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Evaluation of salinity tolerance of Yemeni chilli pepper genotypes during germination by using different statistically models

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Abstract: Evaluating the genotypes of vegetables is a critical component in establishing effective plant breeding programs. In this study, nine genotypes of Yemeni *Capsicum spp.* were collected from various regions in Yemen to assess their germination capabilities under different salinity levels (0, 50, 100, 150, 200, and 250 mM). The experiment was conducted using a factorial completely randomized design (CRD) with three replicates. Results indicated that increasing salinity levels led to a gradual decline in germination percentage (GRP), mean germination rate (MGR), germination time (MGT), and seedling dry matter (DM%). Additionally, variations in the genotypes' responses to salt stress were evaluated using four models: the slope of the regression line (*b*), the integrated evaluation approach (*DV*), Principal components, and the genotypes' salinity susceptibility index (GSSI). All the classified of genotypes was different by analysis models. Based on the integrated value (*DV*), the genotypes were classified into four sensitivity categories: resistant (*A*, *D*, and *G*), moderately resistant (*F* and *V2*), sensitive (*S* and *Z*), and highly sensitive (*H* and *V3*) to salinity stress. The findings demonstrate that the slope of the regression line is a reliable indicator for assessing genotype sensitivity to salinity, aligning consistently with the integrated value model (*DV*). The insights gained from this research are expected to significantly inform breeding strategies aimed at developing salt-tolerant chilli pepper cultivars, which are essential for successful cultivation in challenging environmental conditions.

1. Introduction

Hot peppers (*Capsicum spp*.) are an important vegetable crop cultivated globally in warm and temperate regions for various purposes (Comparini *et al.*, 2021).They are highly valued for their nutritional content, particularly their vitamin C and capsaicin levels, which provide notable health benefits (Taiti *et al.*, 2024) and antimicrobial activity (Serio *et al.*, 2024). This adaptable crop can be consumed fresh, as a spice, or in dried form (Taiti *et al.*, 2015; Arraf and Al-Madhagi, 2025). Over the past

50 years, global production has steadily increased (FAO, 2022). In 2022, Yemen contributed approximately 18,22 tons of hot peppers, cultivated on 3,24 hectares, representing roughly 2.3% of global production (FAO, 2022). Globally, hot peppers were grown on an estimated 689,33 hectares, yielding a remarkable 788,032.04 tons (FAO, 2022).

Salinity poses a significant challenge to agriculture in arid and semi-arid regions due to the accumulation of dissolved salts caused by soil processes, irrigation practices, drainage patterns, and overuse of fertilizers (Khondoker *et al.*, 2023). Urban expansion and competition for water resources further exacerbate the issue (Suarez, 2001; Sahbeni *et al.*, 2023).

Yemen features a range of climates, including semi-humid, semi-arid, and arid tropical types (Alhadi *et al.*, 2023).

Yemen's extensive coastal region, characterized by a warm climate conducive to pepper cultivation, particularly during the autumn and winter seasons, faces significant challenges related to excessive salinity. An estimated 37,100 hectares of non-desert agricultural land are affected by salinity, while an additional 12 million hectares experience erosion. Furthermore, 3.8 million hectares suffer from varying degrees of salinity, with 3-5% of the land at risk of desertification (USAID, 2010; Gregory *et al.*, 2018).

Yemen is home to numerous chilli genotypes (Colonna *et al.*, 2019), distributed across regions with diverse climates, altitudes, and soil properties (Aldobai and Al-shabi, 2010). Salinity significantly impairs plant growth through mechanisms such as cell membrane destabilization (Hasegawa *et al.*, 2000; Mushtaq *et al.*, 2020), disruption of photosynthesis (Momenpour and Imani, 2018; Zhou *et al.*, 2023), nutrient imbalances (Munns, 1993), and cellular damage (Hasanuzzaman *et al.*, 2021; Ahmad *et al.*, 2022).

Salt tolerance varies across species, genotypes, and cultivars (Khoshsokhan *et al.*, 2012), driven by mechanisms such as ion partitioning and proline synthesis (Hasegawa *et al.*, 2000; Farooqi *et al.*, 2021). These adaptations, along with oxidative stress management and regulated growth responses (Binzel *et al.*, 1985; Long *et al.*, 1994; Maggio *et al.*, 2007; Hasanuzzaman *et al.*, 2021), mitigate stress effects but often reduce overall yield, resulting in smaller plants (Greenway and Munns, 1980; Naeem *et al.*, 2020). Furthermore, the response to salt stress is contingent on the growth stage, with certain studies indicating variations in tolerance across different developmental phases (Mangal *et al.*, 2023; Roșca *et al.*, 2023). Notably, vegetable plants, particularly during early life stages, exhibit heightened sensitivity to salt stress, especially during germination and seedling growth (Miceli *et al.*, 2021).

Research on salt stress tolerance in various crops, including pepper (Qiu *et al.*, 2017) and fenugreek (Al-Maqtary *et al.*, 2024), often focuses on specific salt concentrations and exposure durations. Plant responses to salt stress also vary based on climatic conditions and soil characteristics (Läuchli and Epstein, 1990; Munns and Gilliham, 2015). Elevated salinity levels impede seed germination by reducing water absorption due to osmotic stress, followed by ionic stress. Increased salt concentrations in the germination medium negatively affect seed embryo vitality by disrupted ion transport (Zowain, 2014). An negative correlation exists between salinity and germination in various vegetable plants, including cucumbers (Bolton and Simon, 2019), sweet peppers (Chartzoulakis and Klapaki, 2000; Hannachi and Van Labeke, 2018; Karalija *et al.*, 2024), and tomatoes (Singh *et al.*, 2012). For example, chilli pepper and tomato seeds failed to germinate at 200 mM NaCl (Loganayaki *et al.*, 2020).

Increased salinity prolongs germination time and lowers germination rates (Al-swedi *et al.*, 2020; Dawd and Abdulla, 2020). However, Aktas *et al.* (2006) observed genetic variability in salt accumulation and leaf damage in peppers exposed to 150 mM NaCl for 10 days, indicating potential yield discrepancies. Different vegetable genotypes exhibit varying levels of resistance to salt stress, as demonstrated in studies of 26 tomato genotypes (Devi and Arumugam, 2019), 17 chilli pepper genotypes (Howlader *et al.*, 2018), and 13 *Cucurbita* genotypes (Horuz *et al.*, 2022).

The degree of genotype tolerance to salinity depends on inherent resistance mechanisms, including metabolic responses activated during salt stress (Horuz *et al.*, 2022). Chilli peppers are classified as either sensitive (Lycoskoufis *et al.*, 2005; Giorio *et al.*, 2020; Ntanasi *et al.*, 2024) or moderately salt-tolerant (Maas and Hoffman, 1977; Chartzoulakis and Klapaki, 2000; Zamljen *et al.*, 2022). Among the vegetable plants tested by Loganayaki *et al.* (2020), chilli exhibits greater salinity sensitivity compared to tomatoes and cucumbers. Salinity and alkalinity, as critical abiotic stresses, significantly reduce the growth and productivity of pepper plants (Chartzoulakis and Klapaki, 2000;

Demir and Mavi, 2008; Amirinejad *et al.*, 2017).

Ongoing research efforts by institutes and universities aim to develop agricultural techniques to mitigate the adverse effects of salinity on vegetable crop production. These efforts include breeding salt-tolerant plants (Zhu *et al.*, 2000; Singla-Pareek *et al.*, 2003; Yang *et al.*, 2005), employing grafting techniques on vegetables (Santa-Cruz *et al.*, 2002; Edelstein *et al.*, 2005; Estan *et al.*, 2005) or fruit (Momenpour and Imani, 2018), utilizing growth regulators (Sakamoto and Murata, 2001; Abrahám *et al.*, 2003; Hamdia *et al.*, 2004; Amirinejad *et al.*, 2017), and managing soil salinity through excessive irrigation (Semiz *et al.*, 2014; Sahbeni *et al.*, 2023; Tarolli *et al.*, 2024).

Exploring genetic diversity and understanding the physiological traits of various vegetable genotypes will provide a foundation for future research, including selective breeding and grafting. Therefore, the aim of this study is to evaluate the salinity sensitivity stress of Yemeni chilli genotypes. This research could significantly inform breeding strategies for chilli by examining local genotypes based on significant physiological traits.

2. Materials and Methods

Chilli seed collection

Chilli pepper seeds from local genotypes were collected from various regions in Yemen (Fig. 1, Table 1). Additionally, the F1 Shamakh pepper cultivar, designated as the F code, was included in the study.

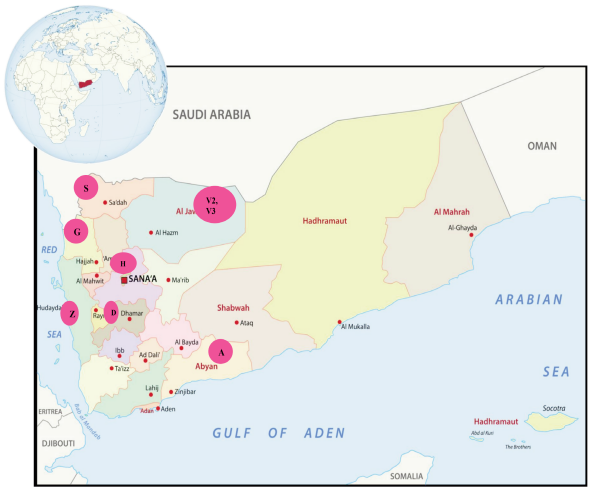

Fig. 1 - The map of Yemen shows the geographic origin of the chili pepper genotypes used in this experiment. The sample names reflect the geographic origin of the samples.

This cultivar, commonly grown in Yemen, was supplied by Agro Star Company, the exclusive agent in Yemen for United Genetics Company (USA) (Fig. 2).

Experimental layout

The study was carried out in the horticultural laboratory using a factorial experimental design based on a completely randomized design (CRD). The experiment included three replicates, with each replicate comprising 10 seeds. Seeds from different genotypes were collected and stored in specially labeled glass containers for future experimental use.

Table 1 - Name and origin of nine chili genotypes used in the study

Research code	Species	Common name	Area of distribution (latitude)	No. fruit per node	Fruit attitude	Spiciness
A	*C. annuum*	Abyani	Abyan (13° 02' 60.00" N) * lahij (13° 02' 60.00" N)	1	hanging	sweet
Z	*C. frutescens*	Zaaitri	Hudaidah (14° 12'00" N)* Taiz (13° 33' 59.99") Ibb (13° 58' 0.01" N)	1	upright	hot
H	*C. frutescens*	Haimi	Sana'a (15.36 N, 44.191006	2	upright	hot
D	*C. annuum*	Dhamari	Dhamar (15° 39' 59.99" N)* Ibb (13° 58' 0.01" N)	1	hanging	hot
V2	*C. chinense*	Jawfi 2	Al-jawf (16° 46' 59.99" N)*	2	Semi upright	hot
V3	*C. chinense*	Jawfi 3	Al-jawf (16° 46' 59.99" N)*	2	hanging	hot
G	*C. annuum*	Hajjai	Hajjai (15° 41' 59.99" N)*	1	hanging	hot
S	*C. frutescens*	Sa'ddi	Sa'dah (16° 56' 5.39" N)*	1	hanging	hot
F	*C. annuum*	Shamakh		1	hanging	

* Main regions where Yemeni chili genotypes were gathered for the research.

