



## Original article

Sensitivity of different flax (*Linum usitatissimum* L.) genotypes to salinity determined by GE biplot

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## ABSTRACT

Plants respond differently to salt stress depending on their genetic structure and the severity of the stress. Salinity reduces seed germination, delays plant emergence, and inhibits seedling growth. The selection of the tolerant genotypes, however, plays a vital role in increasing agricultural output since various genotypes greatly vary for their tolerance to salinity. Therefore, this study determined the impact of five different NaCl levels (i.e., 0, 50, 100, 150 and 200 mM) on seed germination and growth attributes of 10 flax (*Linum usitatissimum* L.) genotypes. The germination and growth characteristics of the genotypes under study were examined using the biplot approach at varied salt levels. The results indicated that individual and interactive effects of genotypes and salinity levels significantly ( $p \leq 0.01$  or  $p \leq 0.05$ ) affected several seed germination traits. The relations of genotype  $\times$  germination traits indicated that 'G4' and 'G6' were the most stable genotypes with the highest performance regarding seed germination characteristics. The genotype 'G2' was associated with shoot length, while 'G7' was linked with salinity tolerance index. The biplot divided the germination characteristics into five different groups according to sector analysis. Most of the germination parameters had higher values under 100 mM, while some of the parameters had better values under 0, 50 and 200 mM NaCl levels. The tested genotypes varied for their seed germination and growth response depending on the NaCl levels. The genotypes 'G4', 'G5' and 'G6' proved more tolerant to high NaCl levels. Therefore, these genotypes can be used to improve flax productivity under saline soils.

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## 1. Introduction

Flax (*Linum usitatissimum* L.) is a member of the Linaceae family and commonly known as linseed. It is one of the commercially important industrial plants in the world. Flax is produced and consumed for its oil and fiber, and intensively used in several sectors. It is important industrial plants with several uses (Zuk et al., 2015). Flax can grow in semi-arid climatic conditions and is less affected by stressful environments. Therefore, the response of flax varieties to different stress conditions should be determined for selecting the best suited ones (Moghaddam et al., 2018).

Salinity in the growing environment is one of the limiting factors in crop production. The salt ratio in the environment alters

numerous biochemical and physiological events in plants (Tarchoun et al., 2022). Plant breeding efforts are highly affected by salinity in the environment, especially at different developmental stages of crop plants. Since the germination is the first step in the life cycle of plants, it is important to determine the sensitivity of plants to salinity during this phase (Önen et al., 2018; Zamani et al., 2010). High salt concentration in the soil inhibits seed germination or induces dormancy at low levels (Farooq et al., 2015). Salinity negatively seed germination and disrupts several processes at physiological and metabolic levels, including changes in the enzymatic activities (Tarchoun et al., 2022). Flax is a moderately salinity-tolerant plant and a yield decrease of 10 %, 25 % and 50 % has been reported under 2.5, 3.8 and 5.9 mM salinity, respectively (Dubey et al., 2020). Flax seeds had a long and oval structure, and the average weight of a thousand grains is 6.61 g (Dumanoglu, 2020).

Fast and consistent seed germination and healthy seedling establishment leads to better crop growth, development, yield, and financial returns. This is especially true for plants cultivated in dry environments, where a number of variables have a detrimental impact on seed germination (Tan et al., 2017). Researchers

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have looked at how salt affects the germination of seeds in a variety of plant species, including weeds (Farooq et al., 2019). For example earlier studies have determined seed germination response of *Limonium stocksii* (Hameed et al., 2014), *Linum usitatissimum* (Moghaddam et al., 2018), *Gypsophila oblongeolata* (Sekmen et al., 2012), Basil (Zahedi et al., 2011), and sunflower (Kaya et al., 2019) to different salinity levels. Seedling development is also suppressed and delayed under salinity stress (Jaleel et al., 2007).

Variable impacts of environmental factors have been observed on genotype evolution. One of the most important features desired for breeding is the ability to choose genotypes that perform well across a wide range of environmental or stressful conditions. This may be achieved by selecting stable genotypes whose interaction rate decreases with the exposure to new environments. The studies should be aimed at choosing stable genotypes, since stability or the attribute of low interaction with the environment is a heritable trait. It will be possible to have better yields under large production zones if the most stable genotypes are chosen (Kendal, 2019; Orawu et al., 2017).

Interaction is defined as the relationship between genotypes and different environmental conditions. The genotype by environment interaction is of great significance for seed germination traits. Genetic traits and the immediate environment play important roles in determining the stability of genotypes. Accordingly, researchers use several methods to illuminate the effects of genetics, environment, and their interaction. One of these methods is GE biplot. The GE biplot is important for developing variety because of quantification and visualization (Kendal, 2020). The selection of the most stable genotypes is possible by conducting genotype trials in different environments and determining the effects of genotype, environment, and their interaction (Li et al., 2017; Rastogi et al., 2011). The GGE biplot model is highly suitable for identifying environmental groups, ideal environments, and the best genotypes for the most suitable environment. This method has been used by several researchers to reveal the effect of genotype and environment interaction on different plants (Farias et al., 2016); however, it has not been applied to upland Flax in Turkey. For this reason, GGE biplot method was used to determine the effect of genotypes and salinity on seed germination and growth traits of different flax genotypes.

The primary objectives of this work were to (1) explain the effect of salt concentration on seed germination measures, and (2) use a biplot to determine the genotype-salinity interaction for these parameters. It was hypothesized that the traits under study would be profoundly affected by salinity levels, genotypes, and the interactions between the two. The results will improve flax productivity and economic advantages by identifying the most tolerant genotypes.

## 2. Materials and methods

### 2.1. Experimental treatments

This research was done in 2022 to find out how certain flax genotypes responded to salt (NaCl) stress during germination and the early phases of seedling development. Salinity levels were the primary element in the experiment, whereas genotypes were considered a minor effect. The experiment was set up using a factorial experiment method. Ten flax genotypes and five different NaCl concentrations (0, 50, 100, 150, and 200 mM) were used in the research. The experiment had four replications. The information regarding the flax genotypes included in the study are given in Table 1.

The Petri dishes used in the experiment were sterilized in an autoclave. Furthermore, flax seeds were surface sterilized before

the initiation of the experiment. For surface sterilization, 30 flax seeds belonging to each genotype were treated with 70 % ethanol for 10 s. These seeds were then mixed with sodium hypochlorite for 1 min. Afterwards, the seeds were washed 4 times with distilled water. The seeds were then washed with benomyl solution of 2 ppt (parts per thousand) for 1 min and again washed with distilled water to cover the surface.

### 2.2. Seed germination test

The flax seeds were disinfected and placed on two layers of Whatman no. 1 filter paper in 9 cm diameter Petri dishes. Various salt solutions, with distilled water acting as a control, were prepared, and added to Petri dishes. Para film was used to seal up the tops of the Petri dishes, and the incubator was set at 20°Celsius with 24 h dark period to avoid evaporation. Germination rates were recorded daily. At the end of the study, normal and abnormal seedlings were counted, root and shoot length, root, and shoot fresh and dry weights (after being dried at 70 °C for 72 h) were measured 9 days later. Dead root tips and cotyledons or cotyledons that were extensively injured were other symptoms of anomaly plants.

Equation (1) from Fang et al. (2006) was used to calculate the proportion of seeds that germinated.

$$G\% = n/N \times 100 \quad (1)$$

where n is the sum of seeds germinated and N is the total number of seeds included in the experiment.

Equation (2) was used to calculate the seed germination rate.

$$R_s = \sum_{i=1}^n S_i/D_i \quad (2)$$

where  $R_s$  represents the germination rate,  $S_i$  stands for the number of germinated seeds at each count,  $D_i$  stands for the number of days till the  $n$ th count day, and  $n$  represents the total number of count days.

using Ellis and Roberts (1981) Eq. (3) mean germination time was computed.

$$MGT = \sum D.N/n \quad (3)$$

where  $\sum$  is the number of seeds that began to sprout on day  $D$ , and  $D$  is the number of days since germination started.

Equation (4) was used to estimate the seed viability index.

$$SVI = G\% \times SL(mm)/100 \quad (4)$$

where  $G\%$  is the germination percentage and  $SL$  is the average seedling length.

Seed germination rate was determined by counting the daily germinating seeds, filter papers were changed at each count and soluble NaCl solution was added to the new filter papers. The seeds were regarded as germinated once 2 mm root was visible. The seed germination percentage was calculated according to ISTA standards.

Similarly, RE (emergence rate), RL (root length), SL (shoot length), STI (salinity tolerance index) DGR (degrees germination rate), RFW (root fresh weight), SFW (shoot fresh weight), RDW (root dry weight), SDW (shoot dry weight) NP (normal plants), and ANP (anormal plants) were recorded for each genotype under all salinity levels.

