abstract

Salinity is one of the main factors responsible for deterioration and poor agricultural productivity in semi-arid and arid regions due to reducing seed germination and seedling establishment. An *in vitro* investigation was carried out at the Laboratory of Department of Plant Breeding and Genetics, Sri Karan Narendra College of Agriculture, Jobner (Rajasthan). This experiment was carried out to assess the genotypic response of ten fenugreek genotypes under different salinity levels using five levels of NaCl salinity *viz.* 0.0 mM, 40 mM, 80 mM, 120 mM and 160 mM. Fifteen seeds of each genotype were sown in sterilized Petridishes and seedling observations were recorded. The genotypes showed significant differences for most of the traits in each of the salinity level and pooled ANOVA exhibited significant differences among genotypes, both salinity levels as well as the interactions between genotype x salinity levels, indicating differential response of genotypes along the salinity gradients for most of the characters. Fenugreek showed moderately tolerant to salinity up to 40 mM NaCl, but varied in degree of salt tolerance as salinity increased, it affected by their seedling traits. The highest GCV and PCV values were observed in radicle fresh weight followed by plumule dry weight and radicle dry weight indicating that variation was high for these characters. Heritability in board sense was generally high for plumule and radicle fresh weight, plumule dry weight, radicle length, plumule to radicle length ratio and seedling length across the salinity levels. Hence, these high heritable traits would be rewarding for selection for better crop improvement programme. Mean value was recorded higher in the control and higher reduction at higher salinity level for most of traits *viz.*, plumule length, radicle length, seedling length, plumule to radicle length ratio, plumule fresh weight, radicle fresh weight, plumule dry weight, radicle dry weight and seedling vigour index. Over different salinity levels S1, S2, S3 and S4 (Sm) and characters, RMt-303, UM-385, RMt-143 and RMt-305 would be found desirable used for better seedling enhancement under salinity. These lines would be used for further crop breeding programme under this climate changing era.

Keywords: Salinity, fenugreek, genetic variability, seedling parameters

Introduction

Fenugreek (*Trigonella foenum-graecum* L.) is a self pollinated, small seeded, annual legume which belongs to family *fabaceae*. It has chromosome number $2n = 2x = 16$. This crop is native to an area extending from Iran to Northern India and widely cultivated in China, India, Egypt, Ethiopia, Morocco, Ukraine, Greece, Turkey, etc. In India, the major fenugreek growing states Rajasthan, Gujrat, Madhya Pradesh, Uttarakhand, Uttar Pradesh, Maharashtra, Haryana and Punjab. It is the third largest seed spice in India after coriander and cumin. India occupies a prime position among the fenugreek growing countries in the world. More than 70 percent area and production of the country is contributed by Rajasthan state alone. In India, the seeds are used in curries as spice for adding nutritive value and flavour, dyes and medicines. Fenugreek leaves and seeds are consumed for different purposes such as, medicinal uses (anti-diabetic, lowering blood sugar and cholesterol level, anti-cancer, anti-microbial, etc.), making food (stew with rice, flavour cheese, syrup and bitter run, mixed seed powder with flour for making flat bread, curries, dyes, young seedlings eaten as a vegetable etc.), roasted grain as coffee-substitute, controlling insects in grain storages, food and forage for cattle and in perfume industries. It is moderately tolerant to salinity which makes it suitable for cultivation in major parts of the state. Salinity is one of the most abiotic factors in arid and semi-arid regions in the world which adversely affected the crop yield due to limits the growth and production of crop. Seedling establishment is a most critical stage that determined the crop production at later stages. Phenotypic variability changes under different environmental conditions while genetic variability remains unchanged and more useful to a plant breeder for

exploitation in selection or hybridization. Heritability is a suitable measure for assessing the magnitude of genetic portion of total variability and genetic advance aids to make improvement in crop by selection for various characters. It is an index of transmissibility of a character from parents to their off springs. Thus, study of heritability coupled with genetic advance is more useful in predicting the resultant effect of selection.

Materials and Methods

The experiment including 10 genotypes and 5 NaCl concentrations was laid out in randomized block design (RBD) with three replications. Five treatments were used in experiment *viz.*, S₀, S₁, S₂, S₃ and S₄ (0, 40, 80, 120 & 160 mM NaCl). The present experiment was conducted to assess the genetic variability on seed germination and subsequent seedling growth of ten genotypes of fenugreek under salinity and effect of salinity on fenugreek. The germination was completed within 7 days of planting and germination was monitored 8th day from the day of seed planting. Observations were recorded on 8th day of planting on different morphological early seedling characters and parameters. Five seedlings were randomly selected from each petridish to record the data on plumule length, radicle length, seedling length, plumule to radicle length ratio, plumule fresh weight, radicle fresh weight, plumule dry weight, radicle dry weight and seedling vigour index.