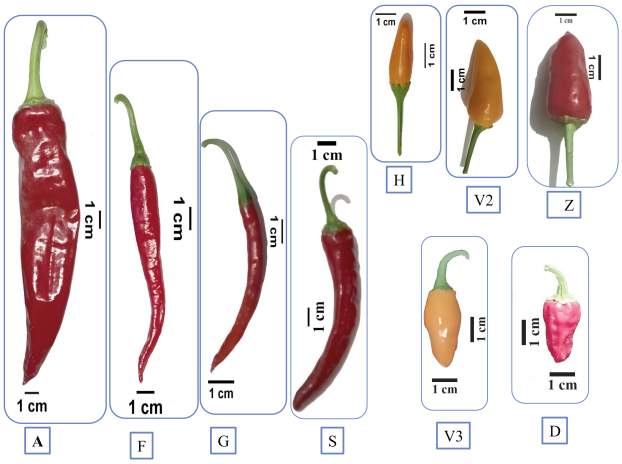

Fig. 2 - Local chilli pepper genotypes utilised in this experiment. The attitude of the peduncle explains the fruit behaviours, with the down peduncle denoted as V2, H, and Z, indicating fruit with upright habits. The length and width of the fruit for different genotypes are shown in cm. The other differences between the fruit of genotypes of chili are clear from colour, size, direction, shape, neck at base of fruit, shape at blossom end, appendage and pedicel with fruit.

Seed sterilization was performed using a solution containing 10% sodium hypochlorite (NaClO), 90% distilled water, and a drop of Tween 20. This process lasted for five minutes. Post-sterilization, the seeds were subjected to a thorough rinsing regime, involving multiple washes with running water, subsequent rinses with distilled water, and finally, a drying phase.

To commence the experimental protocol, 3 milliliters of a sodium chloride (NaCl) solution with different concentrations rate: 0, 50, 100, 200, and 250 mM, were dispensed onto filter paper within Petri dishes. For control treatments, 3 milliliters of distilled water were added to Petri dishes designated for the control group, which did not receive any salinity treatment.

Parameters of study

Data on the seed germination process were carefully recorded daily over a 21-day period, beginning from the start of the experiment. Furthermore, photographic evidence was collected daily for every treatment and replication under examination. The calculated metrics of the germination data is detailed in Table 2.

In the germination equations: N, the total number of seeds in each experimental unit; n_i , the number of seeds germinated in the i^{th} time; k, the last day of germination evaluation; t_i , the period from the commencement of the experiment to the i^{th} observation; G_i, the number of seeds germinated in the i^{th} time; and X_i , the number of days from sowing; SDG denotes the germination standard deviation.

Salinity sensitivity index

The salinity sensitivity index (SSI) values for the each single parameter were calculated separately as (Horuz *et al.*, 2022):

$$SSI = \frac{\text{Salinity level - control}}{\text{Control}} \times 100 \quad (7)$$

Table 2 - The various metrics used to calculate the process of seed germination in the experiment

No.	Measurements	Unit	Equation		References
1	Germination Percentage (GrP)	%	$GrP = \left(\frac{\sum_{i=1}^{k} n_1}{N}\right) \times 100$	1	(Kader, 2005)
2	Mean Germination Time (MGT)	day	$MGT = \frac{\sum_{i=1}^{k} n_i t_i}{\sum_{i=1}^{k} n_i}$	2	(Ranal and Santana, 2006)
3	Mean Germination Rate (MGR)	day^{-1}	$MGR = \frac{1}{MGT}$	3	(Ranal, 1999)
4	Germination speed coefficient (GSC)	%	$GSC = \left(\frac{\sum_{i=1}^{k} G_i}{\sum_{i=1}^{k} G_i X_i}\right) \times 100$	4	(Ranal, 1999)
5	Coefficient of Velocity of Germination (CVG)	%	$CVG = \left(\frac{SDG}{MGT}\right) \times 100$	5	(Ranal, 1999)
6	Dry Matter (DM)	%	$DM = \frac{Dry\ weight}{Fresh\ weight} \times 100$	6	(Al-Madhagi and Al-Sharagi, 2019)

Evaluation of salt tolerance by an integrated evaluation system

The examination of salt tolerance across all genotypes was comprehensively conducted through the application of subordinate function and standard deviation coefficient techniques, utilizing the Stress Intensity (SI) metric to evaluate the effects of salt stress on NaCl concentrations surpassing 100 mM as described by Xie *et al*. (2021). The value of each evaluation index was calculated by the following equations:

$$SI = \frac{\text{Control - Salinity level}}{\text{Control}} \times 100 \quad (8)$$

$$X(u) \quad \frac{x - x\,min}{x\,max - x\,min} \quad (9)$$

$$X(u)\ 1 - \frac{x - x\,min}{x\,max - x\,min} \quad (10)$$

$$Xj = 1/n \sum_{i=1}^{n} xij \quad (11)$$

$$Vj = \frac{\sqrt{\sum_{i=1}^{n}(Xij - \bar{\bar{Xj}})2}}{xj} \quad (12)$$

$$Wj = \frac{Vj \Sigma Vj\, mj}{\sum_{j=1}^{m} vj} \quad (13)$$

$$DV = \sum_{j=1}^{n}[u(xj) \times Wj] \quad (14)$$

Firstly, standardization of index data was conducted using the subordinate function as defined in [Equations (8) and (9)]. For traits negatively correlated with salinity tolerance (NaCl), the dependency value was determined using the inverse subordinate function (Equation 9). Conversely, for traits positively correlated with salinity tolerance, the dependency value was calculated using Equation (8).

In this context, $X(u)$ represents the subordinate function value of the μ^{th} indicator, X denotes the observed indicator value, while X_{max} and X_{min} indicate the maximum and minimum values of the indicator, respectively [Equation (10).

$\bar{\bar{X}}j$ signifies the average of the j^{th} assessment index, with n denoting the total number of genotypes, and Xij referring to the j^{th} evaluation index of the i^{th} genotype [Equation (11)].

Vj represents the standard deviation coefficient of the *jth* evaluation index, with Xj depicting the jth evaluation index of genotypes [Equation (12)].

Wj stands for the weighting coefficient of the j^{th} evaluation index [Equation (13)]. $u(xj)$ corresponds to the subordinate function value of the j^{th} evaluation index.

DV denotes the aggregated values for salt tolerance in chilli pepper [Equation (14)]. A lower in the DV value indicates higher salt tolerance.

Genotypes salinity susceptible index (GSSI)

The tolerance genotypes salinity sensitivity index was calculated for germination percentage by the formula (Afzal *et al.*, 2022):

$$GSSI = (1 - \frac{Gs}{Go})/(1 - \frac{AGS}{AGo}) \quad (15)$$

Where *Gs*: an average of certain genotypes under salinity stress conditions, *Go*: an average of genotypes under optimum conditions, *AGs*: an average of all genotypes under salinity stress conditions, and *AGo*: an average of all genotypes under optimum conditions. The criterion for determining the tolerance level to Salinity stress was this: if the GSSI value is 0.5, then the genotype is tolerant (T), if 0.5 <GSSI≤ 1.0, the genotype is moderate (M), and if GSSI> 1.0 then the genotype is sensitive (S) (Pasaribu *et al.*, 2021).

Estimating genotype sensitivity to salinity using slope of the regression line

The sensitivity of each genotype was evaluated using the *R-square* values and slope coefficients calculated for each parameter. The R-square value serves as an indicator of the significance of a trait, with higher values suggesting greater relevance. In this study, the overall *R-square* values for each trait were considered a measure of their importance in assessing genotype sensitivity to salinity stress. According to the established hypothesis, genotypes exhibiting lower slope values in the context of sub-salinity treatments are classified as resistant. This implies that these genotypes maintain their performance despite increasing salinity levels, thereby demonstrating a higher tolerance to salinity stress compared to those with steeper slope values.

Data analysis

The data were analyzed using the statistical analysis program *GeneStat* 12, then the means of single factors (genotypes or salinity) were compared

using the least significant difference test ($LSD_{0.05}$) ($p< 0.05$). The values of the means of the interactions (genotype × salinity) were compared using a multiple range test ($p< 0.05$). SAS 17 was used for correlation analysis and the principal component, while SPSS 21 was used for regression analysis for each genotype.

3. Results

Germination percentage (GrP)

All factors examined, including salinity stress levels, genotype, and their interaction, had highly significant effects on the germination percentage (GrP) of chilli genotypes ($p<0.001$). Among the sources of variation, genotype explained approximately 73% of the total variation, while salinity stress accounted for 27% of the observed changes in GrP (Table 3).

The mean GrP for the genotypes across all genotypes ranged from a low of 53.9±6.77% for the *G* genotype to a high of 97.2±1.35% for the *D* genotype (Table 4). These values were significantly different (*P < 0.05*) from each other except between the *F* and *Z* genotypes.

Increasing salinity levels dramatically reduced GrP, decreasing from 88.89 ± 2.68% at 0 mM to 62.22 ± 4.90% at 250 mM NaCl. The reduction rate was approximately 0.118% for each additional millimole of NaCl, as described by the regression equation: GrP = 94.97 – 0.118 (NaCl), with an R^2 of 0.539. Among the genotypes, the *D* genotype exhibited the lowest salinity sensitivity in terms of GrP, with the lowest slope value (b = -0.013, R^2 = 0.042), ranking first based on the regression slope value. The remaining genotypes were ranked as follows: *A, S, Z, V2, F, V3*, and *G*.

The *H* genotype showed the highest sensitivity to salinity (b = 0.25, R^2 = 0.62) ranking last (order = 9). Notably, certain genotypes maintained higher GrP at higher salinity levels (250 mM), with *S* (83.3%), *A* (73.3%), and *Z* (73.3%) showing no significant difference from the control treatment (0 mM) (Table 4).

The interaction between genotype and salinity stress revealed that the *D* genotype achieved a GrP of 100% under control condition, significantly differing from the *A* and *V2* genotypes. At the 50 mM NaCl, genotype *A* exhibited the lowest GrP, which was significantly different from the other genotypes. Although the *G* genotype maintained a high GrP in the control treatment, its performance declined with salinity levels exceeding 50 mM, with reductions of 30%, 46.67%, and 36.67% at higher salinity concentrations. Similarly, the *F* hybrid cultivar could not maintain a high GrP beyond 200 mM NaCl (Table 4).

Compared to the control, the *D* genotype displayed significantly greater salt tolerance for GrP across all salinity stress levels, with a positive salt sensitive index (SSI) of 33.3% at 0, 50, 150, and 250 mM NaCl. In contrast, the *V2, H, S*, and *A* genotypes showed significant salt resistance up to 150 mM NaCl. The *G, V3*, and *Z* genotypes exhibited the lowest salt resistance (SSI) up to 50 mM NaCl, while the *F* genotype showed reduced resistance up to 100 mM NaCl (Fig. 3).