### 2.3. Statistical analysis (GT, ST, and GS)

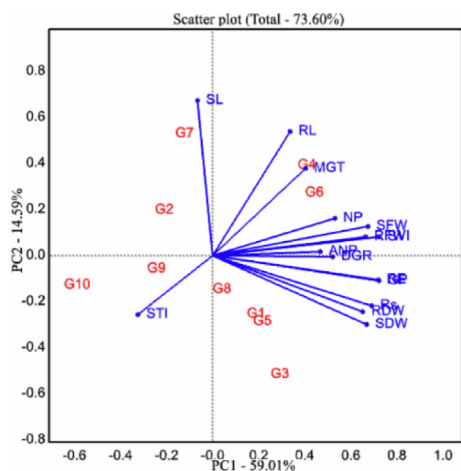
The collected data were analyzed by two-way analysis of variance (ANOVA) by using JMP5 statistical software. The means were compared at 99 and 95 % probability levels using least significant difference test where ANOVA indicated significant differences. On

**Table 1**  
The information about genotypes which used in the study.

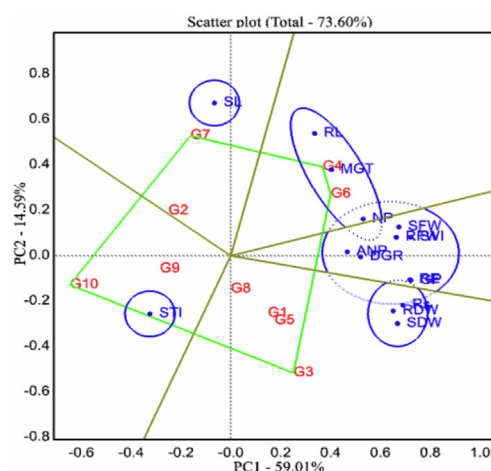
Genotype Codes	Genotype name	1000 seeds weight (g)	Flower color	Seed color	Oil rate (%)	Country of origin	Growing type
G1	Norman	5.70	blue	brown	35.4	Canada	Spring
G2	Midin	7.36	blue	brown	35.8	Romania	Spring
G3	Tsian	6.90	blue	brown	35.6	Russia	Spring
G4	Nareum	6.42	blue	brown	34.7	The USA	Spring
G5	Dufferin	6.19	blue	brown	43.1	Canada	Spring
G6	Somme	6.23	blue	brown	35.8	Canada	Spring
G7	Clli-1400	6.18	blue	brown	38.2	Turkey	Spring
G8	Clli-1412	6.15	light blue	brown	35.3	Turkey	Spring
G9	Clli-1370	5.69	blue	brown	35.0	Turkey	Spring
G10	Clli-1423	5.76	blue	brown	34.6	Turkey	Spring

the other hand, data of the genotypes under salinity levels were analyzed by GT biplot method recommended by Yan and Tinker (2005). The data of all seed germination traits were calculated based on mean of salinity stress and genotypes. Biplot analysis of the data was performed using Genstat version 14. The data were

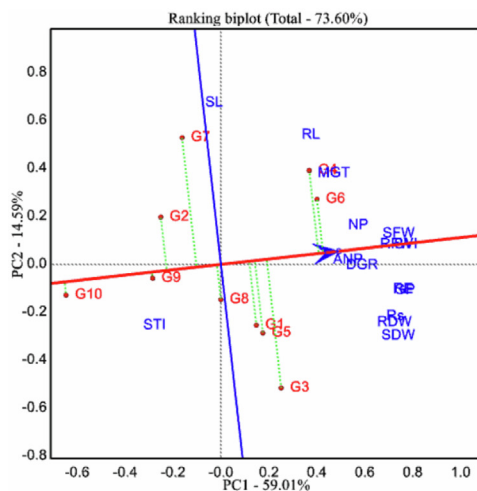
graphically analyzed for the interpretation of GT (genotypes × traits), ST (salinity levels × traits) and GS (genotypes × salinity levels) using GGE biplot software. Fig. 1 (1A-1D) was produced based on the performance of each genotype for each trait (GT). The Fig. 2(2A-2D) was generated based on the



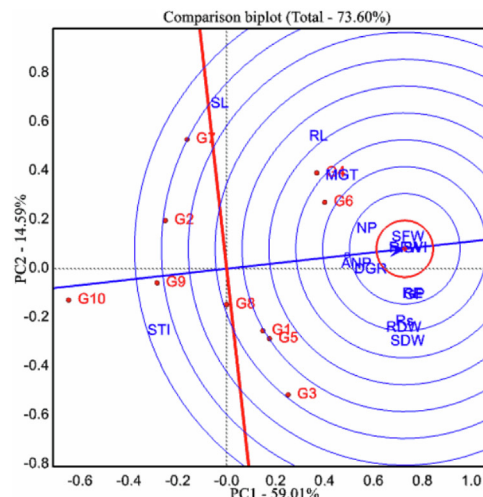
1A The relation of GT biplot based on NaCl concentrations.



1B Which-won-where/what of GT biplot based on NaCl concentrations.

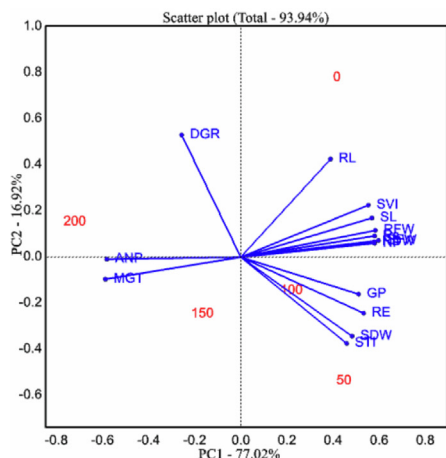


1C The stability of GT biplot based on NaCl concentrations

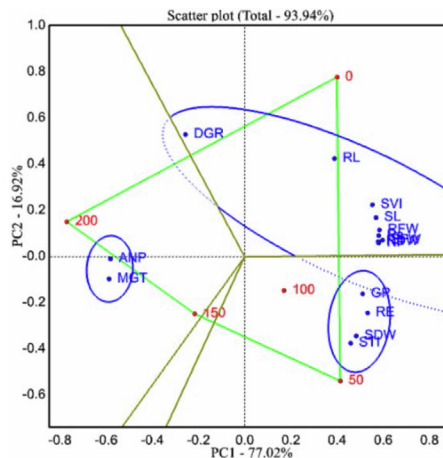


1D The stability of GT biplot based on NaCl concentrations

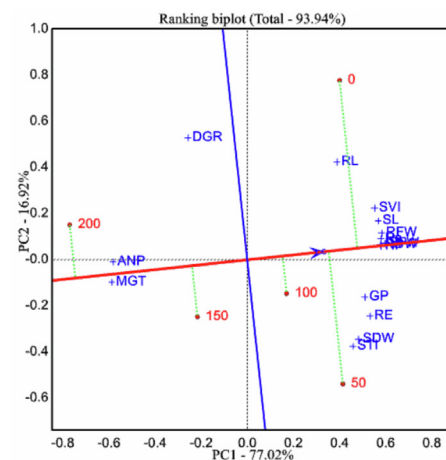
**Fig. 1.** Genotype by traits interaction of different flax genotypes included in the study. Here GP = germination percentage, MGT = mean germination time, Rs = germination rate, SVI = seed variability index, RE = emergence rate, RL = radicle length, SL = shoot length, STI = salinity tolerance index, DGR = degree germination rate, RFW = root fresh weight, SFW = shoot fresh weight, RDW = root dry weight, SDW = shoot dry weight, NP = normal plants, and ANP = abnormal.



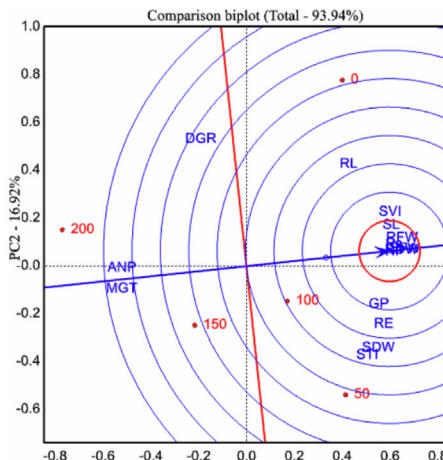
2A The relation of NaCl concentration and traits.



2B Which-won-where of NaCl concentration and traits.



2C Ranking biplot of NaCl concentration and traits



2D Comparison biplot of NaCl concentration and traits

**Fig. 2.** Salinity by trait interaction of different flax genotypes included in the study. Here GP = germination percentage, MGT = mean germination time, Rs = germination rate, SVI = seed variability index, RE = emergence rate, RL = radicle length, SL = shoot length, STI = salinity tolerance index, DGR = degree germination rate, RFW = root fresh weight, SFW = shoot fresh weight, RDW = root dry weight, SDW = shoot dry weight, NP = normal plants, and ANP = anormal.

performance of salinity levels by traits (ST). Similarly, Fig. 3(3A-3D) was generated based on genotype by salinity stress (GS).