Germination percentage

A seed was considered to be germinated at the emergence of both radicle and plumule up to 2 mm length (Chartzoulakis and Klapaki, 2000) [5]. The number of germinated seeds was recorded on 8th day of planting and the germination percentage was determined by using the following formula (Aniat *et al.*, 2012) [2]:

$$\text{Germination Percentage} = \frac{\text{Number of seeds germinated}}{\text{Total number of seeds sown}} \times 100$$

Plumule length (cm)

The plumule length of germinated seeds was recorded on 8th day of planting. Five seedlings from each petridish were randomly selected from each replication in each salinity level and each genotype. Then they were divided into two parts *viz.*, plumule and radicle. The plumule length (the distance from crown to leaf tip) was measured by using a measuring scale in centimeter and average was recorded. The hypocotyl length was also included in plumule length.

Radicle length (cm)

The radicle length (the distance from crown to root tip) was measured by using a measuring scale in centimeter from the same five seedlings which were selected previously from each replication and in each genotype and averaged.

Seedling length (cm)

The seedling length was derived by adding plumule length and radicle length of the same five seedlings which were selected previously from each replication and in each genotype and averaged.

Plumule to radicle length ratio

The plumule to radicle length ratio of seedling was calculated

by the following formula (Kagan *et al.*, 2010) [10].

$$\text{Plumule to Radicle Length Ratio} = \frac{\text{Plumule length}}{\text{Radicle length}}$$

Plumule fresh weight (mg)

The fresh weight of plumule from the same five seedlings from each replication and from each genotype was measured in milligram by using a sensitive electronic balance and averaged.

Radicle fresh weight (mg)

The fresh weight of radicle from the same five seedlings from each replication and from each genotype was measured in milligram by using a sensitive electronic balance and averaged.

Plumule dry weight (mg)

The plumules which were taken for fresh weight were kept into paper bags. The name of varieties and levels of salt solutions were written on paper bags by marker for further identification. After taking fresh weight of plumules these were kept in oven at 65°C for 48 hours for drying. After drying, the dried plumules were weighed by sensitive electronic balance in milligram and averaged.

Radicle dry weight (mg)

The radicles which were taken for fresh weight were kept into paper bags. The name of varieties and levels of salt solutions were written on paper bags by marker for further identification. After taking fresh weight of radicles these were kept in oven at 65°C for 48 hours for drying. After drying, the dried radicles were weighed by sensitive electronic balance in milligram and averaged.

Seedling vigour index

The seedling vigour index was determined by multiplying the sum total of mean length of plumule and radicle of a seedling with germination percentage of the respective seedling by the following formula (Iqbal and Rahmati, 1992) [9]:

$$\text{Seedling Vigour Index (SVI)} = (\text{RL} + \text{PL}) \times (\text{GP})$$

Where

RL= Mean radicle length

PL= Mean plumule length

GP= Germination percentage

Statistical analysis

The data obtained from this study were subjected to analysis of variance following standard statistical methods (Panse and Sukhatme, 1985) [13].

Pooled analysis of variance

Pooled analysis of variance was carried out to know the genotype x salinity level interaction.

Results

In this experiment analysis of variance was studied for each character separately in each salinity level and the results are presented in Table 1. Perusal of tables indicated that the genotypes indicated significant differences for all the characters in all the salinity levels (except germination

percentage in salinity level S_0 and S_1), this indicated inherent differences among the genotypes with the salinity levels.

The pooled analysis of variance exhibited significant differences among the genotypes and salinity levels for all the characters (Table 2). This showed that the genotypes responded linearly to the salinity levels. The genotype x salinity interaction indicated significant mean sum of squares for all the traits except for germination percentage. This significant mean sum of square indicated existence of differential response of genotypes under salinity levels.

Genetic Variability parameters

As the genotype x salinity interaction was significant for all the traits, the range, genotypic and phenotypic coefficients of variation, heritability in broad sense and genetic advance as percentage of mean were estimated in each salinity level separately and are presented in Table 3.

Germination percentage

Perusal of Table 3 showed that the germination percentage ranged from 91.11% (RMt-354) to 100% (RMt-1, RMt-303 and UM-385) in S_0 , 88.89% (RMt-1) to 97.78% (RMt-303) in S_1 , 82.22% (RMt-351) to 95.55% (RMt-305 and RMt-303) in S_2 and 80.00% (RMt-351) to 95.55% (RMt-305 and RMt-303) in S_3 , 75.55% (RMt-365 and UM-385) to 91.11% in S_4 salinity level. The range was wider in S_3 and S_4 as compared to S_0 , S_1 and S_2 salinity levels.

The estimates of phenotypic coefficient of variation (PCV) in general were higher than estimates of genotypic coefficient of variation (GCV) for all the salinity levels indicating predominant influence of salinity. The GCV was 4.37%, 4.90% and 5.57% in S_2 , S_3 and S_4 level, respectively. The PCV was 6.83%, 7.51% and 8.18% in S_2 , S_3 and S_4 level, respectively. The GCV, PCV, h^2 and GA was not determined for salinity level S_0 and S_1 due to non-significant difference between these genotypes. GCV and PCV increased with increasing salinity level. The GCV and PCV was maximum in S_4 (5.57 and 8.18, respectively).