Mean germination time (MGT)

The mean germination time (MGT) of all chilli genotypes was significantly influenced by salinity stress levels, genotype, and their interaction (genotype × salinity) compared to the control treatment ($p<0.001$). Genotype accounted for approximately 62% of the total effect (100%), while the remaining 38% was attributed to the influence of salinity on MGT (Table 3). Across the genotypes, MGT varied from the shortest time of 5.82 days for the *D* genotype to the longest times of 11.52 days and 11.16 days for the *G* and *V2* genotypes, respectively (Table 5). These differences were statistically significant (*P<0.05*).

Table 3 - The predictive capabilities that explaining the contribution of salinity and genotypes to the variation in the total score (100%) that affected the germination parameters. The chosen model is a forward stepwise

Factors	GrP	MGT	MGR	GSC	CVG	DM%
Genotypes	73.0	62.0	70.0	70.2	68.0	100
NaCl	27.0	38.0	30.0	29.8	32.0	0

GrP= Germination percentage; MGT= Mean germination time; MGR= Means germination rate; DM%= Dry matter, GSC= Germination speed coefficient; CVG= Coefficient of velocity of germination.

Table 4 - Interaction effects of Yemeni chili genotypes and NaCl levels on the germination percentage (GrP) after 21 days

Genotypes	NaCl mM						Mean genotypes	R2	Coefficient		Order**
	0	50	100	150	200	250			c	b	
A	76.67 ± 14.53 d-g	73.33 ± 6.67 e-h	73.33 ± 6.67 e-h	76.67 ± 6.67 d-g	56.67 ± 8.82 h-j	73.33 ± 8.82 e-h	71.67 ± 3.55 e	0.045	76.15	-0.036	2
D	96.67 ± 3.33 a-c	100 ± 0a	100 ± 0a	100 ± 0 a	86.67 ± 3.33 a-e	100 ± 0a	97.22 ± 1.35 a	0.042	98.88	-0.013	1
F	100 ± 0 a	100 ± 0a	100 ± 0a	83.33 ± 6.67 a-f	90 ± 10 a-e	56.67 ± 3.33 h-j	88.33 ± 4.14 b	0.56	107.14	-0.150	6
G	83.33 ± 6.67 a-f	90 ± 5.77a-e	36.67 ± 18.56 kl	30 ± 0 l	46.67 ± 3.33 j-l	36.67 ± 14.53 kl	53.89 ± 6.77 f	0.41	80.31	-0.21	8
H	93.33 ± 3.33 a-d	96.67 ± 3.33 a-c	96.67 ± 3.33 a-c	93.33 ± 3.33 a-d	50 ± 5.77 i-k	36.67 ± 13.33 kl	77.78 ± 6.39 de	0.62	108.30	-0.25	9
S	93.33 ± 6.67 a-d	96.67 ± 3.33 a-c	93.33 ± 3.33 a-d	100 ± 0 a	76.67 ± 3.33 b-g	83.33 ± 8.82 a-f	90.57 ± 2.62 b	0.21	97.93	-0.059	3
V2	66.66 ± 3.33 f-i	86.67 ± 8.82 a-e	86.67 ± 8.82 a-e	86.67 ± 6.67 a-e	60 ± 20.82 g-j	50 ± 11.55 i-k	72.78 ± 5.29 e	0. 13	84.44	-0.093	5
V3	96.67 ± 3.33 a-c	96.67 ± 3.33 ab	90 ± 0 a-e	93.33 ± 3.33 a-d	63.33 ± 18.56 g-j	50 ± 15.28 i-k	81.68 ± 5.62 cd	0.48	105.23	-0.188	7
Z	93.33 ± 3.33 a-d	100 ± 0 a	83.33 ± 12.02 a-f	83.33 ± 3.33 a-f	93.33 ± 3.33 a-d	73.33 ± 3.33 e-h	87.79 ± 2.87 bc	0.24	96.34	-0.069	4
Mean NaCl	88.89 ± 2.68 ab	93.33± 2.06 a	84.44± 4.34bc	82.96± 4.13c	69.26±4.43d	62.22±4.90e	GrP = 94.97 – 0.118 (NaCl), (R2 = 0.539) *				

Means containing the same Latin letters are not considered significant, as determined by LSD 0.05 for single factors (genotypes or salinity) or by the multiple range Duncan test (MRDT) for the interaction (genotypes × salinity).
Genotypes: A= Abyani; Z =Zaaitri ; H= Haimi; D=Dhamari; V2 = Jawfi 2; V3 = Jawfi 3; G= Hajjai; S = Sa'ddi; F = Shamakh.
The values for R^2 and the regression coefficients, where c = the intercept and b = slope of the line, are provided for the simple regression analysis of each genotype.
* Simple regression equation was performed for the mean of all genotypes (df = 18).

Table 5 - Interaction effects of Yemeni chili genotypes and NaCl levels on the mean germination time (MGT) after 21 days

Genotypes	NaCl mM						Mean Genotypes	*R2*	Coefficient		Order **
	0	50	100	150	200	250			*c*	*b*	
A	9.28 ± 0.7 l-r	7.64 ± 1.27 r-w	7.47 ± 0.83 s-w	10.93 ± 0.15 f-l	11.71 ± 1.4 d-i	14.10± 0.05 ab	10.191 ± 0.65	0.53	7.34	0.023	7
D	4.32 ± 0.63 A	4.23 ± 0.33 A	6.57 ± 1.11 v-y	5.6 ± 0.38 x-A	8.14± 1.16 q-v	6.1± 2.01 w-z	5.83 ± 0.49 g	0.21	4.42	0.011	2
F	8.47 ± 0.33 p-u	8.53 ± 0.18 o-u	9.77 ± 0.23 j-q	10.78 ± 0.57 g-m	11.76± 0.48 c-i	14.16± 0.32 ab	10.58 ± 0.49 bc	0.86	7.78	0.022	5
G	9.85 ± 0.39 j-p	9.61 ± 0.44 k-q	12.32 ± 0.88 c-g	14.33 ± 2.19 a	11.37± 0.64 e-j	11.67 ± 0.33 d-i	11.52 ± 0.55 a	0.137	10.35	0.009	1
H	5.58 ± 0.33 x-A	6.56 ± 0.87 v-y	8.82 ± 0.45 n-t	10.88 ± 0.33 g-l	13.11± 1.34 a-d	12.93 ± 1.16 a-e	9.65± 0.77 de	0.82	5.46	0.033	9
S	4.44 ± 0.16 zA	4.46 ± 0.29 zA	4.5± 0.10 zA	5.43 ± 0.53 y-A	7.91 ± 0.37 r-v	9.75 ± 0.98 j-q	6.08 ± 0.52 g	0.73	3.38	0.022	5
V2	9.14 ± 0.92 m-s	10.52 ± 1.23 h-n	10.22 ± 0.62 i-o	11.08 ± 0.28 f-k	12.61 ± 1.56 b-f	13.41 ± 0.9 a-c	11.16 ± 0.49 ab	0.46	9.12	0.016	3
V3	5.73 ± 0.08 x-A	6.94 ± 0.58 u-y	6.93 ± 0.55 u-y	10.41 ± 0.9 i-n	12.28± 1.02 c-g	12.14 ± 0.77 c-h	9.07 ± 0.67 e	0.791	5.39	0.029	8
Z	4.74 ± 0.39 zA	5.53 ± 0.35 y-A	8.12 ± 0.61 q-v	7.89 ± 0.88 r-v	7.25 ± 0.35 t-x	11.25± 0.41 e-k	7.47 ± 0.54 f	0.677	4.79	0.021	4
Mean NaCl	6.84±0.45 e	7.14±0.45 e	8.30±0.46 d	9.704±0.59 c	10.68±0.50 b	11.72±0.53 a	MGT= 6.45 + 0.0208 (NaCl) (*R2*= 0.775) *				

Means containing the same Latin letters are not considered significant, as determined by LSD 0.05 for single factors (genotypes or salinity) or by the multiple range Duncan test (MRDT) for the interaction (genotypes × salinity).
Genotypes: A= Abyani; Z =Zaaitri ; H= Haimi; D=Dhamari; V2 = Jawfi 2; V3 = Jawfi 3; G= Hajjai; S = Sa'ddi; F = Shamakh.
The values for R^2 and the regression coefficients, where c = the intercept and b = slope of the line, are provided for the simple regression analysis of each genotype.
* Simple regression equation was performed for the mean of all genotypes (df = 18).
** The genotypes are listed in descending order according on the values of the regression slope line (*b*).

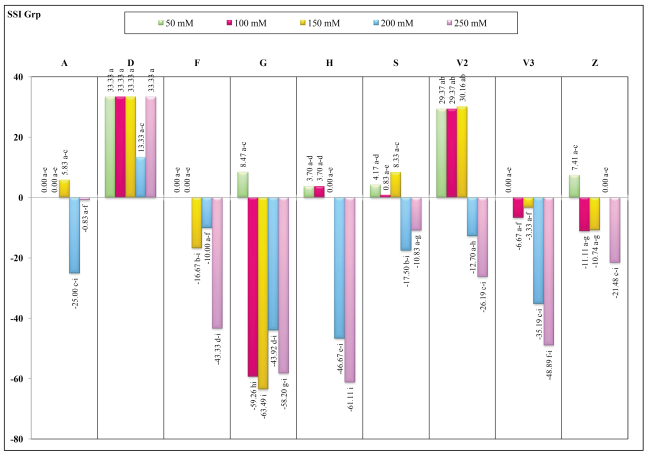

Fig. 3 - Salinity sensitivity index (SSI) for Germination Percentage (GrP) in chili genotypes. Values represent the mean of three replicates. Different letters denote significant differences according to the Duncan Multiple Range Test (DMRT).

Furthermore, the MGT for all genotypes significantly increased ($p < 0.05$) with rising salt levels compared to the control, escalating from 6.84 ± 0.45 days at 0 mM to 11.72 ± 0.53 days at 250 mM. Regression analysis indicated an increase of approximately 0.0202 days for every 1 mM NaCl addition to the control level (MGT = 6.45 + 0.0208 NaCl) ($R^2 = 0.775$). The genotypes were arranged in descending order of MGT response as follows: *G, D, V2, Z, F, S, A, V3*, and *H*. Genotype *G* exhibited the least change in MGT ($b = 0.009$, $R^2 = 0.137$), while the *H* genotype showed the most substantial change ($b = 0.033$, $R^2 = 0.815$).

The interaction between genotypes and salinity stress showed a variation of results. MGT of the *G* genotype was significantly higher (9.85 ± 0.39 days) than that of the other genotypes in the control treatment (0 mM). At salinity levels ranging from 50 to 250 mM, the MGT for the *G* and *V2* genotypes was significantly greater than that of the other genotypes ($p<0.05$). Notably, the *D* genotype consistently exhibited the lowest MGT across all salinity levels. While several genotypes demonstrated increased MGT at the highest salinity levels, genotypes *F*, *H*, and *S* maintained their MGT up to 150 mM NaCl, whereas *G*, *V3*, and *Z* maintained their MGT up to 100 mM NaCl (Table 5).