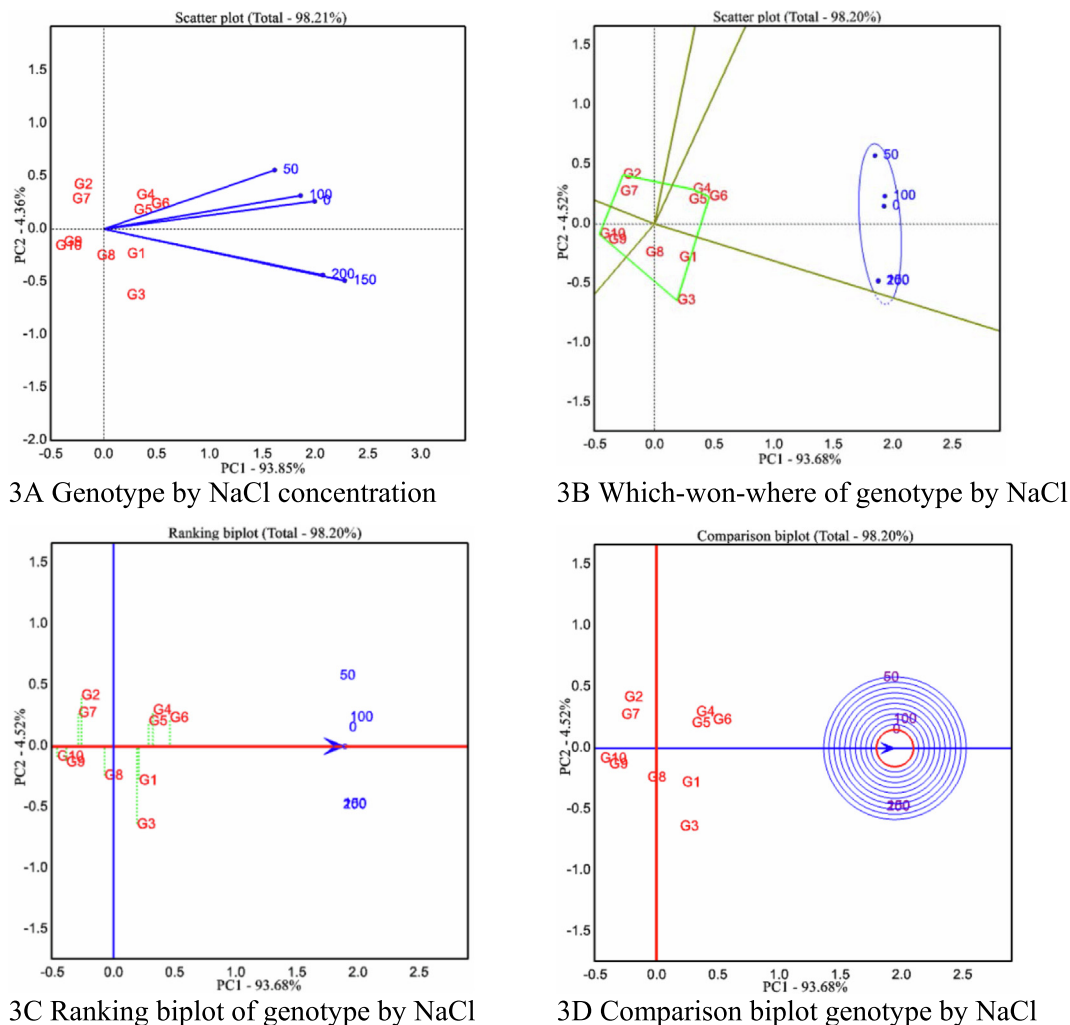
### 3. Results

The ANOVA table indicates the significance of different studied traits (Table 2). The ANOVA indicated that genotype, salinity, or their interaction were significant ( $p \leq 0.01$ ) for seed germination characteristics. Furthermore, data relating to seed germination traits and the formed groups are given in Table 3, Table 4, and Table 5. The pairwise correlation of germinations traits is given in Table 6. In the GT biplot model, PC1 represented 59.01 % of the variation, PC2 represented 14.59 % variation making a total of 73.60 % in total. In ST biplot model, PC1 and PC2 represented 77.02 % and 16.92 % of the variation, respectively explaining a total of 93.94 % variation. In the GS biplot model, PC1 represented 93.85 % and PC2 represented 4.52 % of the variation and explained 98.20 % variation in total. The effect of PC1 is always greater than PC2 in stability analysis; however, PC1 is desired to be greater in the total variation. Principal component analysis is appropriate when a small number of components explain a significant amount of the total

variance (e.g., the top two to five components explain > 60 % of the total variation) or when components are selected with eigenvalues larger than one. Therefore, components with values greater than one were selected for this study, and these values ended up explaining a substantial amount of variation.

#### 3.1. Biplot of genotype by germination traits

Fig. 1A visualizes the relationship between germination characteristics and flax genotypes included in the current study. These graphs are interpreted in two ways as indicated below. The GT biplot shows the relationship between two traits, relationship of a trait with other traits, or the genotypes by traits relationship using the angles between the vectors of the traits. The angle of vectors between two parameters is known as Pearson correlation. The biplot indicates a positive relationship between the vectors of two germination traits if the angle value ( $>0$  and  $<90^\circ$ ) gets narrower, and a negative relationship as the angle value ( $>90$  and  $<180^\circ$ ) gets wider. All interpretations are made according to the angles between the vectors of seed germination traits and the genotypes located in the trait regions.



**Fig. 3.** Genotype by salinity interaction of different flax genotypes included in the study G1 = Norman, G2 = Midin, G3 = Tsian, G4 = Nareum, G5 = Dufferin, G6 = Somme, G7 = Clii-1400, G8 = Clii-1412, G9 = Clii-1370, and G10 = Clii-1423.

**Table 2**

The sum of squares for germination traits of ten flax genotypes included in the study across various NaCl levels.

Germination Traits/DF	Variation Source							CV (%)
	Model 79	Genotype 9	Levels 4	Error 1 30	Gen*Lev. 36	Error 2 120	C. Total 199	
GP	111042.3	105162.0**	435.5**	533.2	4911.7**	2392.8	113435.1	7.3
MGT	7.491	1.536**	4.705**	0.537	0.713 ns	2.111	9.602	3.0
Rs	240.564	185.375**	37.625**	2.187	15.377**	4.508	245.072	7.2
SVI	1977.052	1077.280**	606.929**	4.745	288.093**	24.852	2001.904	7.9
RE	110882.3	101809.0**	1126.5**	537.2	7409.7**	2748.6	113630.9	8.2
RL	269.44	69.29**	89.13**	5.88	105.14**	20.42	289.86	10.1
SL	1072.79	31.66**	986.48**	5.49	49.16**	24.65	1097.44	8.6
STI	133534.5	42234.6**	35631.4**	1225.8	54442.7**	4983.2	138517.6	6.1
DGR	33081.6	14603.2**	2179.1**	581.5	15717.7**	2500.0	35581.6	4.5
RFW	0.125	0.048**	0.054**	0.001	0.023**	0.003	0.128	6.6
SFW	3.315	0.501**	2.395**	0.041	0.378**	0.146	3.461	11.1
RDW	0.001	0.000**	0.000**	0.000	0.000**	0.000	0.001	6.9
SDW	111042.3	105162.0**	435.5**	533.2	4911.7**	2392.8	113435.1	9.6
NP	92714.4	57318.8**	12035.9**	139.6	23220.1**	447.2	93161.6	4.1
ANP	58773.5	18478.0**	22500.7**	54.9	17740.0**	181.4	58954.9	8.0

Here, GP = germination percentage, MGT = mean germination time, Rs = germination rate, SVI = seed variability index, RE = emergence rate, RL = radicle length, SL = shoot length, STI = salinity tolerance index, DGR = degree germination rate, RFW = root fresh weight, SFW = shoot fresh weight, RDW = root dry weight, SDW = shoot dry weight, NP = normal plants, and ANP = anormal plants.