Broad sense heritability estimates vary from one salinity level to the other. Heritability increased with increasing salinity level. It was 40.88%, 42.54% and 46.40%, in S_2 , S_3 and S_4 level, respectively. It was highest in S_4 salinity level.

Regarding genetic advance as percentage of mean, an increasing trend was observed with increase in salinity level. It was 5.75%, 6.58% and 7.82% in S_2 , S_3 and S_4 level, respectively. It was highest in S_4 salinity level.

Plumule length (cm)

This investigation revealed that the plumule length ranged from 5.71 cm (RMt-361) to 7.79 cm (UM-383) in S_0 , 6.51 cm (RMt-351) to 7.87 cm (UM-385) in S_1 , 5.07 cm (RMt-361) to 6.61 cm (UM-385) in S_2 , 3.40 cm (RMt-305) to 5.19 cm (RMt-143) in S_3 and 2.05 cm (RMt-305) to 3.20 cm (UM-383) in S_4 salinity level. The maximum range was observed in S_0 and minimum in S_4 salinity level.

The estimates of phenotypic coefficient of variation (PCV) in general were higher than estimates of genotypic coefficients of variation (GCV) in all the salinity levels indicating predominant influence of salinity. The GCV was 7.68%, 4.82%, 5.61%, 15.33% and 10.59% in S_0 , S_1 , S_2 , S_3 and S_4 level, respectively. The PCV was 9.59%, 7.53%, 9.44%, 16.52% and 12.52% in S_0 , S_1 , S_2 , S_3 and S_4 level, respectively. The variation was maximum in S_3 and minimum in S_1 .

Broad sense heritability estimates vary from one salinity level to the other. Heritability decreased with increasing salinity levels in S_0 , S_1 , S_2 and S_4 whereas it increased in S_3 . It was 64.10%, 40.89%, 35.28%, 86.10% and 71.56% in S_0 , S_1 , S_2 , S_3 and S_4 level, respectively. It was lowest in S_2 and highest in S_3 salinity level.

Regarding genetic advance as percentage of mean, an irregular trend was observed with increase in salinity level. It was 12.66%, 6.34%, 6.86%, 29.31% and 18.46% in S_0 , S_1 , S_2 , S_3 and S_4 level, respectively. It was lowest in S_1 and highest in S_3 salinity level.

Radicle length (cm)

This experiment revealed that the radicle length ranged from 3.67 cm (RMt-305) to 5.39 cm (UM-385) in S_0 , 3.47 cm (RMt-365) to 5.38 cm (RMt-143) in S_1 , 3.11 cm (UM-383) to 4.79 cm (RMt-143) in S_2 , 3.17 cm (RMt-365) to 4.51 cm (RMt-303) in S_3 and 2.29 cm (RMt-143) to 3.16 cm (RMt-303) in S_4 salinity level. The range was maximum in S_1 and minimum in S_4 salinity level.

The estimates of phenotypic coefficient of variation (PCV) in general were higher than estimates of genotypic coefficients of variation (GCV) in all the salinity levels indicating predominant influence of salinity. The GCV was 13.07%, 13.72%, 11.24%, 10.86% and 11.61% in S_0 , S_1 , S_2 and S_3 level, respectively. The PCV was 14.07%, 14.99%, 13.59%, 12.51% and 13.48% in S_0 , S_1 , S_2 , S_3 and S_4 level, respectively. The variation was maximum in S_1 and minimum in S_3 .

Broad sense heritability estimates vary from one salinity level to the other. Heritability exhibited irregular response with increasing salinity levels. It was 86.32%, 83.74%, 68.36%, 75.32% and 74.24% in S_0 , S_1 , S_2 , S_3 and S_4 level, respectively. It was lowest in S_2 and highest in S_0 salinity level.

Regarding genetic advance as percentage of mean, an irregular trend was observed with increase in salinity level. It was 25.01%, 25.86%, 19.14%, 19.41% and 20.61% in S_0 , S_1 , S_2 , S_3 and S_4 level, respectively. It was lowest in S_2 and highest in S_1 salinity level.

Seedling length (cm)

The seedling length ranged from 9.40 cm (RMt-361) to 13.12 cm (UM-385) in S_0 , 10.06 cm (RMt-361) to 12.21 cm (RMt-143) in S_1 , 8.49 cm (UM-383) to 10.93 cm (UM-385) in S_2 , 6.85 cm (RMt-305) to 9.67 cm (RMt-143 and RMt-303) in S_3 and 4.35 cm (RMt-305) to 6.01 cm (RMt-303) in S_4 salinity level. The range was maximum in S_0 and minimum in S_4 salinity level (Table 3).

The estimates of phenotypic coefficient of variation (PCV) in general were higher than estimates of genotypic coefficients of variation (GCV) in all the salinity levels indicating predominant influence of salinity. The GCV was 9.19%, 6.24%, 6.83%, 11.66% and 9.32% in S_0 , S_1 , S_2 , S_3 and S_4 level, respectively. The PCV was 10.04%, 7.48%, 8.97%, 12.37% and 10.59% in S_0 , S_1 , S_2 , S_3 and S_4 level, respectively. The variation was maximum in S_3 and minimum in S_1 (Table 3).