Salinity sensitivity index (SSI) compared to the control indicated that the *A* genotype exhibited a negative sensitivity to salinity up to 100 mM. MGT values for both 50 mM and 100 mM NaCl were lower than those of the control, the *G* genotype showed negative sensitivity at 50 mM NaCl. In contrast, all other genotypes displayed positive SSI across all salinity levels. The SSI for the *H, V3, S*, and *F* genotypes increased linearly with rising salinity levels. The highest SSI for MGT was recorded at the 250 mM salinity level (139.2%) for the *Z* genotype, whereas the lowest SSI was at 100 mM NaCl (-19.8%) for the *A* genotype (Fig. 4).

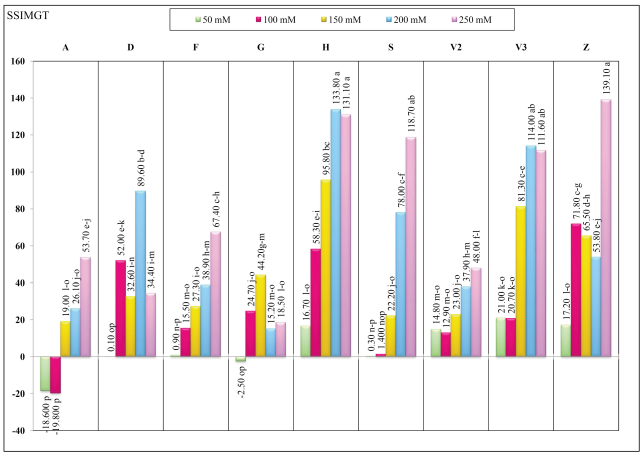

Fig. 4 - Salinity sensitivity index (SSI) for Mean Germination Time (MGT) in chili genotypes. Values represent the mean of three replicates. Different letters denote significant differences according to the Duncan Multiple Range Test (DMRT) at p<0.05.

Germination speed coefficient (GSC)

Germination speed coefficient (GSC) of chilli genotypes was significantly influenced by salinity stress, genotype, and their interaction (genotype × salinity) compared to the control treatment ($p < 0.001$). As shown in Table 3, genotype accounted for approximately 70.2% of the total variation, with the remaining 29.8% attributed to the effect of salinity on GSC.

GSC values between genotypes ranged from the lowest (8.94 ± 0.35%) in genotype *G* to the highest (19.146 ± 1.42%) in genotype *D* (Table 6). These values were statistically different from other genotypes, except for genotype *S*, where no significant differences were observed between *D* and *S*, or between *H* and *V3*.Salinity stress led to a significant reduction in GSC across all genotypes as salt concentrations increased beyond 50 mM NaCl ($p < 0.05$). GSC decreased from 16.4 ± 1.09% at 0 mM to 9.5 ± 0.88% at 250 mM NaCl.

Regression analysis indicated that for every 1 mM increase in NaCl concentration, GSC declined by approximately 0.030% (GSC = 16.518 - 0.030 × NaCl,

Table 6 - Interaction effects of Yemeni chili genotypes and NaCl levels on Germination Speed Coefficient (GSC) after 21 days

Genotypes	NaCl mM					Mean	*R2*	Coefficient		Order **
	0	50	100	150	200	250	Genotypes		*c*	*b*	
A	10.91±0.89 k-s	13.81±2.21 g-j	13.71±1.47 g-j	9.15±0.13 p-x	8.76±0.94 q-x	7.09±0.03 x	10.57±0.74 d	0.39	13.34	-0.022	4
D	24.07±3.15 a	23.93±1.97 ab	16.32±3.23 e-g	18.03±1.26 d-f	12.88±2.08 h-l	19.65±4.98 cd	19.146±1.42 a	0.2	22.97	-0.031	5
F	11.85±0.45 i-o	11.73±0.25 i-p	10.25±0.24 l-u	9.33±0.52 o-x	8.53±0.35 r-x	7.07±0.16 x	9.79±0.43 de	0.9	12.25	-0.02	3
G	10.18±0.4 n-v	10.45±0.49 k-t	8.24±0.59 t-x	7.38±1.32 wx	8.85±0.51 q-x	8.59±0.25 r-x	8.94±0.35 e	0.21	9.924	-0.008	1
H	18.05±1.04 d-f	15.74±1.85 fg	11.4±0.59 i-q	9.21±0.29 o-x	7.78±0.73 u-x	7.86±0.7 t-x	11.67±1.01 c	0.81	17.17	-0.044	8
S	22.57±0.83 ab	22.61±1.56 ab	22.24±0.48 a-c	18.73±1.67 de	12.71±0.58 h-m	10.47±1.09 k-t	18.22±1.25 a	0.78	24.92	-0.054	9
V2	11.16±1.09 j-r	9.77±1.15 o-w	9.86±0.63 n-w	9.04±0.23 q-x	8.22±1.16 t-x	7.53±0.54 v-x	9.26±0.41 e	0.46	10.95	-0.014	2
V3	17.46±0.26 d-f	14.59±1.12 gh	14.62±1.15 gh	9.75±0.84 o-w	8.25±0.66 t-x	8.3±0.49 s-x	12.16±0.91 c	0.83	17.14	-0.04	6
Z	21.39±1.87 bc	18.22±1.13 d-f	12.45±0.89 i-n	13.04±1.64 h-k	13.85±0.67 g-i	8.91±0.34 q-x	14.64±1.07 b	0.69	19.99	-0.043	7
Mean NaCl	16.4±1.09 a	15.65±1.02 a	13.23±0.86 b	11.52±0.82 c	9.98±0.52 d	9.5±0.88 d	*GSC = 16.517917 - 0.030433 (NaCl) (*R2* = 0.758)				

Means containing the same Latin letters are not considered significant, as determined by LSD 0.05 for single factors (genotypes or salinity) or by the multiple range Duncan test (MRDT) for the interaction (genotypes × salinity).
Genotypes: A= Abyani; Z =Zaaitri ; H= Haimi; D=Dhamari; V2 = Jawfi 2; V3 = Jawfi 3; G= Hajjai; S = Sa'ddi; F = Shamakh.
The values for R^2 and the regression coefficients, where c = the intercept and b = slope of the line, are provided for the simple regression analysis of each genotype.
* Simple regression equation was performed for the mean of all genotypes (df = 18).
** The genotypes are listed in descending order according on the values of the regression slope line (b).

$R^2 = 0.758$). Genotype *S* exhibited the greatest reduction in GSC ($b = -0.05$, $R^2 = 0.78$), ranking 9th in the rate of change, whereas genotype *G* exhibited the smallest change ($b = -0.01$, $R^2 = 0.216$), ranking 1st. Genotypes *V2, F, A, D, V3, Z*, and *H* ranked 2nd through 8th, respectively, in the table 6 are reported the values of the genotypes according to their variation rate.

In terms of the genotype × salinity interaction, genotype *D* displayed the highest GSC (24.07 ± 3.15%) at 0 mM NaCl ($p<0.05$), with no significant difference from genotype *S*. At salinity levels between 50 and 250 mM, genotypes *D* and *S* exhibited significantly higher GSC than other genotypes ($p<0.05$), with genotype *D* maintaining the highest GSC at 250 mM NaCl.

The salinity sensitivity index (SSI) analysis for GSC revealed that genotype *A* exhibited a positive SSI up to 100 mM NaCl, exceeding the control values. Genotypes *D* and *G* also demonstrated positive SSI at 50 mM NaCl. Conversely, genotypes *Z, V3, V2, H*, and *F* exhibited negative SSI across all salinity levels, with SSI values for genotypes *F, H, S, V3*, and *V2* decreasing linearly as salinity levels increased. The highest SSI for GSC was observed at 100 mM NaCl (25.3%) in genotype *A*, while the lowest was recorded at 200 mM NaCl (-57.97%) in genotype *H* (Fig. 5).

Mean germination rate (MGR)

The mean germination rate (MGR) of chilli

Fig. 5 - Salinity sensitivity index (SSI) for Germination Speed Coefficient (GSC) in chili genotypes. Values represent the mean of three replicates. Different letters denote significant differences according to the Duncan Multiple Range Test (DMRT) at p<0.05. Genotypes: A = Abyani; Z = Zaaitri ; H= Haimi; D=Dhamari; V2 = Jawfi 2; V3 = Jawfi 3; G= Hajjai; S = Sa'ddi; F = Shamakh.

genotypes was significantly influenced by salinity stress levels, genotype variations, and their interaction (genotype × salinity) compared to control conditions (*p <0.001*). The genotype effect accounted for approximately 70% of the total variation (100%), while salinity contributed 30% to the observed changes in MGR (Table 3). Across the examined genotypes, MGR varied significantly, with the lowest rate recorded for genotypes *F, G*, and *V2* (0.09 seeds/day) and the highest for genotype *D* (0.19 seeds/day) (Table 7). These differences were statistically significant (*p<0.05*); however, no significant difference in MGR was observed between genotypes *D* and *S*.

A marked decline in MGR was observed across all genotypes when salinity levels exceeded 50 mM compared to the control treatment (*p<0.05*). Specifically, MGR decreased from 0.16 ± 0.01 seeds/day at 0 mM NaCl to 0.09 ± 0.008 seeds/day at 250 mM NaCl. Regression analysis indicated that for every 1 mM increase in NaCl, MGR decreased by approximately 0.0003 seeds/day, represented by the equation: MGR = 0.165153 - 0.000304 (NaCl) (R^2 *= 0.758*).The genotypic ranking based on the slope (*b*) of MGR responses to salinity is presented in Table 7. Genotype *S* demonstrated the greatest decline (*b* = -0.00053, R^2 = 0.78), (order 9), whereas genotype *G* exhibited the least decline (b = -0.00008, R^2 = 0.216), while remaining genotypes *V2, F, A, D, V3, Z*, and *H* were ranked in between of them, respectively.

In terms of the genotype × salinity interaction, MGR for genotype *D* was significantly higher (*p < 0.05*) than that of other genotypes under control conditions (0 mM NaCl), except for genotypes *S* and *Z*. At salinity levels ranging from 50 to 250 mM, MGR for genotypes *D* and *S* was significantly higher than that of the remaining genotypes, with genotype *D* achieving the highest MGR (0.19 ± 0.05) at 250 mM (Table 7).

The salinity sensitivity index (SSI) for MGR was positive for genotypes *D, G*, and *S* at 50 mM NaCl, while genotype *A* maintained a positive SSI up to 100 mM NaCl. In contrast, genotypes *Z, V3, V2, H*, and *F* exhibited negative SSI values for MGR across all salinity levels. The decline in SSI was linear for genotypes *F, H, S, V2*, and *V3* with increasing salinity. The highest SSI value for MGR (24.9%) was recorded at 100 mM NaCl for genotype *A*, while the lowest SSI (-58.08%) was observed at 250 mM NaCl for genotype *Z* (Fig. 6).