**Table 3**  
Seed germination and seedling growth traits of flax genotypes under different salinity levels.

Genotype	NaCl levels (mM)					Means	NaCl levels (mM)					Means
	0	50	100	150	200		0	50	100	150	200	
	GP (Germination percentage)						MGT (Mean germination time)					
<b>G1</b>	87 <sup>ad</sup>	85 <sup>af</sup>	79 <sup>fg</sup>	79 <sup>fg</sup>	50 <sup>ik</sup>	<b>76<sup>D</sup></b>	4.4	4.3	4.4	4.6	5.0	<b>4.5<sup>A</sup></b>
<b>G2</b>	33 <sup>mo</sup>	39 <sup>lm</sup>	34 <sup>mo</sup>	31 <sup>np</sup>	35 <sup>mo</sup>	<b>34<sup>G</sup></b>	4.3	4.3	4.3	4.6	4.6	<b>4.4<sup>BC</sup></b>
<b>G3</b>	88 <sup>ac</sup>	76 <sup>g</sup>	81 <sup>dg</sup>	89 <sup>ab</sup>	82 <sup>cg</sup>	<b>83<sup>BC</sup></b>	4.2	4.2	4.4	4.6	4.6	<b>4.4<sup>CD</sup></b>
<b>G4</b>	84 <sup>bf</sup>	85 <sup>af</sup>	85 <sup>af</sup>	88 <sup>ac</sup>	91 <sup>a</sup>	<b>87<sup>A</sup></b>	4.2	4.4	4.4	4.7	4.8	<b>4.5<sup>AB</sup></b>
<b>G5</b>	80 <sup>eg</sup>	81 <sup>dg</sup>	81 <sup>dg</sup>	88 <sup>ac</sup>	81 <sup>dg</sup>	<b>82<sup>C</sup></b>	4.2	4.2	4.3	4.5	4.5	<b>4.3<sup>DE</sup></b>
<b>G6</b>	89 <sup>ab</sup>	91 <sup>a</sup>	86 <sup>ae</sup>	79 <sup>fg</sup>	80 <sup>eg</sup>	<b>85<sup>AB</sup></b>	4.4	4.4	4.5	4.6	4.7	<b>4.5<sup>A</sup></b>
<b>G7</b>	48 <sup>jk</sup>	48 <sup>jk</sup>	44 <sup>kl</sup>	48 <sup>jk</sup>	48 <sup>jk</sup>	<b>47<sup>F</sup></b>	4.4	4.4	4.6	4.6	4.6	<b>4.5<sup>A</sup></b>
<b>G8</b>	51 <sup>ij</sup>	58 <sup>h</sup>	54 <sup>hj</sup>	56 <sup>hi</sup>	58 <sup>h</sup>	<b>55<sup>E</sup></b>	4.1	4.2	4.3	4.4	4.5	<b>4.2<sup>E</sup></b>
<b>G9</b>	36 <sup>mn</sup>	37 <sup>mn</sup>	38 <sup>lm</sup>	35 <sup>mo</sup>	39 <sup>lm</sup>	<b>37<sup>G</sup></b>	4.2	4.1	4.3	4.5	4.6	<b>4.3<sup>DE</sup></b>
<b>G10</b>	23 <sup>qr</sup>	29 <sup>oq</sup>	26 <sup>pr</sup>	22 <sup>r</sup>	21 <sup>r</sup>	<b>24<sup>H</sup></b>	4.2	4.1	4.3	4.5	4.5	<b>4.3<sup>DE</sup></b>
<b>Means</b>	<b>70<sup>A</sup></b>	<b>63<sup>A</sup></b>	<b>61<sup>B</sup></b>	<b>62<sup>B</sup></b>	<b>59<sup>C</sup></b>		<b>4.2<sup>D</sup></b>	<b>4.3<sup>D</sup></b>	<b>4.4<sup>C</sup></b>	<b>4.6<sup>B</sup></b>	<b>4.6<sup>A</sup></b>	
	RS (Germination rate)						SVI (Seed variability index)					
<b>G1</b>	4.0 <sup>de</sup>	3.9 <sup>ef</sup>	3.4 <sup>i</sup>	2.9 <sup>km</sup>	1.3 <sup>wy</sup>	<b>3.1<sup>C</sup></b>	10.1 <sup>ef</sup>	9.0 <sup>gh</sup>	6.3 <sup>k</sup>	4.7 <sup>lo</sup>	2.3 <sup>vw</sup>	<b>6.5<sup>C</sup></b>
<b>G2</b>	1.7 <sup>tv</sup>	1.9 <sup>rt</sup>	1.6 <sup>tv</sup>	1.2 <sup>yz</sup>	1.3 <sup>xy</sup>	<b>1.5<sup>F</sup></b>	4.2 <sup>op</sup>	3.6 <sup>qr</sup>	3.1 <sup>rt</sup>	2.5 <sup>tw</sup>	2.4 <sup>uw</sup>	<b>3.2<sup>E</sup></b>
<b>G3</b>	4.8 <sup>a</sup>	4.2 <sup>cd</sup>	3.7 <sup>fh</sup>	3.4 <sup>hi</sup>	3.0 <sup>k</sup>	<b>3.8<sup>A</sup></b>	11.1 <sup>d</sup>	6.4 <sup>jk</sup>	6.6 <sup>jk</sup>	6.1 <sup>k</sup>	5.0 <sup>lm</sup>	<b>7.1<sup>B</sup></b>
<b>G4</b>	4.7 <sup>ab</sup>	3.9 <sup>ef</sup>	3.7 <sup>fg</sup>	3.1 <sup>k</sup>	3.0 <sup>kl</sup>	<b>3.7<sup>A</sup></b>	12.0 <sup>c</sup>	10.3 <sup>e</sup>	9.5 <sup>fg</sup>	7.3 <sup>i</sup>	6.3 <sup>k</sup>	<b>9.1<sup>A</sup></b>
<b>G5</b>	4.5 <sup>ab</sup>	4.5 <sup>bc</sup>	3.7 <sup>fh</sup>	3.5 <sup>gi</sup>	3.1 <sup>jk</sup>	<b>3.9<sup>A</sup></b>	10.1 <sup>ef</sup>	7.3 <sup>i</sup>	7.0 <sup>ij</sup>	6.5 <sup>kl</sup>	4.8 <sup>lo</sup>	<b>7.2<sup>B</sup></b>
<b>G6</b>	3.9 <sup>ef</sup>	3.9 <sup>ef</sup>	3.4 <sup>ij</sup>	2.9 <sup>km</sup>	2.8 <sup>ln</sup>	<b>3.3<sup>B</sup></b>	15.4 <sup>a</sup>	13.0 <sup>b</sup>	8.8 <sup>h</sup>	4.9 <sup>lm</sup>	3.9 <sup>pq</sup>	<b>9.2<sup>A</sup></b>
<b>G7</b>	2.2 <sup>pq</sup>	2.2 <sup>pq</sup>	1.6 <sup>uv</sup>	1.8 <sup>su</sup>	1.8 <sup>su</sup>	<b>1.9<sup>E</sup></b>	6.2 <sup>k</sup>	5.2 <sup>l</sup>	5.3 <sup>l</sup>	4.9 <sup>ln</sup>	3.8 <sup>pq</sup>	<b>5.1<sup>D</sup></b>
<b>G8</b>	3.0 <sup>k</sup>	3.0 <sup>kl</sup>	2.7 <sup>mno</sup>	2.5 <sup>no</sup>	2.4 <sup>op</sup>	<b>2.7<sup>D</sup></b>	7.0 <sup>ij</sup>	6.5 <sup>jk</sup>	4.9 <sup>lm</sup>	4.4 <sup>mp</sup>	3.3 <sup>qs</sup>	<b>5.2<sup>D</sup></b>
<b>G9</b>	2.0 <sup>qs</sup>	2.1 <sup>pr</sup>	1.9 <sup>tu</sup>	1.4 <sup>wv</sup>	1.5 <sup>vx</sup>	<b>1.8<sup>E</sup></b>	5.1 <sup>l</sup>	4.3 <sup>np</sup>	3.5 <sup>qr</sup>	1.9 <sup>wx</sup>	1.9 <sup>wx</sup>	<b>3.3<sup>E</sup></b>
<b>G10</b>	1.3 <sup>xy</sup>	1.7 <sup>sv</sup>	1.3 <sup>xy</sup>	0.9 <sup>z</sup>	0.8 <sup>z</sup>	<b>1.2<sup>G</sup></b>	3.0 <sup>tu</sup>	2.8 <sup>sv</sup>	2.3 <sup>uw</sup>	1.6 <sup>x</sup>	0.8 <sup>y</sup>	<b>2.1<sup>F</sup></b>
<b>Means</b>	<b>3.2<sup>A</sup></b>	<b>3.1<sup>A</sup></b>	<b>2.7<sup>B</sup></b>	<b>2.4<sup>C</sup></b>	<b>2.1<sup>D</sup></b>		<b>8.4<sup>A</sup></b>	<b>6.8<sup>B</sup></b>	<b>5.7<sup>C</sup></b>	<b>4.5<sup>D</sup></b>	<b>3.5<sup>E</sup></b>	
	RE (rate emergence)						RL (Radicle length)					
<b>G1</b>	77 <sup>eg</sup>	80 <sup>ef</sup>	73 <sup>g</sup>	76 <sup>fg</sup>	31 <sup>nr</sup>	<b>67<sup>D</sup></b>	4.08 <sup>kq</sup>	3.28 <sup>tw</sup>	2.97 <sup>vx</sup>	3.39 <sup>sw</sup>	2.29 <sup>yz</sup>	<b>3.20<sup>F</sup></b>
<b>G2</b>	28 <sup>ps</sup>	33 <sup>m</sup>	33 <sup>m</sup>	27 <sup>qt</sup>	35 <sup>lo</sup>	<b>31<sup>H</sup></b>	4.85 <sup>eh</sup>	2.61 <sup>xy</sup>	3.56 <sup>pu</sup>	4.37 <sup>hn</sup>	4.10 <sup>jp</sup>	<b>3.90<sup>CD</sup></b>
<b>G3</b>	86 <sup>ac</sup>	78 <sup>dg</sup>	83 <sup>af</sup>	83 <sup>ae</sup>	78 <sup>dg</sup>	<b>82<sup>BC</sup></b>	5.09 <sup>cf</sup>	3.10 <sup>ux</sup>	3.50 <sup>qv</sup>	3.50 <sup>qv</sup>	3.92 <sup>ms</sup>	<b>3.82<sup>DE</sup></b>
<b>G4</b>	84 <sup>ad</sup>	88 <sup>a</sup>	87 <sup>ab</sup>	81 <sup>bf</sup>	87 <sup>ab</sup>	<b>85<sup>A</sup></b>	5.63 <sup>bc</sup>	4.56 <sup>nl</sup>	4.94 <sup>dh</sup>	4.24 <sup>io</sup>	3.89 <sup>ms</sup>	<b>4.65<sup>B</sup></b>
<b>G5</b>	79 <sup>dg</sup>	79 <sup>dg</sup>	77 <sup>eg</sup>	88 <sup>a</sup>	76 <sup>fg</sup>	<b>80<sup>C</sup></b>	4.97 <sup>dg</sup>	3.10 <sup>ux</sup>	3.42 <sup>sv</sup>	3.74 <sup>ot</sup>	2.70 <sup>xy</sup>	<b>3.59<sup>E</sup></b>
<b>G6</b>	87 <sup>ab</sup>	89 <sup>a</sup>	84 <sup>ad</sup>	77 <sup>eg</sup>	77 <sup>eg</sup>	<b>83<sup>AB</sup></b>	9.03 <sup>a</sup>	5.96 <sup>b</sup>	4.97 <sup>dg</sup>	3.38 <sup>sw</sup>	3.00 <sup>ux</sup>	<b>5.27<sup>A</sup></b>
<b>G7</b>	40 <sup>jl</sup>	43 <sup>jk</sup>	44 <sup>jk</sup>	46 <sup>ij</sup>	45 <sup>ij</sup>	<b>44<sup>F</sup></b>	4.41 <sup>gm</sup>	3.57 <sup>pu</sup>	5.60 <sup>bc</sup>	5.33 <sup>ce</sup>	4.19 <sup>jo</sup>	<b>4.62<sup>B</sup></b>
<b>G8</b>	51 <sup>hi</sup>	56 <sup>h</sup>	51 <sup>hi</sup>	54 <sup>h</sup>	53 <sup>h</sup>	<b>53<sup>E</sup></b>	4.79 <sup>ei</sup>	3.83 <sup>nt</sup>	3.85 <sup>mt</sup>	4.65 <sup>fk</sup>	3.79 <sup>ot</sup>	<b>4.18<sup>CD</sup></b>
<b>G9</b>	33 <sup>m</sup>	36 <sup>ln</sup>	40 <sup>im</sup>	34 <sup>p</sup>	37 <sup>kn</sup>	<b>36<sup>G</sup></b>	5.50 <sup>bd</sup>	4.06 <sup>lr</sup>	4.21 <sup>jo</sup>	2.99 <sup>ux</sup>	2.95 <sup>vx</sup>	<b>3.94<sup>CD</sup></b>
<b>G10</b>	23 <sup>st</sup>	29 <sup>os</sup>	25 <sup>rt</sup>	21 <sup>t</sup>	21 <sup>t</sup>	<b>24<sup>I</sup></b>	4.41 <sup>gn</sup>	2.82 <sup>wy</sup>	3.84 <sup>mt</sup>	4.67 <sup>ji</sup>	1.95 <sup>z</sup>	<b>3.54<sup>E</sup></b>
<b>Means</b>	<b>59<sup>B</sup></b>	<b>61<sup>AB</sup></b>	<b>61<sup>AB</sup></b>	<b>59<sup>B</sup></b>	<b>54<sup>C</sup></b>		<b>5.28<sup>A</sup></b>	<b>3.69<sup>C</sup></b>	<b>4.09<sup>B</sup></b>	<b>4.02<sup>B</sup></b>	<b>3.28<sup>D</sup></b>	

Here, GP = germination percentage, MGT = mean germination time, Rs = germination rate, SVI = seed variability index, RE = emergence rate, RL = radicle length, SL = shoot length, STI = salinity tolerance index, DGR = degree germination rate, RFW = root fresh weight, SFW = shoot fresh weight, RDW = root dry weight, SDW = shoot dry weight, NP = normal plants, and ANP = abnormal plants, G1 = Norman, G2 = Midin, G3 = Tsian, G4 = Nareum, G5 = Dufferin, G6 = Somme, G7 = Clli-1400, G8 = Clli-1412, G9 = Clli-1370, and G10 = Clli-1423. The means followed by different letters are statistically different from each other.