Broad sense heritability estimates vary from one salinity level to the other. Heritability exhibited irregular response with increasing salinity levels. It was 83.79%, 69.58%, 58.01%, 88.83% and 77.46% in S_0 , S_1 , S_2 , S_3 and S_4 level, respectively. It was lowest in S_2 and highest in S_3 salinity level.

Regarding genetic advance as percentage of mean, an irregular trend was observed with increase in salinity level. It

was 17.32%, 10.73%, 10.72%, 22.64% and 16.90% in S₀, S₁, S₂, S₃ and S₄ level, respectively. It was lowest in S₂ and highest in S₃ salinity level.

Plumule to radicle length ratio

According to Table 3 the plumule to radicle length ratio ranged from 1.44 (UM-385) to 2.00 (RMt-305) in S₀, 1.27 (RMt-143) to 2.00 (UM-385 and RMt-365) in S₁, 1.25 (RMt-361) to 1.73 (UM-383) in S₂, 0.85 (UM-385) to 1.32 (RMt-365) in S₃ and 0.88 (RMt-354) to 1.32 (UM-383) IN S₄ salinity level. The range was maximum in S₁ and minimum in S₄ salinity level.

Perusal of Table 3 for trait plumule to radicle length ratio revealed that the estimates of phenotypic coefficient of variation (PCV) in general were higher than estimates of genotypic coefficients of variation (GCV) in all salinity levels indicating predominant influence of salinity. The GCV was 9.68%, 13.16%, 10.43%, 13.55% and 13.13% in S₀, S₁, S₂, S₃ and S₄ level, respectively. The PCV was 12.41%, 16.00%, 14.17%, 16.51% and 16.34% in S₀, S₁, S₂, S₃ and S₄ level, respectively. The variation was maximum in S₃ and minimum in S₀.

Broad sense heritability estimates vary from one salinity level to the other. Heritability exhibited irregular response with increasing salinity levels. It was 60.94%, 67.61%, 54.17%, 67.36% and 64.64% in S₀, S₁, S₂, S₃ and S₄ level, respectively. It was lowest in S₂ and highest in S₁ salinity level.

Regarding genetic advance as percentage of mean, an irregular trend was observed with increase in salinity level. It was 15.17%, 22.29%, 15.82%, 22.90% and 21.75% in S₀, S₁, S₂, S₃ and S₄ level, respectively. It was lowest in S₀ and highest in S₃ salinity level.

Plumule fresh weight (mg)

The plumule fresh weight ranged from 95.53 mg (UM-383) to 138.83 mg (RMt-303) in S₀, 78.91 mg (RMt-1) to 138.76 mg (RMt-303) in S₁, 70.93 mg (RMt-365) to 119.41 mg (RMt-303) in S₂, 60.22 mg (RMt-1) to 81.13 mg (RMt-143) in S₃ and 45.40 mg (RMt-305) to 68.56 mg (RMt-303) in S₄ salinity level. The range was maximum in S₁ and minimum in S₃ salinity level (Table 3).

Perusal of Table 3 revealed that the estimates of phenotypic coefficient of variation (PCV) in general were higher than estimates of genotypic coefficients of variation (GCV) in all the salinity levels indicating predominant influence of salinity. The GCV was 12.35%, 13.89%, 14.94%, 8.03% and 14.19% in S₀, S₁, S₂, S₃ and S₄ level, respectively. The PCV was 12.41%, 13.99%, 15.09%, 8.33% and 14.45% in S₀, S₁, S₂, S₃ and S₄ level, respectively. The variation was maximum in S₂ and minimum in S₃.

Broad sense heritability estimates vary from one salinity level to the other. Heritability decreased with increasing salinity level, though higher in S₄ as compared to S₃. It was 98.94%, 98.65%, 98.06%, 92.93% and 96.45% in S₀, S₁, S₂, S₃ and S₄ level, respectively. It was lowest in S₃ and highest in S₀ salinity level.

An irregular trend was observed in genetic advance as percentage of mean with increase in salinity level. It was 25.30%, 28.43%, 30.48%, 15.95% and 28.70% in S₀, S₁, S₂, S₃ and S₄ level, respectively. It was lowest in S₃ and highest in S₄ salinity level.

Radicle fresh weight (mg)

Perusal of Table 3 showed that the radicle fresh weight ranged from 20.91 mg (RMt-303) to 39.56 mg (RMt-305) in S₀, 23.17 mg (RMt-351) to 42.14 mg (RMt-303) in S₁, 22.60 mg (RMt-365) to 39.38 mg (RMt-303) in S₂, 24.15 mg (RMt-1) to 34.69 mg (RMt-303) in S₃ and 13.94 mg (RMt-365) to 17.86 mg (RMt-354) in S₄ salinity level. The range was wider in S₁ and shorter in S₄ salinity level.

