



## RESEARCH PAPER

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## Evaluation and selection of synthetic hexaploid wheat and their derivatives at seedling stage targeted for salt tolerance

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### Abstract

Novel sources of salt tolerance need to be identified for the development of crop on saline prone areas in order to meet the food demands of increasing human population. We have evaluated 136 Hexaploid synthetic wheat and their derivatives with local checks varieties at seedling stage for salt tolerance in petridishes at 0, 75 and 150mM NaCl solution using different physiological indices like shoot and root length stress tolerance index, shoot fresh and dry weight tolerance index and root dry weight tolerance index. The collected data were analyzed by statistical techniques as analysis of variance, descriptive statistics, and correlation analysis to evaluate the variations among the studied germplasm against salt tolerance. Mean square values by the analysis of variance and interaction mean values between the genotypes and traits expressed significant variation among all the traits. Highly significant and positive correlation was found between shoot and root length, shoot fresh weight, shoot and root dry weight. Salt tolerant genotypes with accession number 23, 897, 892, 80, 3, 44, , 50, 33, 433, 605, 52, 551, 5, 593, 20, 866, 53, 906, Pasban-90, Shorawaki, and S-24 has been identified which performed best and expressed higher plant fresh/dry biomass and root/shoot length and resulted lower biomass and growth reduction when exposed to 75 and 150mM NaCl with Stress tolerance index (STI) ranges from 70-100% . In order validate these findings the selected lines will be further investigated at the maturity stage in saline field condition for agronomic and yield related traits as thousand kernel weight and harvest index.

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## Introduction

About 800 million hectares of cultivated land worldwide is affected by soil salinization. The growth and yield production of crop plants become severely declined under the saline environmental conditions due to salt stress. Due to salinity there is an annual loss of 12 billion US dollar to the world economy, which is still on rise (Lauchli and Lutttge, 2004). It is a major threat to the net income of breeders and farmers because of higher salt effected land and economic yield loss.

Wheat is an important domesticated cereal crop in many countries all over the world. In Pakistan during 2015-2016, the net production of wheat was 25.5 million tons from an area of 9.23 million hectare than the expected yield of 26.5 million tons (GOP, 2016). Reduction in wheat yield is due to various biotic and abiotic stresses like salinity, drought and heat in the arid and semiarid regions of the world (Ashraf, 2004). Salinity is major abiotic threat especially in the arid and semi-arid regions of the world that reduces the productivity of agricultural crops with adverse effect on plant germination, growth vigour, crop yield due to osmotic and toxic stress of salt ions that affect various morphological, biochemical and physiological processes which contribute towards seed germination and seedling survival (Zhang *et al.*, 2010; Ashraf, 2004). Increasing salt tolerance of crops is a feasible approach for tackling salinity. Wheat is a major cereal crop which is grown throughout the world on both irrigated and rainfed land. However, much of the arable land worldwide is affected by salinity, leading to significant limitations on wheat production. One approach to tackling this problem is to increase the salinity tolerance of wheat cultivars (Munns *et al.* 2006).

As plants are sensitive at all the growth stages to salinity, the seedling stage is studied to be most sensitive in many plant species (Munns, 2002). Genetic variability has been exhausted in wheat due to genetic bottlenecks wheat passed through in the process of evolution and domestication (Appels and Lagudah, 1990).

Salt tolerant wheat germplasm can be used to cultivate these saline soils. Therefore wheat germplasm need to be identified having genetic variation against salt stress. One way of incorporating wild stress tolerant genes into modern wheat is through synthetic hexaploid wheat, produced by crossing tetraploid durum (AABB) with diploid *Ae. tauschii* (DD) (Trethowan and van Ginkel, 2009). For the development of high yielding and salt tolerant varieties effective screening techniques would be beneficial.

In vitro screening of wheat germplasm at seedling stage is important for the selection of genotypes having genetic potential against salt stress at different level of induced salinity. At germination and early seedling stage genetic diversity among the wheat genotypes for morphological and physiological indices has been studied by various researchers (Ashraf, 2004; Munns, 2007). They found that increase in salt level causes higher reduction in plant biomass and yield in susceptible genotypes as compared to the salt tolerant genotypes.