It is possible to get a rough idea of a genotype's overall adaptability by looking at the angle between its vector and its germination characteristic. If the angle is small, the genotype's performance in terms of seed germination is outstanding; if it's wide open, it's terrible. Inferring a genotype's propensity or deficit for particular seed germination features may be done by measuring the length or shortness of the vector. According to these explanations, tested genotypes had positive correlation with several seed germination traits, except shoot length (SL) and salinity tolerance index (STI) (Fig. 1A). On the other hand, genotypes 'G4' and 'G6' were positively associated with all seed germination parameters, except SL and STI. Moreover, genotype 'G7' was correlated with SL and 'G9' and 'G10' with STI. It was observed that tested genotypes considerably differed for the observed germination traits. These explanations are confirmed by the correlation values in Fig. 1A, Table 2 and Table 3.

The effects of salinity levels on seed germination traits are visualized in Fig. 1B by biplot polygon. The axis is divided from the center by bold lines, and the regions are separated by bold lines called "sector" and starts at the bottom right of the graph with numbers 1, 2, 3, etc. If the genotypes and germination parameters are in the same sector, there exists a link between them. Fig. 1B is divided into 5 main sectors (separated from each other by a bold line). The genotypes 'G1', 'G3', 'G5' and 'G8' were in sector 1 with shoot dry weight (SDW), root dry weight (RDW) and germination rate

(Rs). The genotypes 'G4' and 'G6' were in sector 3 along with mean germination time (MGT), root length (RL), and normal plants (NP). Similarly, genotypes 'G2' and 'G7' were in sector 4 with SL, and genotypes 'G9' and 'G10' were in sector 5 with STI. The traits including abnormal plants (ANP), degree germination rate (DGR), shoot fresh weight (SFW) and RFW were in sector 2 and did not correlate with any genotypes.

The stability and performance of the genotypes were visualized according to the average of the germination traits (Fig. 1C). The vertical axis with the average data and the horizontal stability axis with the performances of the cultivars were interpreted according to their distance from the axes. The genotypes cannot be preferred if these are located below the vertical axis, whereas those located above the axis are preferable genotypes. On the other hand, if the genotypes are close to or in the middle of the horizontal line (stability line), these are interpreted as stable, and those located away from the horizontal line have low stability. Based on these explanations, genotypes 'G3' and 'G7' were unstable. The genotypes 'G9' and 'G10' were unpredictable as these were located under the vertical axis. Nevertheless, genotypes 'G1', 'G4', 'G5' and 'G6' were located above vertical line; therefore, these are preferable based on seed germination traits.

Fig. 1D visualizes the representative abilities of the genotypes based on seed germination traits. A representative "ideal center" is formed based on the mean values of these traits, and the most