Perusal of Table 3 revealed that the estimates of phenotypic coefficient of variation (PCV) in general were higher than estimates of genotypic coefficients of variation (GCV) in all the salinity levels indicating predominant influence of salinity. The GCV was 16.22%, 17.84%, 17.00%, 10.86% and 8.83% in S₀, S₁, S₂, S₃ and S₄ level, respectively. The PCV was 17.28%, 18.44%, 17.51%, 11.73% and 9.72% in S₀, S₁, S₂, S₃ and S₄ level, respectively. The variation was maximum in S₂ and minimum in S₄.

Broad sense heritability estimates vary from one salinity level to the other. Heritability exhibited irregular response with increasing salinity level. It was 88.08%, 93.59%, 94.21%, 85.74% and 82.38% in S₀, S₁, S₂, S₃ and S₄ level, respectively. It was lowest in S₄, and highest in S₂ salinity level.

Regarding genetic advance as percentage of mean, an irregular trend was observed with increase in salinity level. It was 31.36%, 35.56%, 33.98%, 20.71% and 16.50% in S₀, S₁, S₂, S₃ and S₄ level, respectively. It was lowest in S₄ (16.50%) and highest in S₁ (35.56%).

Plumule dry weight (mg)

Perusal of Table 3 exhibited that the plumule dry weight ranged from 5.92 mg (RMt-365) to 10.25 mg (RMt-303) in S₀, 5.87 mg (RMt-1) to 10.33 mg (RMt-303) in S₁, 6.10 mg (RMt-1) to 10.45 mg (RMt-303) in S₂, 5.48 mg (RMt-351) to 8.58 mg (UM-385) in S₃ and 5.34 mg (RMt-365) to 9.33 mg (RMt-303) in S₄ salinity level. The range was maximum in S₁ and minimum in S₃ salinity level.

Perusal of Table 3 showed that the estimates of phenotypic coefficient of variation (PCV) in general were higher than estimates of genotypic coefficients of variation (GCV) in all the salinity levels indicating predominant influence of salinity. The GCV was 15.76%, 18.13%, 18.08%, 15.99% and 15.48% in S₀, S₁, S₂ and S₃ level, respectively. The PCV was 17.21%, 18.59%, 18.69%, 16.16% and 15.67% in S₀, S₁, S₂, S₃ and S₄ level, respectively. The variation was maximum in S₂ and minimum in S₄.

Broad sense heritability estimates vary from one salinity level to the other. Heritability exhibited irregular response with increasing salinity level. It was 83.93%, 95.13%, 93.53%, 97.90% and 97.70% in S₀, S₁, S₂, S₃ and S₄ level, respectively. It was lowest in S₀ and highest in S₃ salinity level.

Regarding genetic advance as percentage of mean, an irregular trend was observed with increase in salinity level. It was 29.75%, 36.44%, 36.01%, 32.60% and 31.53% in S₀, S₁, S₂, S₃ and S₄ level, respectively. It was lowest in S₀ and highest in S₁ salinity level.

Radicle dry weight (mg)

Perusal of Table 3 revealed that the radicle dry weight ranged from 0.90 mg (RMt-354) to 1.69 mg (RMt-361) in S₀, 0.91 mg (RMt-1) to 1.35 mg (RMt-361) in S₁, 0.99 mg (RMt-1) to 1.36 mg (UM-385) in S₂, 0.84 mg (RMt-365) to 1.22 mg

(RMt-361) in S₃ and 0.74 mg (RMt-365) to 1.17 mg (UM-385) in S₄ salinity level. The range was maximum in S₀ and minimum in S₂ salinity level.

Perusal of Table 3 revealed that the estimates of phenotypic coefficient of variation (PCV) in general were higher than estimates of genotypic coefficients of variation (GCV) in all the salinity levels indicating predominant influence of salinity. The GCV was 17.89%, 11.10%, 11.10%, 12.83% and 13.85% in S₀, S₁, S₂, S₃ and S₄ level, respectively. The PCV was 18.96%, 12.81%, 12.81%, 14.02% and 14.96% in S₀, S₁, S₂, S₃ and S₄ level, respectively. The variation was maximum in S₀ and minimum in S₁ and S₂.

Broad sense heritability estimates vary from one salinity level to the other. Heritability exhibited irregular response with increasing salinity level. It was 89.05%, 75.13%, 75.13%, 83.75% and 85.70% in S₀, S₁, S₂, S₃ and S₄ level, respectively. It was lowest in S₁ and S₂ and highest in S₀ salinity level.

Regarding genetic advance as percentage of mean, an irregular trend was observed with increase in salinity level. It was 34.78%, 19.83%, 19.83%, 24.19% and 26.41% in S₀, S₁, S₂, S₃ and S₄ level, respectively. It was lowest in S₁ and S₂ and highest in S₀ salinity level.

Seedling vigour index: Perusal of Table 3 exhibited that the seedling vigour index ranged from 917.94 (RMt-361) to 1312.00 (UM-385) in S₀, 933.10 (RMt-351) to 1141.20 (RMt-143) in S₁, 716.24 (UM-383) to 996.61 (UM-385) in S₂, 647.90 (RMt-361) to 925.22 (RMt-303) in S₃ and 369.72 (UM-385) to 548.31 (RMt-303) in S₄ salinity level. The range was wider in S₀ and shorter in S₄ salinity level.