Table 7 - Interaction effects of Yemeni chili genotypes and NaCl levels on the mean germination rate (MGR) after 21 days

Genotypes	NaCl mM						Mean Genotypes	*R2*	Coefficient		Order **
	0	50	100	150	200	250			*c*	*b*	
A	0.11 ± 0.01 j-q	0.14 ± 0.02 g-j	0.14 ± 0.01 g-j	0.09± 0.001 n-s	0.09 ± 0.01 n-s	0.07± 0.00 s	0.11 ± 0.007 d	0.391	0.134	-0.00022	4
D	0.24± 0.03 a	0.24± 0.02 a	0.16± 0.03 f-g	0.18± 0.01 de	0.13 ± 0.02 h-l	0.19± 0.05 b-d	0.19± 0.014 a	0.199	0.230	-0.00030	5
F	0.12 ± 0.004 i-n	0.12± 0.002 i-n	0.10± 0.002 k-s	0.09± 0.01 m-s	0.09 ± 0.003 n-s	0.07± 0.001 s	0.09± 0.004 de	0.895	0.122	-0.00019	3
G	0.10± 0.004 k-s	0.11 ± 0.004 k-r	0.08± 0.01 o-s	0.07± 0.01 rs	0.09 ± 0.005 n-s	0.09 ± 0.002 n-s	0.09 ± 0.004 e	0.216	0.99	-0.00008	1
H	0.18±0.010 de	0.16 ± 0.02 e-h	0.11± 0.01 j-o	0.09± 0.003 n-s	0.08 ±0.01 q-s	0.08±0.01 p-s	0.12 ± 0.01 c	0.805	0.172	-0.00044	8
S	0.23±0.01 a	0.23 ± 0.02 a	0.22± 0.005 ab	0.19 ± 0.02 c-e	0.13±0.01 h-l	0.11 ±0.01 k-r	0.18± 0.013 a	0.781	0.249	-0.00053	9
V2	0.11±0.01 j-p	0.09± 0.01 l-s	0.09± 0.01 k-s	0.09± 0.002 n-s	0.08±0.01 o-s	0.08 ±0.01 rs	0.09± 0.004 e	0.459	0.110	-0.00013	2
V3	0.18 ± 0.002 d-f	0.15± 0.01 f-i	0.15 ± 0.01 f-i	0.09± 0.01 l-s	0.08±0.01 o-s	0.08±0.01 o-s	0.12± 0.009 c	0.822	0.172	-0.00039	6
Z	0.21± 0.02 a-c	0.18± 0.01 de	0.12± 0.01 i-m	0.13± 0.02 h-k	0.14 ±0.01 g-j	0.09± 0.003 n-s	0.15 ± 0.011 b	0.686	0.200	-0.00043	7
Mean NaCl	0.16±0.01 a	0.16±0.01 a	0.13±0.008 b	0.12±0.008 c	0.09±0.005 d	0.09±0.008 d	MGR= 0.165153 - 0.000304 (NaCl), ($R2$=0.758)				

Means containing the same Latin letters are not considered significant, as determined by LSD 0.05 for single factors (genotypes or salinity) or by the multiple range Duncan test (MRDT) for the interaction (genotypes × salinity).
Genotypes: A= Abyani; Z =Zaaitri ; H= Haimi; D=Dhamari; V2 = Jawfi 2; V3 = Jawfi 3; G= Hajjai; S = Sa'ddi; F = Shamakh.
The values for R^2 and the regression coefficients, where c = the intercept and b = slope of the line, are provided for the simple regression analysis of each genotype.
* Simple regression equation was performed for the mean of all genotypes (df = 18).
** The genotypes are listed in descending order according on the values of the regression slope line (b).

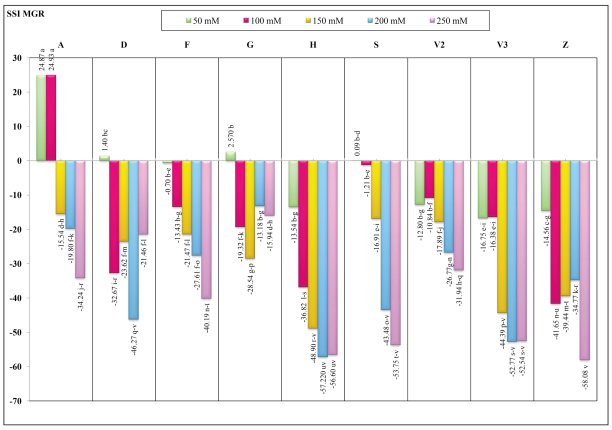

Fig. 6 - Salinity sensitivity index (SSI) for Mean Germination Rate (MGR) for chili genotypes. Values represent the mean of three replicates. Different letters denote significant differences according to the Duncan Multiple Range Test (DMRT) at p<0.05. Genotypes: A= Abyani; Z= Zaaitri ; H= Haimi; D= Dhamari; V2= Jawfi 2; V3= Jawfi 3; G= Hajjai; S = Sa'ddi; F = Shamakh.

Coefficient of velocity of germination (CVG)

The coefficient of velocity of germination (CVG) for all chilli genotypes was significantly influenced by salinity stress levels, genotype differences, and their interaction (genotype × salinity) compared to the control treatment (*p<0.001*). Genotype alone accounted for approximately 68% of the total variation (100%), while salinity contributed an additional 32% to the CVG (Table 3). Among the genotypes, CVG ranged from 18.75±1.45 for genotype *F* to 37.37±3.61 for genotype *V3* (Table 8), with significant differences observed (*p < 0.05*). However, no significant differences were noted among genotypes *V3, A, D, H, S*, and *Z*. Furthermore, increasing salinity levels led to a dramatic decrease in CVG compared to the control (0 mM), with values dropping from 38.48±3.65 (at 0 mM) to 25.69 ± 2.10 (at 250 mM). No significant differences were observed between the 50, 100, and 150 mM NaCl treatments, or between the 200 and 250 mM NaCl treatments (Table 8).

The regression analysis indicated that for every 1 mM increase in NaCl, CVG decreased by approximately 0.0485, as described by the equation: CVG = 37.725 - 0.0485 (NaCl) (R^2 = 0.166). The genotypes were ranked according to their CVG response, with *S, H, F, D, A, Z, G, V3*, and *V2* arranged from 1 to 9, respectively. The *S* genotype exhibited the least impact from salinity (*b* = -0.010, R^2 = 0.004), ranking first, while the *V2* genotype showed the greatest impact (*b* = -0.106, R^2 = 0.53), placing last

Table 8 - Interaction effects of Yemeni chili genotypes and NaCl levels on the Coefficient of velocity of germination (CVG) after 21 days

Genotypes	NaCl mM					Mean	*R2*	Coefficient		Order **
	0	50	100	150	200	250	Genotypes		c	b	
A	45.72± 12.31 a-f	31.36± 8.77 c-o	24.7± 3.03 i-o	36.81± 5.76 a-k	31.03± 8.73 d-o	31.12± 1.39 c-o	33.46± 3.06 ab	0.057	37.87	-0.035	5
D	40.89± 9.68 a-j	29.92± 4.13 e-o	52.68± 17.34 a	23.77± 6.19 j-o	40.96± 5.74 a-j	28.48± 12.21 f-o	36.12± 4.24 a	0.026	40.25	-0.033	4
F	14.17± 4.75 o	20.02± 1.05 k-o	15.96± 4.87 no	19.77± 4.85 k-o	21.66± 1.51 k-o	20.95± 3.49 k-o	18.75± 1.45 d	0.121	15.70	-0.024	3
G	43.07± 7.24 a-h	27.61± 4.35 g-o	30.55± 0.15 e-o	18.09± 9.09 l-o	14.79± 2.26 o	21.82± 0.43 k-o	25.99± 3.21 c	0.42	37.21	-0.087	7
H	31.36± 9.37 c-o	34.19± 11.77 b-l	50.39± 3.52 ab	43.69± 4.06 a-g	32.72± 3.12 c-n	25.64± 7.38 h-o	36.33± 3.33 a	0.021	39.16	-0.023	2
S	33.74± 4.92 b-m	32.49± 6.24 c-n	19.72± 4.31 k-o	42.03± 15.31 a-i	29.23± 3.27 f-o	34.79± 10.11 b-l	32± 3.32a b	0.004	30.72	0.010	1
V2	40.53± 6 a-j	36.37± 6.3 a-k	33.98± 5.3 b-m	24.84± 6.31 i-o	18.4l± 5.53 m-o	16.01± 5.66 no	28.35± 3.004 bc	0.535	41.61	-0.106	9
V3	48.33± 11.17 a-d	52.59± 7.09 a	30.79± 2.22 e-o	36.53± 5.6 a-k	33.2± 11.54 b-n	22.77± 2.72 k-o	37.37± 3.61 a	0.349	50.24	-0.103	8
Z	48.48± 22.35 a-c	35.32± 12.02 b-l	41.35± 1.2 a-i	47.3± 13.64 a-e	17.2± 1.79 m-o	29.66± 4.84f -o	36.55± 4.87 a	0.12	46.73	-0.081	6
Mean NaCl	38.48±3.65a	33.32±2.66 b	33.35±2.99 b	32.54±3.16 b	26.58±2.30 c	25.69±2.10 c	* CVG= 37.725 - 0.0485(NaCl), ($R2$=0.166)				

Means containing the same Latin letters are not considered significant, as determined by LSD 0.05 for single factors (genotypes or salinity) or by the multiple range Duncan test (MRDT) for the interaction (genotypes × salinity).
Genotypes: A= Abyani; Z =Zaaitri ; H= Haimi; D=Dhamari; V2 = Jawfi 2; V3 = Jawfi 3; G= Hajjai; S = Sa'ddi; F = Shamakh.
The values for R^2 and the regression coefficients, where c = the intercept and b = slope of the line, are provided for the simple regression analysis of each genotype.
* Simple regression equation was performed for the mean of all genotypes (df = 18).
** The genotypes are listed in descending order according on the values of the regression slope line (b).

(Table 8).

Interaction between genotype and salinity stress, under control conditions (0 mM), genotype *Z* showed a CVG of (48.48 ± 22.35) higher than the lower values observed for genotypes *F* (14.17 ± 4.75) and *H* (31.36 ± 9.37) (Table 8). At salinity levels ranging from 50 to 250 mM, the CVG for genotype *F* was statistically lower than that of the other genotypes. The genotype *F* showed a positive salinity sensitivity index (SSI) for CVG across all salinity levels. In contrast, genotypes *V2, A*, and *G* exhibited negative SSI values for CVG at all salinity levels, with genotype *V3* showing negative values above 50 mM NaCl. The *H* genotype maintained a positive SSI up to 200 mM NaCl, while genotype *Z* exhibited positive SSI values at the initial two salinity levels. The highest SSI value for CVG was observed at the 200 mM NaCl (98.5%) for genotype *F*, whereas the lowest was recorded at 200 mM NaCl (-65.46%) for genotype *G* (Fig. 7).