**Table 4**  
Seedling growth traits of flax genotypes under different salinity levels.

Genotype	NaCl levels (mM)						NaCl levels (mM)					
	0	50	100	150	200	Means	0	50	100	150	200	Means
	SL (shoot length)						STI (salinity tolerance index)					
<b>G1</b>	7.52 <sup>c</sup>	7.34 <sup>cd</sup>	5.04 <sup>jl</sup>	2.53 <sup>qt</sup>	2.14 <sup>tu</sup>	<b>4.92<sup>DE</sup></b>	100 <sup>or</sup>	104 <sup>mq</sup>	105 <sup>lq</sup>	103 <sup>nq</sup>	<b>108<sup>ko</sup></b>	<b>104<sup>C</sup></b>
<b>G2</b>	7.89 <sup>bc</sup>	5.80 <sup>sh</sup>	3.93 <sup>lm</sup>	2.86 <sup>os</sup>	6.61 <sup>e</sup>	<b>5.42<sup>B</sup></b>	100 <sup>or</sup>	139 <sup>c</sup>	120 <sup>eh</sup>	80 <sup>s</sup>	<b>67<sup>f</sup></b>	<b>101<sup>C</sup></b>
<b>G3</b>	7.58 <sup>c</sup>	5.37 <sup>hi</sup>	4.65 <sup>jk</sup>	3.34 <sup>mo</sup>	2.18 <sup>tu</sup>	<b>4.62<sup>F</sup></b>	100 <sup>or</sup>	106 <sup>lq</sup>	105 <sup>mqq</sup>	110 <sup>in</sup>	<b>97<sup>qr</sup></b>	<b>104<sup>C</sup></b>
<b>G4</b>	8.72 <sup>a</sup>	7.51 <sup>c</sup>	6.51 <sup>ef</sup>	4.00 <sup>l</sup>	3.01 <sup>or</sup>	<b>5.95<sup>A</sup></b>	100 <sup>or</sup>	103 <sup>mqq</sup>	107 <sup>lp</sup>	92 <sup>r</sup>	<b>55<sup>u</sup></b>	<b>91<sup>E</sup></b>
<b>G5</b>	7.69 <sup>c</sup>	5.88 <sup>fh</sup>	5.22 <sup>hj</sup>	3.68 <sup>ln</sup>	3.17 <sup>np</sup>	<b>5.13<sup>CD</sup></b>	100 <sup>or</sup>	112 <sup>hm</sup>	110 <sup>jn</sup>	114 <sup>gl</sup>	<b>45<sup>v</sup></b>	<b>96<sup>D</sup></b>
<b>G6</b>	8.74 <sup>a</sup>	8.37 <sup>ab</sup>	5.26 <sup>hj</sup>	2.83 <sup>os</sup>	1.87 <sup>uv</sup>	<b>5.42<sup>B</sup></b>	100 <sup>or</sup>	119 <sup>ei</sup>	128 <sup>de</sup>	121 <sup>eg</sup>	<b>116<sup>fk</sup></b>	<b>117<sup>B</sup></b>
<b>G7</b>	8.51 <sup>ab</sup>	7.29 <sup>cd</sup>	6.33 <sup>eg</sup>	4.26 <sup>kl</sup>	2.69 <sup>pt</sup>	<b>5.81<sup>A</sup></b>	100 <sup>or</sup>	119 <sup>ei</sup>	106 <sup>lp</sup>	44 <sup>v</sup>	<b>44<sup>v</sup></b>	<b>83<sup>F</sup></b>
<b>G8</b>	8.87 <sup>a</sup>	7.42 <sup>cd</sup>	5.1 <sup>hj</sup>	3.15 <sup>nq</sup>	2.09 <sup>tu</sup>	<b>5.33<sup>BC</sup></b>	100 <sup>or</sup>	120 <sup>eh</sup>	123 <sup>eg</sup>	118 <sup>fi</sup>	<b>124<sup>df</sup></b>	<b>117<sup>B</sup></b>
<b>G9</b>	8.71 <sup>a</sup>	7.39 <sup>cd</sup>	4.86 <sup>ik</sup>	2.38 <sup>tu</sup>	2.07 <sup>tu</sup>	<b>5.08<sup>CE</sup></b>	100 <sup>or</sup>	107 <sup>lp</sup>	118 <sup>fi</sup>	99 <sup>p<sup>r</sup></sup>	<b>76<sup>s</sup></b>	<b>100<sup>CD</sup></b>
<b>G10</b>	8.44 <sup>ab</sup>	6.83 <sup>de</sup>	5.26 <sup>hj</sup>	2.30 <sup>tu</sup>	1.35 <sup>v</sup>	<b>4.84<sup>EF</sup></b>	100 <sup>or</sup>	201 <sup>a</sup>	148 <sup>b</sup>	104 <sup>mqq</sup>	<b>132<sup>cd</sup></b>	<b>137<sup>A</sup></b>
<b>Means</b>	<b>8.26<sup>A</sup></b>	<b>7.00<sup>B</sup></b>	<b>5.41<sup>C</sup></b>	<b>3.24<sup>D</sup></b>	<b>2.34<sup>E</sup></b>		<b>100<sup>C</sup></b>	<b>123<sup>A</sup></b>	<b>117<sup>B</sup></b>	<b>98<sup>C</sup></b>	<b>86<sup>D</sup></b>	
	DGR (Degrees germination rate)						RFW (root fresh weight)					
<b>G1</b>	98 <sup>io</sup>	96 <sup>fl</sup>	90 <sup>bf</sup>	90 <sup>be</sup>	57 <sup>a</sup>	<b>86<sup>A</sup></b>	0.09 <sup>eh</sup>	0.07 <sup>lo</sup>	0.08 <sup>lo</sup>	0.07 <sup>mp</sup>	0.04 <sup>w</sup>	<b>0.07<sup>E</sup></b>
<b>G2</b>	96 <sup>gl</sup>	121 <sup>v</sup>	99 <sup>ip</sup>	93 <sup>ci</sup>	104 <sup>mr</sup>	<b>103<sup>D</sup></b>	0.08 <sup>im</sup>	0.08 <sup>im</sup>	0.07 <sup>mp</sup>	0.05 <sup>v</sup>	0.04 <sup>wx</sup>	<b>0.06<sup>F</sup></b>
<b>G3</b>	98 <sup>io</sup>	85 <sup>b</sup>	91 <sup>bg</sup>	100 <sup>jp</sup>	92 <sup>ch</sup>	<b>93<sup>B</sup></b>	0.09 <sup>ef</sup>	0.09 <sup>st</sup>	0.08 <sup>fi</sup>	0.08 <sup>fi</sup>	0.07 <sup>nq</sup>	<b>0.08<sup>D</sup></b>
<b>G4</b>	98 <sup>io</sup>	100 <sup>iq</sup>	101 <sup>kq</sup>	104 <sup>nr</sup>	107 <sup>rt</sup>	<b>102<sup>D</sup></b>	0.12 <sup>a</sup>	0.11 <sup>cd</sup>	0.11 <sup>cd</sup>	0.08 <sup>im</sup>	0.05 <sup>v</sup>	<b>0.09<sup>B</sup></b>
<b>G5</b>	98 <sup>in</sup>	100 <sup>jp</sup>	100 <sup>jp</sup>	109 <sup>ru</sup>	99 <sup>jp</sup>	<b>101<sup>D</sup></b>	0.11 <sup>cd</sup>	0.07 <sup>qr</sup>	0.08 <sup>in</sup>	0.08 <sup>fi</sup>	0.02 <sup>z</sup>	<b>0.07<sup>E</sup></b>
<b>G6</b>	98 <sup>io</sup>	101 <sup>lq</sup>	95 <sup>el</sup>	87 <sup>bc</sup>	88 <sup>bd</sup>	<b>94<sup>BC</sup></b>	0.12 <sup>ab</sup>	0.11 <sup>cd</sup>	0.11 <sup>bc</sup>	0.08 <sup>kn</sup>	0.06 <sup>tt</sup>	<b>0.10<sup>A</sup></b>
<b>G7</b>	97 <sup>hm</sup>	98 <sup>hn</sup>	90 <sup>be</sup>	98 <sup>in</sup>	98 <sup>hn</sup>	<b>96<sup>C</sup></b>	0.08 <sup>fi</sup>	0.08 <sup>ei</sup>	0.06 <sup>tu</sup>	0.03 <sup>xv</sup>	0.03 <sup>z</sup>	<b>0.06<sup>G</sup></b>
<b>G8</b>	98 <sup>hm</sup>	112 <sup>su</sup>	105 <sup>or</sup>	107 <sup>rt</sup>	113 <sup>tu</sup>	<b>107<sup>E</sup></b>	0.09 <sup>e</sup>	0.09 <sup>eg</sup>	0.09 <sup>eg</sup>	0.08 <sup>hl</sup>	0.07 <sup>pq</sup>	<b>0.08<sup>C</sup></b>
<b>G9</b>	97 <sup>gl</sup>	100 <sup>iq</sup>	105 <sup>pr</sup>	94 <sup>dk</sup>	106 <sup>qs</sup>	<b>100<sup>D</sup></b>	0.08 <sup>gk</sup>	0.07 <sup>qs</sup>	0.07 <sup>oq</sup>	0.05 <sup>v</sup>	0.04 <sup>wx</sup>	<b>0.06<sup>F</sup></b>
<b>G10</b>	94 <sup>dj</sup>	151 <sup>x</sup>	135 <sup>w</sup>	103 <sup>mr</sup>	115 <sup>uv</sup>	<b>120<sup>F</sup></b>	0.05 <sup>v</sup>	0.05 <sup>uv</sup>	0.06 <sup>t</sup>	0.04 <sup>wx</sup>	0.03 <sup>yz</sup>	<b>0.04<sup>H</sup></b>
<b>Means</b>	<b>97<sup>A</sup></b>	<b>106<sup>A</sup></b>	<b>101<sup>A</sup></b>	<b>98<sup>A</sup></b>	<b>98<sup>A</sup></b>		<b>0.09<sup>A</sup></b>	<b>0.09<sup>B</sup></b>	<b>0.08<sup>B</sup></b>	<b>0.06<sup>C</sup></b>	<b>0.04<sup>D</sup></b>	
	SFW (shoot fresh weight)						RDW (root dry weight)					
<b>G1</b>	0.44 <sup>sg</sup>	0.42 <sup>fi</sup>	0.34 <sup>lp</sup>	0.25 <sup>tw</sup>	0.15 <sup>yz</sup>	<b>0.32<sup>C</sup></b>	0.008 <sup>fi</sup>	0.0066 <sup>mo</sup>	0.0075 <sup>il</sup>	0.0085 <sup>cf</sup>	0.0048 <sup>tt</sup>	<b>0.0071<sup>D</sup></b>
<b>G2</b>	0.37 <sup>jm</sup>	0.38 <sup>il</sup>	0.32 <sup>nr</sup>	0.22 <sup>vx</sup>	0.124 <sup>z</sup>	<b>0.30<sup>D</sup></b>	0.0079 <sup>fi</sup>	0.0066 <sup>mo</sup>	0.0064 <sup>np</sup>	0.0049 <sup>rs</sup>	0.0034 <sup>ww</sup>	<b>0.0058<sup>E</sup></b>
<b>G3</b>	0.47 <sup>bd</sup>	0.36 <sup>ko</sup>	0.36 <sup>kn</sup>	0.31 <sup>or</sup>	0.24 <sup>w</sup>	<b>0.35<sup>B</sup></b>	0.0092 <sup>b</sup>	0.0084 <sup>dg</sup>	0.0092 <sup>b</sup>	0.0084 <sup>cf</sup>	0.0078 <sup>fi</sup>	<b>0.0086<sup>A</sup></b>
<b>G4</b>	0.55 <sup>a</sup>	0.51 <sup>ab</sup>	0.46 <sup>cf</sup>	0.29 <sup>qt</sup>	0.14 <sup>yz</sup>	<b>0.39<sup>A</sup></b>	0.0089 <sup>bd</sup>	0.0083 <sup>dg</sup>	0.0077 <sup>gk</sup>	0.0065 <sup>np</sup>	0.0039 <sup>uv</sup>	<b>0.0071<sup>D</sup></b>
<b>G5</b>	0.46 <sup>bf</sup>	0.29 <sup>qt</sup>	0.34 <sup>lp</sup>	0.31 <sup>p<sup>s</sup></sup>	0.07 <sup>z</sup>	<b>0.30<sup>D</sup></b>	0.0104 <sup>a</sup>	0.0080 <sup>fi</sup>	0.0082 <sup>eh</sup>	0.0088 <sup>be</sup>	0.0028 <sup>wx</sup>	<b>0.0076<sup>C</sup></b>
<b>G6</b>	0.42 <sup>ei</sup>	0.53 <sup>a</sup>	0.39 <sup>kg</sup>	0.27 <sup>ru</sup>	0.25 <sup>tw</sup>	<b>0.37<sup>A</sup></b>	0.0095 <sup>b</sup>	0.0090 <sup>bc</sup>	0.0094 <sup>b</sup>	0.0076 <sup>hk</sup>	0.0064 <sup>np</sup>	<b>0.0084<sup>AB</sup></b>
<b>G7</b>	0.43 <sup>d<sup>h</sup></sup>	0.48 <sup>bc</sup>	0.35 <sup>kp</sup>	0.12 <sup>z</sup>	0.10 <sup>z</sup>	<b>0.30<sup>CD</sup></b>	0.0075 <sup>il</sup>	0.0076 <sup>hl</sup>	0.0072 <sup>km</sup>	0.0025 <sup>x</sup>	0.0023 <sup>x</sup>	<b>0.0054<sup>F</sup></b>
<b>G8</b>	0.47 <sup>b<sup>e</sup></sup>	0.45 <sup>cf</sup>	0.37 <sup>jm</sup>	0.23 <sup>ux</sup>	0.21 <sup>wx</sup>	<b>0.34<sup>B</sup></b>	0.0081 <sup>fi</sup>	0.0074 <sup>il</sup>	0.0082 <sup>eh</sup>	0.0080 <sup>fi</sup>	0.0094 <sup>b</sup>	<b>0.0082<sup>B</sup></b>
<b>G9</b>	0.46 <sup>cf</sup>	0.39 <sup>hl</sup>	0.32 <sup>nr</sup>	0.18 <sup>xy</sup>	0.11 <sup>z</sup>	<b>0.29<sup>D</sup></b>	0.0069 <sup>in</sup>	0.0059 <sup>pq</sup>	0.0062 <sup>op</sup>	0.0049 <sup>rs</sup>	0.0042 <sup>tu</sup>	<b>0.0056<sup>EF</sup></b>
<b>G10</b>	0.26 <sup>s<sup>v</sup></sup>	0.33 <sup>m<sup>q</sup></sup>	0.23 <sup>ux</sup>	0.13 <sup>z</sup>	0.10 <sup>z</sup>	<b>0.21<sup>E</sup></b>	0.0024 <sup>x</sup>	0.0046 <sup>st</sup>	0.0054 <sup>qr</sup>	0.0033 <sup>vw</sup>	0.0034 <sup>w</sup>	<b>0.0038<sup>G</sup></b>
<b>Means</b>	<b>0.43<sup>A</sup></b>	<b>0.41<sup>B</sup></b>	<b>0.35<sup>C</sup></b>	<b>0.23<sup>D</sup></b>	<b>0.15<sup>E</sup></b>		<b>0.0079<sup>A</sup></b>	<b>0.0072<sup>C</sup></b>	<b>0.0075<sup>B</sup></b>	<b>0.0063<sup>D</sup></b>	<b>0.0048<sup>E</sup></b>	

Here, GP = germination percentage, MGT = mean germination time, Rs = germination rate, SVI = seed variability index, RE = emergence rate, RL = radicle length, SL = shoot length, STI = salinity tolerance index, DGR = degree germination rate, RFW = root fresh weight, SFW = shoot fresh weight, RDW = root dry weight, SDW = shoot dry weight, NP = normal plants, and ANP = anormal plants, G1 = Norman, G2 = Midin, G3 = Tsian, G4 = Nareum, G5 = Dufferin, G6 = Somme, G7 = Clli-1400, G8 = Clli-1412, G9 = Clli-1370, and G10 = Clli-1423. The means followed by different letters are statistically different from each other.

suitable genotype can be interpreted according to the proximity or distance from the ideal center. If the genotype is in this ideal center, it is the most ideal, if close to the center and above the average vertical axis, it can be preferred. However, genotypes located below the vertical axis are undesirable. Based on these explanations, genotypes ‘G4’ and ‘G6’ were ideal since they were located upon to perpendicular axis and near to the “ideal center”. On the other hand, genotype ‘G10’ was located under perpendicular axis and far from the “ideal center. Hence, this genotype was undesirable based on seed germination parameters.