Perusal of Table 3 revealed that the estimates of phenotypic coefficient of variation (PCV) in general were higher than estimates of genotypic coefficients of variation (GCV) in all the salinity levels indicating predominant influence of salinity. The GCV was 9.48%, 6.56%, 8.82%, 12.89% and 10.53% in S₀, S₁, S₂, S₃ and S₄ level, respectively. The PCV was 11.46%, 8.90%, 11.34%, 14.46% and 12.12% in S₀, S₁, S₂, S₃ and S₄ level, respectively. The variation was maximum in S₃ and minimum in S₁.

Broad sense heritability estimates vary from one salinity level to the other. Heritability exhibited irregular response with increasing salinity levels. It was 68.38%, 54.35%, 60.49%, 79.37% and 75.47% in S₀, S₁, S₂, S₃ and S₄ level, respectively. It was lowest in S₁ and highest in S₃ salinity level.

Regarding genetic advance as percentage of mean, an irregular trend was observed with increase in salinity level. It was 16.14%, 9.96%, 14.13%, 23.65% and 18.85% in S₀, S₁, S₂, S₃ and S₄ level, respectively. It was lowest in S₁ and highest in S₃ salinity level.

The comparison between mean of different genotypes in control (S₀) versus S_m (mean of S₁, S₂, S₃ and S₄) for each character is presented in table 4 Perusal of this table revealed that overall mean was highest in control as compared to the overall mean of salinity levels for all the characters. Mean performance of most of the genotypes was also observed to be high in S₀ as compared to S_m for all the characters. Based upon the rank totals of a genotype over different salinity levels S₁, S₂, S₃ and S₄ (S_m) and characters, the genotype RMt-303 was found to be most desirable as it had a desirable rank total followed by UM-385, RMt-143 and RMt-305.

Table 1: ANOVA for Ten various traits at Five salinity level S₀, S₁, S₂, S₃ and S₄ (0, 40, 80, 120 & 160 mM NaCl)

Source of variation	Salinity levels	d.f.	Mean sum of squares (M.S.S.)									
			Germination (%)	Plumule length (cm)	Radicle length (cm)	Seedling length (cm)	Plumule/Radicle length ratio	Plumule fresh weight (mg)	Radicle fresh weight (mg)	Plumule dry weight (mg)	Radicle dry weight (mg)	Seedling vigour index
Replications	S ₀	2	28.159	0.205	0.087	0.386	0.015	6.467	9.455	0.051	0.003	8062.11
Genotypes		9	23.712	1.076**	1.092**	3.657**	0.089**	533.002**	81.540**	4.874**	0.144**	39665.02**
Error		18	13.334	0.169	0.055	0.222	0.016	1.896	3.521	0.292	0.006	5296.905
Replications	S ₁	2	57.716	0.029	0.072	0.072	0.029	1.269	5.959	0.133	0.017	10326.971
Genotypes		9	23.034	0.502*	1.065**	1.677**	0.172**	712.536**	96.570**	6.199**	0.054**	18029.065**
Error		18	16.621	0.163	0.065	0.213	0.024	3.247	2.155	0.104	0.005	3943.818
Replications	S ₂	2	10.359	0.684	0.040	0.641	0.038	8.428	0.386	0.021	0.004	6219.661
Genotypes		9	67.285*	0.508*	0.714**	1.675**	0.088**	609.980**	85.868**	6.039**	0.048**	21769.984**
Error		18	21.888	0.193	0.095	0.326	0.019	3.997	1.724	0.136	0.005	3892.960
Replications	S ₃	2	23.683	0.054	0.001	0.070	0.002	0.185	0.052	0.032	0.011	352.402
Genotypes		9	81.620*	1.336**	0.625**	2.879**	0.073**	98.907**	30.601**	3.820**	0.062**	28599.746**
Error		18	25.343	0.068	0.062	0.116	0.010	2.447	1.607	0.027	0.004	2280.498
Replications	S ₄	2	31.122	0.040	0.063	0.047	0.022	2.389	0.503	0.085	0.008	670.173
Genotypes		9	88.245**	0.280**	0.334**	0.844**	0.062**	181.193**	6.701**	3.532**	0.047**	7395.051**
Error		18	24.531	0.033	0.035	0.075	0.010	2.197	0.446	0.028	0.002	722.880

* and ** represent significant at 5% and 1% level of significance, respectively

Table 2: Pooled ANOVA for various traits of fenugreek seedlings under salinity conditions

Source of variation	d.f.	Mean sum of squares (M.S.S.)									
		Germination (%)	Plumule length (cm)	Radicle length (cm)	Seedling length (cm)	Plumule/Radicle length ratio	Plumule fresh weight (mg)	Radicle fresh weight (mg)	Plumule dry weight (mg)	Radicle dry weight (mg)	Seedling vigour index
Genotypes	9	167.217**	1.417**	1.399**	4.957**	0.071**	1056.196**	84.874**	15.756**	0.193**	53086.070**
Salinity	4	866.278**	107.260**	14.140**4**	191.53**	2.893**	17887.158**	1270.848**	6.065**	0.505**	2201315.825**
Replication/Salinity	10	30.207	0.203	0.053	0.243	0.022	3.747	3.271	0.065	0.008	5126.265