In wheat breeding due to the limited genetic variation against salt tolerance we are lagging behind its genetic improvement for yield related traits in terms of thousand kernel weight, spikes per plant and harvest index (Dreccer *et al.*, 2004). In order to explore the genetic variations in wide array of germplasm against salinity tolerance, a rapid, reliable and effective approach for screening methods is very important (Munns and James, 2003).

Due to the fluctuating and irregular seasonal rainfall and heterogenous nature of soil salinity it is quite difficult to handle the initial screening in the saline field conditions. Majority of crop evaluation methods are performed in controlled environmental conditions among which the *in vitro* screening in petridishes is simple and quite effective approach at seedling stage initially. *In vitro* screening is important to propose the selected germplasm for saline environment. SHW have more tolerance to salinity as compared to bread wheat, therefore their screening and selection will help wheat breeding to develop salt tolerant germplasm.

The objective of the present study was to evaluate the 136 wheat genotypes at early seedling stage in petridishes at three different level of salinity for the selection of salt tolerant genotypes.

## Material and methods

### Plant material

Plant material of 136 wheat genotypes having 117 synthetic hexaploid wheat (SHW), 12 SHW derivatives, 3 durum wheat and 4 local check varieties were used in this study (Table. 1 and 2).

**Table 1.** Pedigree and accession number of the germplasm used in study.

S. No	Acc. No	Pedigree	S. No	Acc. No	Pedigree
1	433	ALTAR 84/Ae. tauschii (1012)	63	853	D67.2/P66.270//Ae. tauschii (633)
2	908	ALTAR 84/Ae. tauschii (1068)	64	854	D67.2/P66.270//Ae. tauschii (634)
3	1010	ALTAR 84/Ae. tauschii (1094)	65	855	D67.2/P66.270//Ae. tauschii (635)
4	3	ALTAR 84/Ae. tauschii (178)	66	260	D67.2/P66.270//Ae. tauschii (646)
5	5	ALTAR 84/Ae. tauschii (188)	67	823	D67.2/P66.270//Ae. tauschii (657)
6	8	ALTAR 84/Ae. tauschii (191)	68	861	D67.2/P66.270//Ae. tauschii (658)
7	12	ALTAR 84/Ae. tauschii (192)	69	261	D67.2/P66.270//Ae. tauschii (659)
8	17	ALTAR 84/Ae. tauschii (193)	70	865	D67.2/P66.270//Ae. tauschii (665)
9	20	ALTAR 84/Ae. tauschii (198)	71	866	D67.2/P66.270//Ae. tauschii (666)
10	23	ALTAR 84/Ae. tauschii (205)	72	867	D67.2/P66.270//Ae. tauschii (668)
11	33	ALTAR 84/Ae. tauschii (211)	73	875	D67.2/P66.270//Ae. tauschii (709)
12	48	ALTAR 84/Ae. tauschii (219)	74	803	D67.2/P66.270//Ae. tauschii (731)
13	49	ALTAR 84/Ae. tauschii (220)	75	804	D67.2/P66.270//Ae. tauschii (741)
14	52	ALTAR 84/Ae. tauschii (221)	76	884	D67.2/P66.270//Ae. tauschii (788)
15	57	ALTAR 84/Ae. tauschii (223)	77	885	D67.2/P66.270//Ae. tauschii (791)
16	64	ALTAR 84/Ae. tauschii (224)	78	887	D67.2/P66.270//Ae. tauschii (796)
17	918	ALTAR 84/Ae. tauschii (237)	79	888	D67.2/P66.270//Ae. tauschii (797)
18	464	ALTAR 84/Ae. tauschii (244)	80	889	D67.2/P66.270//Ae. tauschii (828)