### 3.2. Biplot of salinity by germination traits

The biplot of salinity by germination traits (ST) is visualized in Fig. 2A–D. The biplot was generated for salinity concentrations and seed germination traits. The PC1 represented 77.02 % of the variation, whereas PC2 represented 16.92 % and both axes explained a total 93.94 % variation in the data.

Salinity concentrations indicated high variation for seed germination (Fig. 2A). The 100 mM NaCl salinity level was in the center for examined germination traits, while 200 mM NaCl level is far from the center of graph and linked with ANP and MGT. On the other hand, 0-, 50-, and 150-mM salinity levels did not correlate with mean germination traits.

Fig. 2B is divided into main 4 sectors and no salinity level or germination traits were in sector 1. The 50- and 100-mM salinity levels were in sector 2 with GP, RE, SDW and STI, and the control (0 mM) was in sector 2 with RL, SVI, SL, and RFW etc. The 150 and 200 mM NaCl levels were in sector 3 with only ANP and MGT.

The main goal of salinity by germination trait (ST) biplot was to assess the discrimination power and the representativeness of the salinity concentrations (Fig. 2 C). The discriminating ability is reflected by the distance or proximity of a salinity level from the center graph. Hence, the salinity level far from the center has more discriminating ability, and those close to the center show lower discriminative ability. The representative ability refers to the angle between the trait vector and the average tester coordinate (ATC). The smaller angle indicates more representativeness power. The ATC stands for the axis which passes from the biplot origin and the point representing the average of all examined factors. Based on the results, 100 mM NaCl concentration was the most discriminating followed by 0 and 50 mM NaCl. The 150 and 200 mM NaCl levels showed the lowest representativeness and discrimination ability based on seed germination.

The 100 mM NaCl concentration proved ideal for seed germination traits since it was located near the “ideal center”. Moreover, 0 and 50 mM were favorable salinity levels as they were on perpendicular axis. On the other hand, the 150- and 200-mM salinity levels were located under perpendicular axis, and far from “ideal

**Table 5**  
Seedling growth traits of flax genotypes under different salinity levels.

Genotype	NaCl levels (mM)						NaCl levels (mM)					
	0	50	100	150	200		0	50	100	150	200	Means
	NP (Normal plants)						SDW (Shoot dry weight)					
<b>G1</b>	70 <sup>g</sup>	31 <sup>st</sup>	43 <sup>n</sup>	49 <sup>kl</sup>	53 <sup>j</sup>	<b>49<sup>D</sup></b>	0.040 <sup>im</sup>	0.041 <sup>fk</sup>	0.0422 <sup>dj</sup>	0.040 <sup>hl</sup>	0.040 <sup>gk</sup>	<b>0.040<sup>BC</sup></b>
<b>G2</b>	64 <sup>h</sup>	88 <sup>b</sup>	56 <sup>i</sup>	27 <sup>uv</sup>	50 <sup>k</sup>	<b>57<sup>C</sup></b>	0.032 <sup>pq</sup>	0.040 <sup>sk</sup>	0.035 <sup>lo</sup>	0.024 <sup>qs</sup>	0.022 <sup>rs</sup>	<b>0.023<sup>D</sup></b>
<b>G3</b>	32 <sup>rs</sup>	24 <sup>wx</sup>	39 <sup>o</sup>	47 <sup>lm</sup>	38 <sup>op</sup>	<b>36<sup>E</sup></b>	0.044 <sup>bh</sup>	0.048 <sup>ac</sup>	0.046 <sup>af</sup>	0.051 <sup>a</sup>	0.043 <sup>dj</sup>	<b>0.046<sup>A</sup></b>
<b>G4</b>	76 <sup>e</sup>	74 <sup>ef</sup>	83 <sup>c</sup>	36 <sup>pq</sup>	25 <sup>wx</sup>	<b>58<sup>B</sup></b>	0.043 <sup>ch</sup>	0.046 <sup>bf</sup>	0.048 <sup>ab</sup>	0.042 <sup>ek</sup>	0.022 <sup>rs</sup>	<b>0.040<sup>BC</sup></b>
<b>G5</b>	79 <sup>d</sup>	72 <sup>fg</sup>	66 <sup>h</sup>	55 <sup>ij</sup>	27 <sup>uv</sup>	<b>59<sup>B</sup></b>	0.038 <sup>jm</sup>	0.047 <sup>ad</sup>	0.045 <sup>bg</sup>	0.046 <sup>ae</sup>	0.019 <sup>su</sup>	<b>0.040<sup>C</sup></b>
<b>G6</b>	87 <sup>b</sup>	94 <sup>a</sup>	86 <sup>b</sup>	72 <sup>fg</sup>	65 <sup>h</sup>	<b>80<sup>A</sup></b>	0.034 <sup>mo</sup>	0.043 <sup>ci</sup>	0.046 <sup>af</sup>	0.045 <sup>bg</sup>	0.043 <sup>ci</sup>	<b>0.042<sup>B</sup></b>
<b>G7</b>	34 <sup>qs</sup>	40 <sup>o</sup>	36 <sup>pq</sup>	14 <sup>z</sup>	23 <sup>x</sup>	<b>29<sup>F</sup></b>	0.034 <sup>mo</sup>	0.041 <sup>fk</sup>	0.032 <sup>np</sup>	0.014 <sup>uv</sup>	0.013 <sup>v</sup>	<b>0.027<sup>E</sup></b>
<b>G8</b>	46 <sup>m</sup>	54 <sup>ij</sup>	50 <sup>k</sup>	46 <sup>m</sup>	47 <sup>lm</sup>	<b>48<sup>D</sup></b>	0.033 <sup>no</sup>	0.041 <sup>fk</sup>	0.042 <sup>dj</sup>	0.041 <sup>gk</sup>	0.042 <sup>ek</sup>	<b>0.040<sup>C</sup></b>
<b>G9</b>	34 <sup>qs</sup>	32 <sup>s</sup>	35 <sup>qr</sup>	28 <sup>u</sup>	20 <sup>y</sup>	<b>29<sup>F</sup></b>	0.032 <sup>op</sup>	0.035 <sup>lo</sup>	0.037 <sup>kn</sup>	0.032 <sup>op</sup>	0.023 <sup>rs</sup>	<b>0.032<sup>D</sup></b>
<b>G10</b>	23 <sup>x</sup>	29 <sup>tu</sup>	26 <sup>uvw</sup>	16 <sup>z</sup>	19 <sup>y</sup>	<b>22<sup>G</sup></b>	0.021 <sup>rt</sup>	0.031 <sup>op</sup>	0.024 <sup>qr</sup>	0.017 <sup>tv</sup>	0.022 <sup>rt</sup>	<b>0.023<sup>F</sup></b>
<b>Means</b>	<b>54<sup>A</sup></b>	<b>53<sup>A</sup></b>	<b>52<sup>B</sup></b>	<b>39<sup>C</sup></b>	<b>36<sup>D</sup></b>		<b>0.035<sup>B</sup></b>	<b>0.041<sup>A</sup></b>	<b>0.040<sup>A</sup></b>	<b>0.0350<sup>B</sup></b>	<b>0.0289<sup>C</sup></b>	
	ANP (Anormal plants)											
<b>G1</b>	10.0 <sup>o</sup>	6.0 <sup>rt</sup>	17.0 <sup>i</sup>	35.0 <sup>f</sup>	45.0 <sup>c</sup>	<b>23.0<sup>B</sup></b>						
<b>G2</b>	21.0 <sup>j</sup>	1.0 <sup>xy</sup>	9.0 <sup>op</sup>	21.0 <sup>j</sup>	6.0 <sup>st</sup>	<b>12.0<sup>D</sup></b>						
<b>G3</b>	3.0 <sup>uv</sup>	1.0 <sup>xy</sup>	4.0 <sup>uv</sup>	42.0 <sup>d</sup>	42.0 <sup>d</sup>	<b>18.0<sup>C</sup></b>						
<b>G4</b>	10.0 <sup>op</sup>	16.0 <sup>im</sup>	5.0 <sup>tu</sup>	46.0 <sup>c</sup>	72.0 <sup>a</sup>	<b>29.0<sup>A</sup></b>						
<b>G5</b>	6.0 <sup>rs</sup>	23 <sup>i</sup>	19.0 <sup>jk</sup>	34.0 <sup>g</sup>	67.0 <sup>b</sup>	<b>30.0<sup>A</sup></b>						
<b>G6</b>	0.1 <sup>y</sup>	0.1 <sup>y</sup>	2.0 <sup>wx</sup>	15.0 <sup>m</sup>	23.0 <sup>i</sup>	<b>8.0<sup>E</sup></b>						
<b>G7</b>	13.0 <sup>n</sup>	8.0 <sup>qr</sup>	7.0 <sup>rs</sup>	38.0 <sup>e</sup>	27.0 <sup>h</sup>	<b>18.0<sup>C</sup></b>						
<b>G8</b>	5.0 <sup>tu</sup>	4.0 <sup>uv</sup>	3.0 <sup>vw</sup>	9.0 <sup>pq</sup>	9.0 <sup>pq</sup>	<b>6.0<sup>G</sup></b>						
<b>G9</b>	1.0 <sup>xy</sup>	5.0 <sup>tu</sup>	4.0 <sup>uv</sup>	6.0 <sup>st</sup>	19.0 <sup>k</sup>	<b>7.0<sup>F</sup></b>						
<b>G10</b>	0.1 <sup>y</sup>	1.0 <sup>xy</sup>	0.1 <sup>y</sup>	4.0 <sup>uv</sup>	2.0 <sup>wx</sup>	<b>1.0<sup>H</sup></b>						
<b>Means</b>	<b>7.0<sup>C</sup></b>	<b>6.0<sup>D</sup></b>	<b>7.0<sup>CD</sup></b>	<b>25.0<sup>B</sup></b>	<b>31.0<sup>A</sup></b>							

Here, GP = germination percentage, MGT = mean germination time, Rs = germination rate, SVI = seed variability index, RE = emergence rate, RL = radicle length, SL = shoot length, STI = salinity tolerance index, DGR = degree germination rate, RFW = root fresh weight, SFW = shoot fresh weight, RDW = root dry weight, SDW = shoot dry weight, NP = normal plants, and ANP = anormal plants, G1 = Norman, G2 = Midin, G3 = Tsian, G4 = Nareum, G5 = Dufferin, G6 = Somme, G7 = Clli-1400, G8 = Clli-1412, G9 = Clli-1370, and G10 = Clli-1423. The means followed by different letters are statistically different from each other.