Genotype x Salinity	36	29.169	0.572**	0.608**	1.444**	0.103**	269.856**	54.101**	2.177**	0.041**	15593.198**
Error	90	20.343	0.125	0.062	0.190	0.016	2.757	1.891	0.117	0.004	3227.412

Table 3: The general mean, range, genotypic (GCV) and phenotypic (PCV) coefficient of variation, heritability (in broad sense) and genetic advance (GA) over different salinity levels for various seedling traits

Variability parameters	Salinity levels									
	Germination percent (%)					Plumule length(cm)				
	S0	S1	S2	S3	S4	S0	S1	S2	S3	S4
mean	96.89	93.33	89.11	88.44	82.67	7.16	6.98	5.78	4.24	2.71
range	91.11 - 100.00	88.89 - 97.78	82.22 - 95.55	80 - 95.55	75.55 - 91.11	5.71-7.79	6.51-7.87	5.07-6.61	3.40-5.19	2.05-3.20
GCV	-	-	4.37	4.90	5.57	7.68	4.82	5.61	15.33	10.59
PCV	-	-	6.83	7.51	8.18	9.59	7.53	9.44	16.52	12.52
h ² (in bs)	-	-	40.88	42.54	46.40	64.10	40.89	35.28	86.10	71.56
GA	-	-	5.75	6.58	7.82	12.66	6.34	6.86	29.31	18.46
Variability parameters	Radicle length(cm)					Seedling length(cm)				
	S0	S1	S2	S3	S4	S0	S1	S2	S3	S4
mean	4.50	4.21	4.05	3.99	2.72	11.65	11.19	9.83	8.23	5.43
range	3.67-5.39	3.47-5.38	3.11-4.79	3.17-4.51	2.29-3.16	9.40 - 13.12	10.06 - 12.21	8.49 - 10.93	6.85 - 9.67	4.35 - 6.01
GCV	13.07	13.72	11.24	10.86	11.61	9.19	6.24	6.83	11.66	9.32
PCV	14.07	14.99	13.59	12.51	13.48	10.04	7.48	8.97	12.37	10.59
h ² (in bs)	86.32	83.74	68.36	75.32	74.24	83.79	69.58	58.01	88.83	77.46
GA	25.01	25.86	19.14	19.41	20.61	17.32	10.73	10.72	22.64	16.9
Variability parameters	Plumule to radicle ratio					Plumule fresh weight(gm)				
	S0	S1	S2	S3	S4	S0	S1	S2	S3	S4
mean	1.61	1.69	1.45	1.07	1.01	107.78	110.68	95.12	70.58	54.45
range	1.44 - 2.00	1.27 - 2.00	1.25 - 1.73	0.85 - 1.32	0.88 - 1.32	95.53 - 138.83	78.91 - 138.76	70.93 - 119.41	60.22 - 81.13	45.40 - 68.56
GCV	9.68	13.16	10.43	13.55	13.13	12.35	13.89	14.94	8.03	14.19
PCV	12.41	16	14.17	16.51	16.34	12.41	13.99	15.09	8.33	14.45
h ² (in bs)	60.94	67.61	54.17	67.36	64.64	98.94	98.65	98.06	92.93	96.45
GA	15.57	22.29	15.82	22.9	21.75	25.3	28.43	30.48	15.95	28.7
Variability parameters	Radicle fresh weight(gm)					Plumule dry weight(gm)				
	S0	S1	S2	S3	S4	S0	S1	S2	S3	S4
mean	31.44	31.44	31.16	28.63	16.36	7.84	7.86	7.76	7.03	6.98
range	20.91 - 39.56	23.17 - 42.14	22.60 - 39.38	24.15 - 34.69	13.94 - 17.86	5.92 - 10.25	5.87 - 10.33	6.10 - 10.45	5.48 - 8.58	5.34 - 9.33
GCV	16.22	17.84	17	10.86	8.83	15.76	18.13	18.08	15.99	15.48
PCV	17.28	18.44	17.51	11.73	9.72	17.21	18.59	18.69	16.16	15.67
h ² (in bs)	88.08	93.59	94.21	85.74	82.38	83.93	95.13	93.53	97.9	97.7
GA	31.36	35.56	33.98	20.71	16.5	29.75	36.44	36.01	32.6	31.53
Variability parameters	Radicle dry weight(gm)					Seedling vigour index				
	S0	S1	S2	S3	S4	S0	S1	S2	S3	S4
mean	1.2	1.15	1.16	1.09	0.88	1129.49	1044.68	875.46	726.85	447.75
range	0.90 - 1.69	0.91 - 1.35	0.99 - 1.36	0.84 - 1.22	0.74 - 1.17	917.94 - 1312	933.10 - 1141.20	716.24 - 996.61	647.90 - 925.22	369.72 - 548.31
GCV	17.89	11.1	11.1	12.83	13.85	9.48	6.56	8.82	12.89	10.53
PCV	18.96	12.81	12.81	14.02	14.96	11.46	8.9	11.34	14.46	12.12
h ² (in bs)	89.05	75.13	75.13	83.75	85.7	68.38	54.35	60.49	79.37	75.47
GA	34.78	19.83	19.83	24.19	26.41	16.14	9.96	14.13	23.65	18.85