19	80	ALTAR 84/Ae. tauschii (291)	81	895	CETA/Ae. tauschii (1085)
20	551	ALTAR 84/Ae. tauschii (319)	82	440	CETA/Ae. tauschii (1024)
21	96	ALTAR 84/Ae. tauschii (328)	83	962	CETA/Ae. tauschii (683)
22	97	ALTAR 84/Ae. tauschii (328)	84	927	CETA/Ae. tauschii (418)
23	318	ALTAR 84/Ae. tauschii (333)	85	930	CETA/Ae. tauschii (442)
24	923	ALTAR 84/Ae. tauschii (380)	86	825	CETA/Ae. tauschii (615)
25	419	ALTAR 84/Ae. tauschii (502)	87	955	CETA/Ae. tauschii (680)
26	572	ALTAR 84/Ae. tauschii (539)	88	903	CETA/Ae. tauschii (373)
27	993	ALTAR 84/Ae. tauschii (793)	89	578	CETA/Ae. tauschii (1055)
28	187	ALTAR 84/Ae. tauschii (JBANGOR)	90	449	CETA/Ae. tauschii (166)
29	186	ALTAR 84/Ae. tauschii (Y86-87 S401)	91	448	CETA/Ae. tauschii (1042)
30	607	D67.2/P66.270//Ae. tauschii (1009)	92	516	CETA/Ae. tauschii (1043)
31	608	D67.2/P66.270//Ae. tauschii (1015)	93	517	CETA/Ae. tauschii (1046)
32	610	D67.2/P66.270//Ae. tauschii (1017)	94	450	CETA/Ae. tauschii (172)
33	906	D67.2/P66.270//Ae. tauschii (1032)	95	446	CETA/Ae. tauschii (1030)
34	785	D67.2/P66.270//Ae. tauschii (1054)	96	477	CETA/Ae. tauschii (371)
35	771	D67.2/P66.270//Ae. tauschii (1057)	97	454	CETA/Ae. tauschii (200)
36	892	D67.2/P66.270//Ae. tauschii (1068)	98	483	CETA/Ae. tauschii (445)
37	894	D67.2/P66.270//Ae. tauschii (1074)	99	513	CETA/Ae. tauschii (1036)
38	896	D67.2/P66.270//Ae. tauschii (1085)	100	511	CETA/Ae. tauschii (1031)
39	899	D67.2/P66.270//Ae. tauschii (1090)	101	515	CETA/Ae. tauschii (1038)
40	909	D67.2/P66.270//Ae. tauschii (1093)	102	452	CETA/Ae. tauschii (184)
41	584	D67.2/P66.270//Ae. tauschii (185)	103	919	CETA/Ae. tauschii (310)
42	34	D67.2/P66.270//Ae. tauschii (211)	104	921	CETA/Ae. tauschii (345)
43	37	D67.2/P66.270//Ae. tauschii (213)	105	897	CETA/Ae. tauschii (1090)
44	44	D67.2/P66.270//Ae. tauschii (217)	106	600	CETA/Ae. tauschii (416)
45	47	D67.2/P66.270//Ae. tauschii (218)	107	429	CETA/Ae. tauschii (540)
46	50	D67.2/P66.270//Ae. tauschii (220)	108	460	CETA/Ae. tauschii (235)
47	53	D67.2/P66.270//Ae. tauschii (221)	109	1008	CETA/Ae. tauschii (1093)
48	614	D67.2/P66.270//Ae. tauschii (1039)	110	786	CETA/Ae. tauschii (356)
49	59	D67.2/P66.270//Ae. tauschii (223)	111	573	CETA/Ae. tauschii (541)
50	590	D67.2/P66.270//Ae. tauschii (239)	112	640	CETA/Ae. tauschii (299)
51	223	D67.2/P66.270//Ae. tauschii (257)	113	655	CETA/Ae. tauschii (408)
52	593	D67.2/P66.270//Ae. tauschii (260)	114	485	CETA/Ae. tauschii (450)
53	781	D67.2/P66.270//Ae. tauschii (288)	115	622	CETA/Ae. tauschii (199)
54	594	D67.2/P66.270//Ae. tauschii (301)	116	479	CETA/Ae. tauschii (391)
55	224	D67.2/P66.270//Ae. tauschii (308)	117	673	CETA/Ae. tauschii (519)
56	595	D67.2/P66.270//Ae. tauschii (320)	118		Pasban-90
57	596	D67.2/P66.270//Ae. tauschii (368)	119		Shorawaki
58	782	D67.2/P66.270//Ae. tauschii (400)	120		PBW-343
59	599	D67.2/P66.270//Ae. tauschii (416)	121		S-24
60	603	D67.2/P66.270//Ae. tauschii (448)	122		ALTAR
61	605	D67.2/P66.270//Ae. tauschii (497)	123		CETA
62	847	D67.2/P66.270//Ae. tauschii (629)	124		D67.2