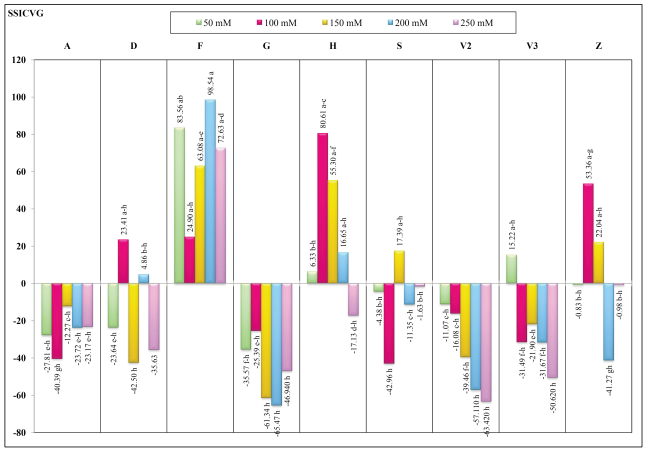

Fig. 7 - Salinity sensitivity index (SSI) of Coefficient of Velocity of Germination (CVG) in chili genotypes. Values represent the mean of three replicates. Different letters denote significant differences according to the Duncan Multiple Range Test (DMRT) at p < 0.05. Genotypes: A = Abyani; Z = Zaaitri ; H= Haimi; D=Dhamari; V2 = Jawfi 2; V3 = Jawfi 3; G= Hajjai; S = Sa'ddi; F = Shamakh.

Dry matter of germinated seed (DM%)

The dry matter percentage (DM%) of all chilli genotypes was significantly influenced by salinity stress levels, genotype differences, and the interaction between genotype and salinity stress when compared to the control treatment (*p < 0.05*).

Across the genotypes, DM% ranged from 7.77 ± 0.74% for genotype *G* to 17.95 ± 1.38% for genotype *Z*. No significant differences were observed among genotypes *S, H, F*, and *A* (Table 9). Furthermore,

Table 9 - Interaction effects of Yemeni chili genotypes and NaCl levels on the percentage of dry matter (DM%) after 21 days

Genotypes	NaCl mM						Mean	*R2*	Coefficient		Order **
	0	50	100	150	200	250	Genotypes		*c*	*b*	
A	10.95± 0.25 g-o	10.33± 1.33 h-o	10.1± 0.89 h-o	10.19± 0.6 h-o	13.01± 0.2 e-l	10.24± 0 h-o	10.8± 0.45 cd	0.40	9.18	0.014	2
D	14.86± 1.72 d-i	16.67± 1.84 b-f	15.01± 5.07 d-h	20.31± 0.62 ab	13.48± 0.87 e-k	16.9± 1.18 b-e	16.2± 1.04 b	0.004	15.72	0.003	3
F	11.95± 1.83 e-m	13.87± 0.92 e-k	9.49± 1.96 k-q	15.55± 1.75 c-g	6.79± 2.84 n-r	5± 0 p-r	10.44± 1.06 d	0.27	13.94	-0.026	8
G	9.98± 0.98 h-o	10.34± 0.51 h-o	9.39± 1.57 k-q	4.5± 0.71 r	4.06± 0.04 r	8.33± 2.15 l-r	7.77± 0.74 e	0.258	10.05	-0.018	5
H	12.28± 1.51 e-m	13.05± 1.96 e-l	11.74± 0.7 f-n	13.37± 1.03 e-l	7.7± 0.3 m-r	4.83± 0 qr	10.5± 0.86 d	0.51	14.19	-0.030	9
S	11.45± 1.9 g-o	10.98± 1.16 g-o	10± 2.13 h-o	14.82± 3.12 d-i	6.53± 2.93 o-r	4.67± 0.6 r	9.74± 1.1 d	0.21	12.77	-0.024	7
V2	9.7± 1.25 j-p	10.02± 0.61 h-o	11.1± 0.23 g-o	11.55± 1.7 g-o	14.71± 1.08 d-j	15.98± 0.35 b-g	12.18± 0.67 c	0.66	8.89	0.026	1
V3	12.23± 1.52 e-m	13.37± 3.28 e-l	14.38± 0.79 d-k	9.86± 2.85 i-o	10.44± 4.5 h-o	13.42± 0 e-k	12.28± 0.99 c	0.008	12.80	-0.004	4
Z	19.81± 6.08 a-c	22.17± 4.23 a	16.71± 3.39 b-f	14.18± 0.78 d-k	19.06± 2.4 a-d	15.78± 1.85 b-g	17.95± 1.38 a	0.074	20.23	-0.018	5
Mean NaCl	12.58±0.93 ab	13.42±0.93 a	11.99±0.82 bc	12.7±0.96 ab	10.64±1.08 cd	10.57±1.07 d	*DM%= 13.253599 -0.010085(NaCl) , (*R2* =0.12)				

Means containing the same Latin letters are not considered significant, as determined by LSD 0.05 for single factors (genotypes or salinity) or by the multiple range Duncan test (MRDT) for the interaction (genotypes × salinity).
Genotypes: A= Abyani; Z =Zaaitri ; H= Haimi; D=Dhamari; V2 = Jawfi 2; V3 = Jawfi 3; G= Hajjai; S = Sa'ddi; F = Shamakh.
The values for R^2 and the regression coefficients, where c = the intercept and b = slope of the line, are provided for the simple regression analysis of each genotype.
* Simple regression equation was performed for the mean of all genotypes (df = 18).
** The genotypes are listed in descending order according on the values of the regression slope line (b).

increasing salinity levels led to a significant decline in DM%, with values decreasing from 12.58 ± 0.93% at 0 mM to 10.57 ± 1.07% at 250 mM. No significant differences were detected between salinity levels from 0 mM to 150 mM (Table 9).The regression analysis indicated the effect of salinity on dry matter, with the order of genotypes ranked as *V2, A, D, V3, G, Z, S, F*, and *H* from 1 to 9, respectively.

According to the R^2 values, salinity had a minimal influence on genotypes *D* (b = -0.003, R^2 = 0.004) and *V3* (b = -0.004, R^2 = 0.008), while it exerted the most significant effect on genotype *H* (b = -0.03, R^2 = 0.51) (Table 9). Regarding the interaction between genotype and salinity stress, the DM% for genotype *Z* was significantly higher than the one of the other genotypes across all salinity levels tested (0, 50, 100, 200, and 250 mM). At 150 mM NaCl, genotype *D* exhibited a significantly higher DM% compared to the other genotypes (Table 9).

In terms of the salinity sensitivity index (SSI) for DM%, genotypes *V2* and *D* displayed positive SSI values across all salinity levels. Genotype *A* showed a positive SSI value under salinity levels up to 150 mM. In contrast, genotype *G* exhibited negative SSI values under salinity levels up to 50 mM. The lowest SSI value for DM% was recorded at the 150 mM salinity level (-71%) for genotype *G*, while the highest SSI value was observed at the 250 mM salinity level (72.7%) for genotype *D* (Fig. 8).

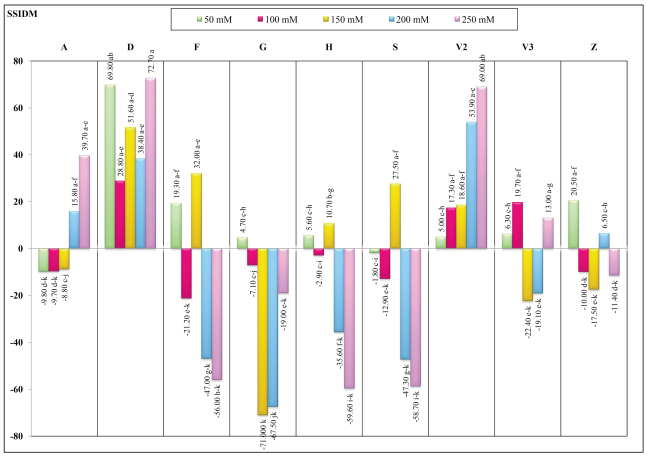

Fig. 8 - Salinity sensitivity index for Dry matter of seedling (DM%) in chili genotypes. Values represent the mean of three replicates. Different letters denote significant differences according to the Duncan Multiple Range Test (DMRT) at p<0.05. Genotypes: A = Abyani; Z = Zaaitri ; H= Haimi; D=Dhamari; V2 = Jawfi 2; V3 = Jawfi 3; G= Hajjai; S = Sa'ddi; F = Shamakh.

Pearson correlation and principal component analysis

The Principal component analysis (PCA) conducted in this study (Table 10) classified the variables into two primary components have eigenvalues greater than 1, which together explained 76.2% of the total variance observed. The first principal component (PC1) exhibited an eigenvalue of 2.75, accounting for 55.11% of the overall variance (Table 10). The coefficients associated with PC1 indicate higher correlations with: DM% (0.713), GrP (0.808), MGT (-0.715), MGR (0.881), and CVG (0.552) (Table 11). The second principal component (PC2) demonstrated an eigenvalue of 1.079, explaining 21.585% of the variance in the data (Table 11). The biplot diagram (Fig. 9) displays both the first and second principal component (PC) scores of the various parameters. Strong positive correlation of PC1 with both CVG and DM%, as confirmed by the Pearson correlation coefficient (r= 0.44, p> *0.01*) (Fig. 10). Additionally, MGR and GrP exhibited a significant positive correlation (r= 0.58, p> *0.01*), indicating their

Table 10 - The Eigenvalue, variability (%) and the cumulative percentage of the principal component for first, second, third, fourth and fifth components

Number of principal component	Cumulative Percentage	Eigenvalue	Percentage
1	55.11	2.755.500	55.11
2	76.69	1.079.260	21.58
3	87.12	0.521455	10.42
4	96.24	0.455748	9.11
5	100.00	0.188037	3.76

Table 11 - The coefficients of the principal component score (Prin) for first to fifth components

Parameters	Prin1	Prin2	Prin3	Prin4	Prin5
DM%	0.71321	0.37635	0.57006	-0.15021	-0.0464
grp	0.80819	-0.01046	-0.00483	0.58824	0.02586
mgt	-0.71563	0.62246	0.07473	0.13852	0.27505
mgr	0.88102	-0.23142	-0.13593	-0.23594	0.31001
cvg	0.55258	0.70463	-0.41521	-0.1109	-0.11599

The principal components are based strongly correlated of parameters with each component. Number with light color means no correlation.

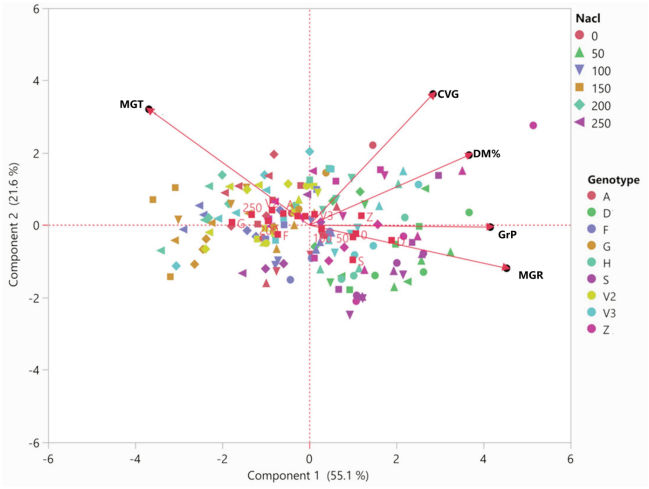

Fig. 9 - Biplot Principal Component Analysis (PCA) of various parameters contributing of MGT, CVG, DM% and GrP to salinity and genotypes. Genotypes: A= Abyani; Z= Zaaitri H= Haimi; D= Dhamari; V2= Jawfi 2; V3= Jawfi 3; G=Hajjai; S = Sa'ddi; F= Shamakh.