Table 4: The rank total of different genotypes based on mean (S_m) of salinity levels S₁, S₂, S₃ and S₄

Genotype	Germination (%)	Plumule length (cm)	Radicle length (cm)	Seedling length (cm)	Plumule/ Radicle length ratio	Plumule fresh weight (mg)	Radicle fresh weight (mg)	Plumule dry weight (mg)	Radicle dry weight (mg)	Seedling vigour index	Total	Rank
RMt-305	2	9	9	9	4	4	5	3	3	5	53	4
RMt-351	9	8	6	6	5	3	10	6	7	10	70	8
RMt-361	3	10	8	10	7	7	3	4	2	8	62	7
RMt-354	9	4	3	3	8	8	6	7	6	4	58	6
RMt-365	7	6	10	8	1	9	9	9	9	9	77	10
UM-383	8	5	7	7	2	6	2	8	4	7	56	5
RMt-1	6	7	5	5	5	10	7	10	10	6	71	9
RMt-143	4	1	1	1	9	5	8	5	8	2	44	3
RMt-303	1	2	2	2	10	1	1	1	4	1	25	1
UM-385	5	3	4	4	3	2	4	2	1	3	31	2

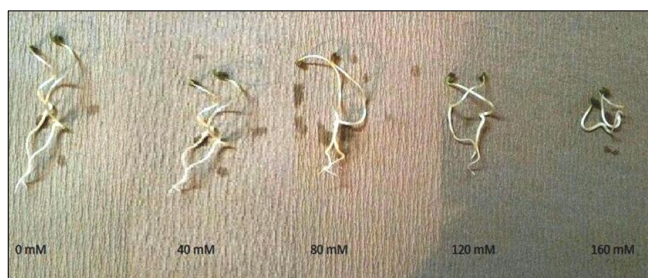


Fig 1: Effect and Response of Fenugreek seedling under different Salinity levels

Discussion

Effect of salinity on variability parameters

In general, the PCV values were higher than GCV values for all the traits. The differences were however, low for all the traits. Further, highest GCV and PCV values for plumule dry weight and radicle dry weight indicating that variation was highest for these characters among the genotypes followed by the plumule length, radicle length, seedling length, plumule to radicle length ratio, plumule fresh weight, radicle fresh weight and seedling vigour index whereas it was lowest for germination percentage indicated that these are the characters having low variability.

Comparison of GCV and PCV values for each character across the salinity levels indicated that while mean values decreased with increasing salinity, the CV values increased, this may indicated complex response mechanism which brought variations among genotypes and possibility of selection of responsive genotypes. This is particularly true for germination percentage, plumule, radicle and seedling length, plumule to radicle length ratio, plumule fresh weight, radicle fresh weight and seedling vigour index. Earlier similar observations were also reported by Ali *et al.* (2007) [1], Ashagre *et al.* (2013) [4] and Jat *et al.* (2014).

Heritability in broad sense was generally very high for the plumule and radicle fresh weight, plumule and radicle dry weight and radicle length across the salinity levels. Similar result was reported by Gupta (1994) [8], Kapoor and Pande (2015) [11] and Chauhan *et al.*, (2016) [6].

Genetic advance as percentage of mean was highest for radicle fresh weight, plumule dry weight and radicle dry weight followed by plumule fresh weight. This was lowest for germination percentage followed by plumule length, radicle length, seedling length, plumule to radicle length ratio. The Genetic advance also showed linear increment with increase in salinity gradient in germination percentage. While, no trend was observed in the rest of the characters studied. Increase in the magnitude of genetic advance across the salinity gradient indicated increase in the inherent variation in the response of genotype to salinity and a possibility of selection of suitable genotypes at higher salinity. Earlier similar findings were also reported by Gupta (1994) [8] and Narayan (1993) [12], Asaadi *et al.* (2009) [3] and Dutta and Bera (2014) [7].

Conclusion

The early seedling parameters of genotype showed significantly variation at higher salinity in comparison to 0 to 40 mM NaCl salinity level for most of the characters. The comparison between mean of different genotypes in control (S_0) versus S_m (mean of S_1 , S_2 , S_3 and S_4) for each character also revealed that overall mean was highest in control as compared to the overall mean of salinity levels for all the

characters.

Various salt tolerance indices were shown to be useful for estimation of stress level and identification of salt tolerant elite genotypes. Based upon the rank totals of a genotype over different salinity levels S_1 , S_2 , S_3 and S_4 (S_m) and characters, the genotype RMt-303 was found to be most desirable followed by UM-385, RMt-143 and RMt-305. Such potential lines could serve for effective exploitation for further hybridization programme as a source for salt-responsive candidate genes suitable for crop improvement in saline land as viable option to ensure food security under this climate change era.

Competing Interests

Authors have declared that no competing interests exist.

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