**Table 2.** Pedigree and accession number of the synthetic hexaploid wheat derivatives.

S. No	Acc. No	Pedigree
125	23	68.111/RGB-U//WARD/3/FGO/4/RABI/5/AE.SQUARROSA (878)/6/CETA/5/68.111/RGB-U//WARD RESEL/3/STIL/4/AE.SQUARROSA(783)
126	32	TURACO/5/CHIR3/4/SIREN//ALTAR84/AE.SQUARROSA(205)/3/3*BUC/6/CNO/7/CROC_1/AE.SQUARROSA(444)
127	25	TURACO/5/CHIR3/4/SIREN//ALTAR84/AE.SQUARROSA(205)/3/3*BUC/6/FCT/6/DOY1/AE.SQUARROSA(458)
128	240	GAN/AE.SQUARROSA(236)//CETA/AE.SQUARROSA(895)/3/MAIZ/4/INQALAB 91/5/ BKH-94
129	251	GAN/AE.SQUARROSA(236)//CETA/AE.SQUARROSA(895)/3/MAIZ/4/INQALAB
130	250	GAN/AE.SQUARROSA(236)//CETA/AE.SQUARROSA(895)/3/MAIZ/4/INQALAB
131	166	OPATA//CETA/AE.SQUARROSA(1027)
132	26	OPATA//CETA/AE.SQUARROSA(895)
133	74	PBW-343*2/CHAPIO/3/D67.2/P66.270//T.BOEOTICUM(66)
134	30	D67.2/P66.270//AE.SQUARROSA(223)3/ARLIN_1/T.MONOCOCCUM(95)
135	88	MH 97/2/D67.2/P66.270//T.BOEOTICUM(66)
136	148	OPATA//CETA/AE.SQUARROSA(615)

### Study area and experimental design

The experiment was conducted in petridishes at the growth chamber of wheat wide crosses of National Agriculture Research Center, Islamabad under controlled environmental conditions following two factorial complete randomized designs with three replications for each genotype by using salt solution of 0, 75 and 150mM NaCl to determine the salt tolerance potential at seedling stage by using the physiological indices as screening tool at the department of wheat wide crosses, NARC Islamabad.

### Methodology

Ten seed of uniform size has been selected from each genotype and were grown in 10cm petridishes. After 16 days of experiment the seedlings were harvested and washed with tap water.

Five seedlings from each replication were selected and measured for the data observations of seedling length (cm), shoot length (cm), root length (cm) and shoot fresh weight (g). Shoot and root dry weight (g) was recorded after complete moisture drying in oven at 70°C for 48 hours. Stress tolerance trait index (STTI) and stress tolerance index (STI) at the seedling stage for shoot length, root length, shoot fresh weight, shoot and root dry weight and plant dry weight were calculated according to the following formula (Ali *et al.*, 2007):

$$STTI = \frac{\text{Trait value under salt stress}}{\text{Trait value under control}} \times 100$$

$$STI = \frac{\text{Sum of Salt tolerance trait index}}{\text{Total number of traits}} \times 100$$

### Statistical Analysis

The experiment was organised following two factorial complete randomized designs with three replications for each genotype.