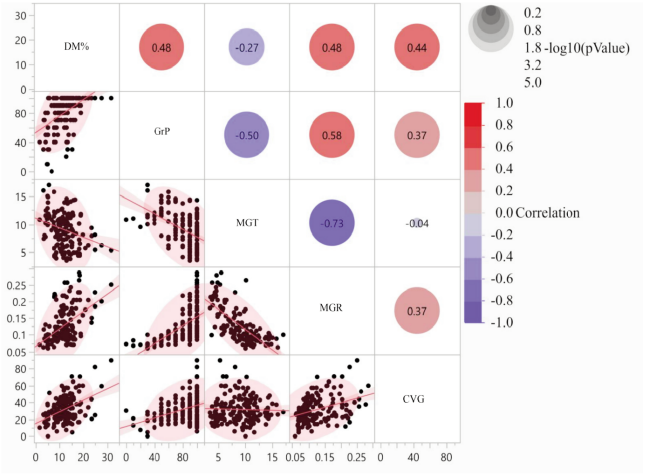

Fig. 10 - The correlation matrix (Pearson) displaying the relationships among parameters investigated in the current study. Significant correlations are detailed below the diagonal, whereas above the diagonal, correlations between parameters under various treatments. The degree of correlations between these parameters under treatment is shown by varying sizes of circles and shades of color that correspond to different correlation values.

effectiveness as prominent indicators of salinity stress resilience.

Conversely, PC1 exhibited a negative correlation with MGT. The analysis revealed a significant negative correlation between MGT and MGR (r= -0.73, $p>0.01$), suggesting that genotypes characterized by shorter MGTs tend to display higher MGR under saline conditions. A similar negative correlation was observed between MGT and GrP (r = -0.50, $p > 0.01$), indicating that genotypes with lower MGTs achieve higher GrP in response to salinity stress.

The PCA biplot (Fig. 9) and data from Table 12 show that the genotypes were distributed across all

Table 12 - The coefficients of the principal component score (Prin) for first to fifth components for genotypes and salinity, with ranking of Yemeni chili genotypes for salinity tolerance, determined by the cumulative coefficients of the principal component score (Prin) for first and second components values

Factors		Prin1	Prin2	Prin3	Prin4	Prin5	Order	Grope
Genotypes	A	-0.59566	0.32256	-0.09868	-0.08734	-0.09748	6	3
	D	189.235	-0.41852	0.10463	-0.20911	0.10728	1	1
	F	-0.72275	-0.25615	0.43255	0.80284	0.18231	8	4
	G	-177.313	0.0807	-0.2378	-0.34424	0.1064	9	4
	H	-0.26658	0.25372	-0.35926	0.03307	-0.0791	5	4
	S	10.002	-0.95791	-0.67273	-0.0669	0.21997	4	1
	V2	-0.85458	0.41669	0.34601	0.11202	-0.01167	7	3
	V3	0.12219	0.29816	-0.15171	0.02071	-0.17465	3	2
	Z	119.796	0.26074	0.637	-0.26106	-0.25305	2	2
	0	107.166	-0.23484	-0.36013	-0.16135	-0.05502		
Salinity	50	100.443	-0.32537	-0.01125	0.09954	-0.01775		
	100	0.28284	-0.0954	-0.11151	0.06181	-0.10089		
	150	-0.09113	0.24656	0.10626	0.19838	-0.05322		
	200	-0.94522	0.11829	0.15719	-0.02344	0.04212		
	250	-132.258	0.29076	0.21944	-0.17494	0.18476		

The principal components are based strongly correlated of parameters with each component. Number with light color means no correlation. Order = the rank of genotypes according to summation of values the prin1 and Prin 2. Genotypes: A = Abyani; Z = Zaaitri ; H= Haimi; D=Dhamari; V2 = Jawfi 2; V3 = Jawfi 3; G= Hajjai; S = Sa'ddi; F = Shamakh.

four quadrants, highlighting significant genetic variation among the tested genotypes. Genotypes D and S appeared in the quadrant with the highest PC1 and lowest PC2 values, indicating tolerance and a strong correlation with MGR and GrP. Genotypes Z and V3 were positioned in the quadrant with the highest PC1 and highest PC2 values, displaying a strong correlation with CVG and DM, suggesting moderate resistance. In contrast, genotypes A and V2 were located in the quadrant with the lowest PC1 and highest PC2 values, indicating sensitivity and a close correlation with MGT. Genotypes F and G were placed in the quadrant with the lowest PC1 and lowest PC2 values, reflecting very high sensitivity and showing no correlation with germination parameters. Based on the cumulative PC1 and PC2 scores, the chilli genotypes were ranked from 1 to 9, with genotype D ranked the highest (Order 1) and genotype G ranked the lowest (Order 9), indicating its heightened sensitivity to salinity stress (Table 12).

PC1 of NaCl showed a positive correlation at concentrations ranging from 0 to 100 mM. However, it was negatively correlated, with no significant effect at 150 mM, and significantly negatively correlated at concentrations of 200 to 250 mM NaCl.

Evaluation of salinity tolerance in Yemeni chilli genotypes by integrated value (DV)

The salt tolerance levels among the chilli genotypes in this experiment were assessed using the integrated value (*DV*), as presented in Table 12. The weighted coefficients indicate the significance of various parameters in measuring the sensitivity of the genotypes to salinity. Notably, germination rate percentage (GrP), mean germination time (MGT), mean germination rate (MGR), and germination speed coefficient (GSC) collectively accounted for over 70% of the overall weight in this study.

The arrangement of integrated values (*DV*) ranked the genotypes according to their salt tolerance, with genotype A occupying the top position (rank 1), indicating higher resistance to salinity. In contrast, genotype *H* ranked last (order 9), reflecting greater sensitivity to salinity. Based on the integrated value (*DV*), the genotypes were categorized into four groups: resistant (*D*, *A*, and *G*), moderately resistant (*F* and *V2*), sensitive (*S* and *Z*), and highly sensitive (*H* and *V3*) to salinity (Fig. 11).

Additionally, the Genotypes Salinity Susceptibility

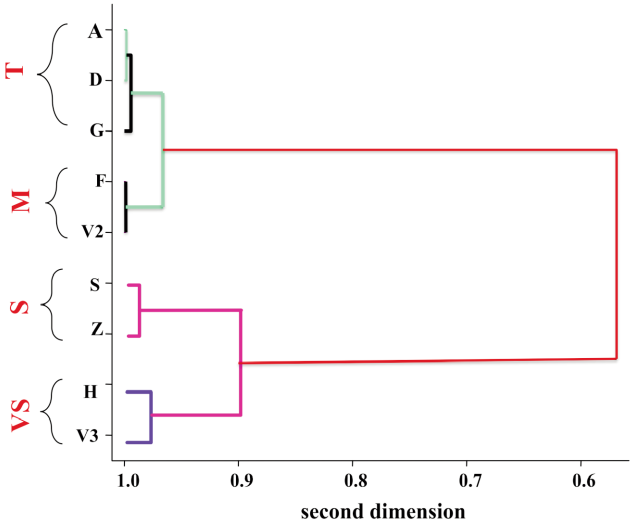

Fig. 11 - Cluster analysis of 9 chilli genotypes using integrated value (VD). The first group contains salinity-resistant (T) genotypes. The second group contains genotypes that are moderately sensitive (M) to salinity; the third group contains genotypes that are sensitive (S) to salinity; and the fourth group contains genotypes that are very sensitive to salinity (VS). Genotypes: A= Abyani; Z =Zaaitri ; H= Haimi; D=Dhamari; V2 = Jawfi 2; V3 = Jawfi 3; G= Hajjai; S = Sa'ddi; F = Shamakh.

Index (GSSI) was calculated based on GrP (Table 13). The results indicated that genotypes *A* and *D* were tolerant to salinity, while genotypes *F*, *G*, *H*, and *V3* were sensitive. Genotypes *V2* and *Z* are exhibited moderate sensitivity to salinity. Interestingly, the ranking of genotypes according to the subordinate function of GrP (O GrP) slightly differed from that of the GSSI, as genotype *A* ranked fifth in O GrP but was classified as tolerant in the GSSI assessment.

Evaluation of salinity tolerance in Yemeni chilli genotypes by regression slop

In this study, the significance of various traits was assessed through the R-square (R^2) values derived from total regression analyses for each genotype across all measured characteristics. Higher R^2 values indicate a greater significance of the trait, while lower values suggest diminished relevance. The R^2 values for germination percentage (GrP), mean germination time (MGT), mean germination rate (MGR), and germination speed coefficient (GSC) were all above 50%, with values of 53, 77, 76, and 76 %, respectively (Table 13). These findings demonstrate that salinity significantly affects these traits, providing a reliable measure of the sensitivity of the

genotypes employed in this experiment. Conversely, the R^2 values for germination velocity coefficient (CVG) and dry matter (DM) were markedly lower, indicating that these traits are less significant, with R^2 values below 0.25.

Table 14 summarizes the slope values obtained from the regression analyses for each genotype across all parameters. Genotypes with higher slope values (*b*) are regarded as being more a*dv*ersely affected by salinity and thus exhibit lower resistance to salt stress. Based on the summation of slope values for each genotype across all parameters, the genotypes were ranked from 1 to 9, with genotype *A* achieving the highest rank, followed by genotype *D*.

Table 13 - The values of the subordinate function, integrated value (DV), and order of each chili genotypes under salt stress. GrP means germination percentage, MGT means germination time, MGR means germination rate, MD% means dry matter, GSC means germination speed coefficient, CVG germination velocity coefficient on the 21th day, GSSI Genotypes Salinity Susceptible Index and Wj is the weighted coefficient

Genotypes	GrP	MGT	MGR	DM%	GSC	CVG	D	Order	O GrP	Grope (GSSI) *
A	0.074	0.238	0.059	0.093	0.060	0.099	0.622	1	5	T
D	0.036	0.261	0.086	0.091	0.079	0.080	0.634	2	1	T
F	0.096	0.251	0.082	0.098	0.085	0.082	0.695	4	6	S
G	0.099	0.245	0.071	0.084	0.073	0.098	0.671	3	7	S
H	0.125	0.325	0.157	0.086	0.162	0.083	0.937	9	9	S
S	0.053	0.314	0.148	0.088	0.153	0.072	0.828	6	3	T
V2	0.072	0.264	0.101	0.091	0.104	0.101	0.733	*5*	4	M
V3	0.103	0.328	0.157	0.079	0.162	0.098	0.926	8	8	S
Z	0.049	0.340	0.163	0.076	0.168	0.080	0.876	7	2	M
WJ	0.18	0.20	0.20	0.11	0.21	0.11				

The principal components are based strongly correlated of parameters with each component. Number with light color means no correlation. Order = the rank of genotypes according to summation of values the prin1 and Prin 2. Genotypes: A = Abyani; Z = Zaaitri ; H= Haimi; D=Dhamari; V2 = Jawfi 2; V3 = Jawfi 3; G= Hajjai; S = Sa'ddi; F = Shamakh.