**Table 6**  
Pairwise correlations for seed germination and seedling traits of flax genotypes under different salinity levels.

	GP	MGT	Rs	SVI	RE	RL	SL	STI	DGR	RFW	SFW	RDW	SDW	NP
MGT	0.13 ns													
Rs	0.88**	-0.29**												
SVI	0.75**	-0.21*	0.84**											
RE	0.96**	0.04 ns	0.90**	0.76**										
RL	0.17*	-0.16*	0.22*	0.60**	0.19*									
SL	0.06 ns	-0.63**	0.35**	0.59**	0.09**	0.51 ns								
STI	-0.15*	-0.30**	-0.03 ns	-0.06 ns	-0.14 ns	-0.18*	0.19*							
DGR	0.26**	0.28**	0.16 ns	0.13 ns	0.21*	0.40**	0.82**	0.35**	0.01 ns	0.85**				
RFW	0.53**	-0.34**	0.66**	0.79**	0.55**	0.50**	0.61**	0.30**	0.029 ns					
SFW	0.34**	-0.50**	0.57**	0.70**	0.35**	0.40**	0.82**	0.35**	0.01 ns	0.85**				
RDW	0.57**	-0.27**	0.69**	0.64**	0.59**	0.30**	0.39**	0.35**	0.13 ns	0.84**	0.71**			
SDW	0.60**	-0.11 ns	0.63**	0.47**	0.60**	-0.04 ns	0.19*	0.44**	0.19*	0.67**	0.58**	0.79**		
NP	0.48**	-0.09 ns	0.51**	0.60**	0.48**	0.29**	0.35**	0.26**	0.10 ns	0.73**	0.55**	0.64**	0.57**	
ANP	0.34**	0.52**	0.06 ns	-0.10 ns	0.28**	-0.24**9	-0.47**	-0.53**	0.23**	-0.35**	-0.47**	-0.26**	-0.14 ns	-0.19*

\*\* : P < 0.01 probability level, \* : P < 0.05 probability level. ns: not significant.

Here, GP = germination percentage, MGT = mean germination time, Rs = germination rate, SVI = seed variability index, RE = emergence rate, RL = radicle length, SL = shoot length, STI = salinity tolerance index, DGR = degree germination rate, RFW = root fresh weight, SFW = shoot fresh weight, RDW = root dry weight, SDW = shoot dry weight, NP = normal plants, and ANP = anormal plants.

center. Hence these NaCl concentrations were undesirable for seed germination.

3.3. Biplot of genotypes by salinity

The biplot of genotype by salinity (GS) across germination traits is shown in Fig. 3A-D. The PC1 accounted for 93.85 % of the variation, whereas PC2 represented 4.52 % making a total of 98.20 % variation explained by these two axes.

The genotypes show high variation based on salinity concentrations (Fig. 3A). The genotypes ‘G4’, ‘G6’ and ‘G5’ were correlated with 0, 50- and 100-mM salinity levels, while ‘G1’ and ‘G3’ were correlated with 150- and 200-mM salinity concentrations. The

remaining genotypes were not correlated with any salinity concentration.

Fig. 3B is divided into main 5 sectors (separated from each other by a dotted line). The genotypes ‘G4’, G5 and ‘G6’ were in sector 1 with all salinity concentrations. This means that there were no differences among salinity concentrations. On the other hand, other genotypes did not correlate with any NaCl concentrations and distributed in different sectors. Therefore, the genotypes ‘G4’, ‘G5’ and ‘G6’ are suitable for saline areas.

The main goal of genotype by salinity (GS) biplot was to assess the discrimination power and the representativeness of the genotypes (Fig. 3C). The genotype ‘G6’ was the most stable based on salinity concentrations. On the other hand, other genotypes (‘G9’,



'G10' etc.) showed the lowest representativeness and discrimination ability to salinity concentration.

The genotype 'G6' proved ideal genotype as it was located upon to perpendicular axis and near center of the "ideal center" (Fig. 3D). On the other hand, genotypes 'G2', 'G7', 'G9' and 'G10' were located under perpendicular axis and far from "ideal center. Therefore, these genotypes were undesirable. Moreover, the genotypes 'G1', 'G3', 'G4', and 'G5' were located upon perpendicular axis; hence, these are desirable to study salinity tolerance.

#### 4. Discussion

Identifying the optimal circumstances is necessary for identifying the stable genotypes under varying stresses (stress, drought, cold). Identification of resistant varieties is crucial since the major goal of all breeding projects is the production of stress (such as salt, drought, cold, etc.) tolerant genotypes. The performance and productivity of genotypes are affected by several factors, including abiotic stresses (Yan, 2014). In addition, GT (genotype  $\times$  trait), ST (salinity  $\times$  trait), and GS (genotype  $\times$  salinity) relationships should be clearly revealed. A realistic strategy is to determine the acceptable levels of a stress condition for more than one trait (Xu et al., 2014). Therefore, several researchers evaluated genotypes based on multiple traits in different plants with GT, ST and GS relationships in the recent years (Kendal, 2019; Rastogi et al., 2011; Sofi et al., 2022; Yan and Tinker, 2006). There is a negative or positive relationship between traits, and the level of this relationship may vary depending on growth conditions and genotypes (Luo et al., 2015). Therefore, it is necessary to determine ST and GT relationships to determine performance of genotypes under drought, salinity, and cold etc. The physicochemical effects of the osmotic-toxic salts in the solution are brought about by the imposition of osmotic pressure (increasing negative osmotic pressure) as salinity increases. Toxicities from high concentrations of cations and anions, as well as increased osmotic pressure (greater negative osmotic pressure), inhibit seed germination and water uptake (Atak et al., 2006).

The results of GT showed that the genotypes varied depending on the multi-traits. The genotypes 'G4' and 'G6' had better seed germination traits, whereas 'G7' had better SL, and 'G9' and 'G10' had high STI (Fig. 1A-D). The genotypes close to the ideal center and stability line ('G4' and 'G6') can be used and studied in the future, while those far from the ideal center ('G2', 'G9', 'G10') should be eliminated from salinity tolerance studies (Tables 3-5). Significant differences have been recorded for germination rate and radicle length of flax under different salinity levels (Yaver and Pasa, 2009). Although the highest germination rate was recorded under 100 mM (100.0 %), 0 mM and 50 mM salinity levels resulted in the highest values for hypocotyl and radicle length in the current study. These results are similar to earlier studies reporting that the number abnormal seedlings were increased and root and hypocotyl lengths decreased under increasing salinity levels (Zahedi et al., 2011). Different responses of flax seeds and seedlings to varying salt solutions were because of salt components on the membrane permeability or cell wall of the seeds (Tobe et al., 2004). de Oliveira et al. (2018) reported that GT emerges from multivariate methodologies since it assessed the genotypes performance based on multiple traits and allows the identification of desirable traits. Qayyum et al. (2019) reported that germination of flax genotypes was negatively affected by increasing salinity.

The results of ST indicated that the germination traits varied depending on the salinity concentrations. The 100 mM NaCl concentration was the most discriminating followed by 0 and 50 mM NaCl. The 150 and 200 mM NaCl levels showed specific adaptation to ANP, MGT, and the lowest representativeness and

discrimination ability based on seed germination traits (Fig. 2A-D). Root length gives us an important clue in terms of the response of plants to salinity stress because roots are in direct contact with the soil. Roots feed the plant by absorbing water and taking nutrients (Atak et al., 2006). In addition, shoot length is indirectly affected by the development of the roots. Therefore, shoot length is also an important parameter to examine the responses of plants to salinity stress, and it provides important information regarding salinity tolerance of plants (Moghaddam et al., 2018). The results of the current study indicated decrease in root and shoot length with increase in salt concentrations. The highest root and shoot lengths were recorded for control treatment (Table 3). The inhibitory effect of salt concentrations on root and shoot length is similar to earlier studies conducted on halophyte *Agropyron* species (Ashkan and Jalal, 2013), *Nepeta persica* (Mohammadizad et al., 2013), *Cucumis melo* (Sohrabikertabad et al., 2013) and *Linum usitatissimum* (Moghaddam et al., 2018). On the other hand, Gholizadeh et al. (2016) reported that flax seeds were more tolerant to salt stress than echinacea and artichoke seeds during the germination period. Similarly, Çamlıca and Yıldız (2017) reported that NaCl significantly affected basil seed germination, shoot and root length. On the other hand, the highest germination percentage, and the highest root length were found under control condition. Likewise, Kiremit et al. (2017) reported that the highest seedling growth parameters of flax were noted under 2 mM salinity level.

The correlation of seed germination traits resulted in five groups. There were high and positive correlations among GP, Rs, SVI, RE, RL, SL, STI, RFW, SFW, RDW, DGR, SDW, NP, while negative correlation with MGT, ANP and these traits (Table 6). The highest significant positive correlation was found between RE and GP ( $r^2 = 0.96$ ) and Rs ( $r^2 = 0.90$ ), while the highest and most significant negative correlation was found between STI and GP ( $r^2 = -0.15$ ).

#### 5. Conclusion

The current study determined that flax genotypes exhibited large variation for salt tolerance during germination and early seedling growth. The differences among genotypes were observed by biplot method, which confirmed that the genotypes 'G4', 'G5' and 'G6' were more tolerant to salinity. Therefore, these genotypes can be used in future studies to develop salinity-tolerant flax genotypes.

#### Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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