### Analysis of Variance

The data obtained from the seedling screening at three level of salt stress and from the greenhouse experiment under control and salt stress were analyzed for analysis of variance (ANOVA) at  $P < 0.05$  level based on general linear model (GLM) procedure to find out the significant differences among the genotypes between all the parameters and their interaction with different treatment by using the SAS statistical software (SAS Institute, 2003).

### Descriptive statistics and correlation analysis

Data collected for different variables at three different level of salt study were analyzed for descriptive statistics, salt tolerance trait indices (STTI), stress tolerance index (STI) and correlation coefficient by using STATISTICA software (Stat Soft Inc. 7.0). Significant and highly positive correlation is found among the root and shoot length, root and shoot dry weight and shoot fresh weight.

### Results and discussions

All the genotypes exhibited variable response to salt stress. Our result clearly shows that plant biomass production has been reduced with increase in salt concentration.

With increase in salt level plant do not uptakes sufficient water due to the development of higher osmotic pressure of external solution which results in decrease in net biomass production. Salt tolerant genotypes respond minimum reduction in biomass, shoot/root length, and Shoot/root dry weight. Mean square values obtained from analysis of variance at seedling stage showed maximum variation for all the recorded observation among the 136 wheat genotypes grown at three different salt concentrations (Table.3). All the traits showed higher variability at ( $p > 0.05$ ) on all treatments. Interaction between accessions and treatment also shows significant variation.

The increase in salt concentration from control to 75mM and 150mM NaCl significantly results in reduction on all the observed traits of seedling length, shoot length, root length, shoot fresh weight, and shoot and root dry weight. In wheat reduction in shoot and root biomass was associated with lower water potential due to osmotic effects created under salt stress (Munns *et al.*, 1995). Relationships among variables were calculated by Pearson coefficient correlation analysis, all the traits under study at three treatment level expressed positive and significant correlation with each other on the level of probability  $p < 0.05$ ,  $p < 0.01$  and  $p < 0.001$  (Table 4).

**Table 3.** Mean squares values and analysis of variance (ANOVA) results for the evaluated traits in wheat genotypes at 0, 75 and 150mM NaCl.

SOV	DF	MS	F	P	DF	MS	F	P
Shoot length				Shoot dry weight				
Rep	2	91.46	111.39	<.0001	2	0.0005	179.95	<.0001
Acc	135	37.05	45.13	<.0001	135	0.0002	60.97	<.0001
Trt	2	9377.32	11419.9	<.0001	2	0.0210	7388.45	<.0001
Acc*Trt	270	6.55	7.97	<.0001	270	0.0000	5.9	<.0001
Shoot fresh weight				Root length				
Rep	2	0.007	177.91	<.0001	2	69.37	61.79	<.0001
Acc	135	0.002	45.11	<.0001	135	28.13	25.06	<.0001
Trt	2	0.401	10633.2	<.0001	2	7238.25	6446.88	<.0001
Acc*Trt	270	0.000	6.88	<.0001	270	4.05	3.61	<.0001
Root dry weight								
Rep	2	0.0002	74.61	<.0001				
Acc	135	0.0000	16.01	<.0001				
Trt	2	0.0120	5406.06	<.0001				
Acc*Trt	270	0.0000	2.01	<.0001				

**Table 4.** Pearson correlation coefficient between the morphological traits at 0, 75,& 150mM NaCl.

	NaCl	SL	SFW	SDW	RL
SFW	0mM	0.67***			
	75mM	0.79***			
	150mM	0.86***			
SDW	0mM	0.62***	0.72***		
	75mM	0.71***	0.81***		
	150mM	0.80***	0.86***		
RL	0mM	0.59***	0.36**	0.39**	
	75mM	0.64***	0.42***	0.45***	
	150mM	0.76***	0.63***	0.66***	
RDW	0mM	0.37**	0.33**	0.52***	0.57***
	75mM	0.57***	0.49***	0.56***	0.76***
	150mM	0.72***	0.62***	0.65***	0.87***

\*, \*\* and \*\*\* indicate values are statistically significant different from each other at the level of  $p < 0.05$ ,  $p < 0.01$  and  $p < 0.001$ , where: SL: Shoot length (cm), RL: Root length (cm), SFW: Shoot fresh weight (g), SDW: Shoot dry weight (g), RDW: Root dry weight (g).