Table 14 - The ranking of Yemeni chili genotypes for salinity tolerance, determined by the cumulative regression line slope values of seed germination parameters. The R^2 values represent the strength of association for each parameter

Genotypes	GrP	MGT	MGR	CVG	DM%	GSC	∑	Order
A	-0.036	0.023	-0.00022	-0.035	0.014	-0.022	-0.0342	1
D	-0.013	0.011	-0.0003	-0.035	0.003	-0.031	-0.0343	2
F	-0.15	0.022	-0.00019	-0.035	-0.026	-0.02	-0.1892	6
G	-0.21	0.009	-0.00008	-0.035	-0.018	-0.008	-0.2541	8
H	-0.25	0.033	-0.00044	-0.035	-0.03	-0.044	-0.2824	9
S	-0.059	0.022	-0.00053	-0.035	-0.024	-0.054	-0.0965	4
V2	-0.093	0.016	-0.00013	-0.035	0.026	-0.014	-0.0861	3
V3	-0.188	0.029	-0.00039	-0.035	-0.004	-0.04	-0.1984	7
Z	-0.069	0.021	-0.00043	-0.035	-0.018	-0.043	-0.1014	5
R2	0.539	0.775	0.758	0.166	0.12	0.758		

The principal components are based strongly correlated of parameters with each component. Number with light color means no correlation. Order = the rank of genotypes according to summation of values the prin1 and Prin 2. Genotypes: A = Abyani; Z = Zaaitri ; H= Haimi; D=Dhamari; V2 = Jawfi 2; V3 = Jawfi 3; G= Hajjai; S = Sa'ddi; F = Shamakh.

In contrast, genotype *H* was ranked last (order 9), indicating its greater susceptibility to salinity stress.

4. Discussion and Conclusions

Natural hybridization in peppers plays a vital role in the development of numerous species and varieties; however, it also complicates their classification due to overlapping traits (Comparini *et al.*, 2021). Of approximately 35 *Capsicum* species found in nature, only five have been domesticated for human use (Comparini *et al.*, 2021; Swamy, 2023).This study focuses on three Yemeni chilli species: *C. frutescens, C. annuum, and C. chinense*, as presented in Table 1. Seed germination marks the beginning of the plant's life cycle and requires specific conditions to ensure successful germination. Salinity hinders seed germination by inducing osmotic stress and ionic toxicity (Hasanuzzaman *et al.*, 2021; Fu and Yang, 2023). Salinity stress disrupts essential physiological processes in plants, , leading to a reduced K^+/Na^+ ratio and imbalances in ascorbate/dehydroascorbic acid and glutathione/oxidized glutathione levels (Kaya *et al.*, 2020). Furthermore, it reduces sugar content, alters organic acid metabolism, and promotes the accumulation of phenolic compounds (Zamljen *et al.*, 2022). These physiological disruptions limit germination percentage, delay germination time, and reduce both germination rate and biomass production (Gupta and Huang, 2014).

The results showed a decrease in germination and biomass of hot chilli genotypes under salt stress, with a more pronounced impact observed in salt-sensitive genotypes compared to moderate and salt-tolerant ones. These findings align with the findings of Sarkar *et al.* (2023). This decline in germination parameters can be attributed to disruptions in nutrient uptake and the accumulation of sodium ions, which lead to ion-specific toxicity and increased osmotic pressure, and nutrient imbalances(Munns, 1993), as well as damage to plant cells and tissues (Hasanuzzaman *et al.*, 2021; Ahmad *et al.*, 2022).

A lower MGT value indicates faster seed germination (Kader, 2005), while a higher GSC value reflects quicker seed germination. In contrast, mean germination rate (MGR), calculated as the inverse of MGT, and represents the rate of seed germination per unit of time. The coefficient of velocity of germination (CVG) is another metric used to assess germination speed; it typically increases with a higher number of germinated seeds and a shorter germination period (Talská *et al.*, 2020).

The gradual reduction in GrP, MGR, CVG, and GSC, but increasing the MGT, is due to salinity's influence and is inevitable, given the limited tolerance of plants to salt. This reduction in salt tolerance is influenced by the plant's capacity to absorb salt concentrations and its response to salt stress, whether by enhancing osmosis through the production of organic compounds like proteins, proline, and sugars or by excluding salt via selective ion permeability (Wien and Stützel, 2020). These response mechanisms vary depending on plant species, varieties, and genotypes (Loganayaki *et al.*, 2020; Ali *et al.*, 2022). The most significant CVG values were observed in the tolerant genotypes examined in this study. Elevated salt concentrations can impede water absorption due to intracellular osmotic pressure, disrupting cell division and elongation, thereby more effectively inhibiting water absorption than reducing seed germination (Meyer and Boyer, 1981; Munns, 1993; Hasegawa *et al.*, 2000; Mushtaq *et al.*, 2020; Hasanuzzaman *et al.*, 2021; Ahmad *et al.*, 2022; Zhou *et al.*, 2023).

Simple correlation analyses are commonly used because they are easy to calculate. Yet, for complex traits, a basic analysis may not be sufficient. In such cases, principal component analysis, or non-linear PCA, can be utilized.

The accumulation of dry matter in seedlings indicates the absorption of NaCl ions and the genotypes' response mechanisms to salt stress. The dry matter percentage decreases with increasing salinity levels; a negative correlation was found between DM% and MGT (r= -0.26, $p>0.01$), the genotypes that content a higher dry matter percentage at high salinity levels are considered resistant, with a positive correlation with GrP (r=0.49, $p>0.01$) and with MGR (r = 0.48, $p>0.01$) (Fig. 10).

Genotype *D* exhibited higher DM% across all salt concentrations compared to the control, while genotype *A* maintained stable DM% levels. Although variations in DM% were observed among genotypes, indicating points of peak resistance, stepwise regression analysis revealed that 100% of the observed effects were attributed to genetic differences (Table 3). This suggests that, while DM% can be indicative of salinity tolerance, its overall significance as a trait was relatively limited in this

study. These findings highlight the potential of DM% as a useful physiological marker for evaluating salinity tolerance, especially during the germination stage.

Numerous researchers have also highlighted the presence of genetic variances in salt tolerance among various vegetable crops, such as in tomato (Devi and Arumugam, 2019) and in pepper (Howlader *et al.*, 2018). Salt stress exerts a*dv*erse effects on seed germination percentage, plant length, root length, root/plant length ratio, as well as fresh and dry weights of seedlings, along with the seedling vigor index (Kayacetin, 2022). Seed germination and seedling growth represent the plant growth stages most susceptible to salt stress (Miceli *et al.*, 2021). In this investigation, the germination rate percentage of most genotypes significantly decreased, but they were able to maintain up to 50% germination even at very high NaCl concentrations (250 mM), indicating that the threshold for poor germination among most Yemeni hot pepper genotypes was 200 to 250 mM NaCl. Similarly, the PCS revealed a negative effect at 200 and 250 mM NaCl concentrations (Table 12).

In this study, distinct variations were observed among hot pepper genotypes regarding their salinity tolerance index. Genotypes *A* and *D* genotypes exhibited superior resistance in terms in both germination percentage and dry matter accumulation. In contrast, these genotypes, showed heightened resistance specifically in terms of germination speed and rate. Consequently, the most salt-tolerant genotype was identified based on the slope of the regression line, the integrated value (*DV*), principal component analysis, and the Genotype Salinity Susceptibility Index (GSSI) indicators.

PCA helps identify key traits impacting salinity tolerance (Negrão *et al.*, 2016; Mubushar *et al.*, 2022). This study used principal component analysis (PCA) to evaluate variables, with the first and second PCs explaining the majority of the variation (76.7%). The distribution of genotypes across the four quadrants highlighted distinct groupings. Salt-tolerant genotypes showed high GrP and MGR values and low MGT. Among all genotypes, D consistently ranked as the most resistant, achieving the first position across all analytical methods. However, the classification of other genotypes differed depending on the analysis model.

The cumulative value of the weighted coefficients (*Wj*) for GrP, MGT, MGR, and GSC exceeded 76% of the overall weights in this study. And the Cumulative Percentage of the first and second PCS (Table 10) was about 79.69% in which similar to *Wj*. Correspondingly, the R-square values for GrP, MGT, MGR, and GSC were all greater than 50%, indicating their reliability in assessing the sensitivity of the genotypes to salinity stress. These findings suggest that these four characteristics could serve as fundamental parameters in a framework designed to evaluate the tolerance of chilli pepper germination to salinity stress. Additionally, the R-square value may be considered a viable alternative to the weighted coefficient (*Wj*) in this assessment.

Despite minor discrepancies between the integrated value (*DV*) and the slope of the regression line in the arrangement of genotypes (Tables 12 and 13), we propose that the slope is a more effective metric for evaluating salinity sensitivity. This is primarily because the slope quantitatively represents the extent of decline in each characteristic as salinity levels increase across all genotypes. In contrast, the *DV* calculation depends on higher salinity levels, which may not fully capture the nuanced responses of genotypes.

Principal components (PCs) effectively highlight the relationship between variables and their respective impacts, while summated regression slope values provide a comprehensive measure of the overall influence across all traits.

When evaluating the impact of salinity on genotypes, the R-squared value is a critical metric for assessing the significance of the parameters. Moreover, our hypothesis regarding the efficacy of the regression line slope (*b*) has been validated. In contrast, the Genotype Salinity Susceptibility Index (GSSI) model is not recommended, as it evaluates parameters independently rather than offering a comprehensive understanding of the genotypes' responses to salinity stress.

Previous scholarly investigations, alongside our findings, indicate that the *DV* value is a superior metric for assessing salt tolerance (Fang *et al.*, 2017; Xie *et al.*, 2021). Cluster analysis based on the *DV* value enabled a comparative evaluation of salt tolerance across different genotypes. The results of this study clearly categorized the genotypes into four clusters: the first cluster, comprising *A* and *D*, exhibited salt tolerance and thus represents a valuable set of materials suitable for cultivation in

saline environments. The analysis effectively delineated varying degrees of salinity sensitivity among the genotypes, classifying them as resistant (*D*, *A*, and *G*), moderately resistant (*F* and *V2*), sensitive (*S* and *Z*), and highly sensitive (*H* and *V3*) to salinity.

Yemeni chilli genotypes exhibit considerable variation in salinity tolerance. Results have identified genotypes A and D as promising candidates for cultivation in saline environments, designating them as elite genotypes. These genotypes offer valuable prospects for hybridization with those exhibiting moderate to low salt tolerance, aiming to enhance resilience and productivity. The study underscores the efficacy of using the regression line slope as a robust method for assessing genotypic sensitivity to salinity. These findings are pivotal for a*dv*ancing the development of salt-tolerant chilli cultivars, optimizing breeding strategies, and promoting sustainable agricultural practices in saline-affected regions.

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