Similar results have also been reported by Ali *et al.*, 2007. Strongest and higher values of positive correlation for all traits were observed at 150mM NaCl. At three level of salinity shoot length shows strongest positive correlation with shoot fresh weight ( $r = 0.67$ ), ( $r = 0.79$ ) and ( $r = 0.86$ ) and shoot dry weight

( $r = 0.62$ ), ( $r = 0.71$ ) and ( $r = 0.80$ ) respectively. Significant positive correlation was recorded between shoot length and root length ( $r = 0.59$ ), ( $r = 0.64$ ) and ( $r = 0.76$ ) and root length and root dry weight ( $r = 0.57$ ), ( $r = 0.76$ ) and ( $r = 0.87$ ) at three salt treatment respectively.

It is not unanticipated as plants with vigorous and long roots can absorb more water and especially under stress, this may result due to higher photosynthetic rate and therefore increased plant biomass. Meneguzzo *et al.*, (2000) reported that in controlled environmental condition genotype showing salinity tolerance were apparently determined by the accumulation of dry plant biomass. However shoot dry weight and root dry weight expressed an average of significant positive correlation ( $r=0.52$ ), ( $r=0.56$ ) and ( $r=0.65$ ) at three different salt level. Descriptive summary statistical results for all the morphological traits, stress tolerance trait indices (STTI), stress tolerance index

(STI) were given in Table. 5 & 6. Coefficient of determination ( $R^2$ ) varies from 0.94 to 0.97, which indicates that regression explains maximum variability among all the variables around their mean values. The observed coefficient of variation (CV %) ranged from 6.95% for shoot length to 9.94% for root dry weight. Munns and James (2003) studied that genetic variations in wheat for salinity tolerance by screening at seedling stage are effective to identify a wide array of genetic resources. Genotypic variations for biomass production were due to decrease in growth rate enforced by the osmotic and toxic effect of salt (Akhtar *et al.*, 2012).

**Table 5.** Descriptive statistics of morphological traits of wheat genotypes at 0, 75, and 150mM NaCl.

Trait	NaCl	Mean	Min	Max	Range	S.D	S.E	$R^2$	CV%	P
SL	0mM	17.817	13.333	23.667	10.333	2.192	0.188	0.97	6.95	***
	75mM	13.010	7.000	18.333	11.333	2.439	0.209			
	150mM	8.232	2.333	14.667	12.333	2.437	0.209			
SFW	0mM	0.118	0.089	0.162	0.073	0.013	0.001	0.97	7.02	***
	75mM	0.087	0.043	0.145	0.102	0.017	0.001			
	150mM	0.056	0.014	0.114	0.100	0.017	0.001			
SDW	0mM	0.031	0.019	0.040	0.020	0.005	0.000	0.96	7.19	***
	75mM	0.024	0.013	0.036	0.023	0.005	0.000			
	150mM	0.016	0.005	0.028	0.024	0.005	0.000			
RL	0mM	16.275	11.333	20.000	8.667	1.870	0.160	0.95	8.82	***
	75mM	11.890	7.000	16.333	9.333	2.072	0.178			
	150mM	7.853	3.333	13.667	10.333	2.071	0.178			
RDW	0mM	0.021	0.015	0.025	0.010	0.002	0.000	0.94	9.49	***
	75mM	0.015	0.011	0.021	0.010	0.002	0.000			
	150mM	0.010	0.005	0.014	0.009	0.002	0.000			

**Table 6.** Descriptive statistics of salt tolerance index (STI) studied in wheat genotypes.

STTI	NaCl	Mean	Min	Max	Range	Variance	SD	SE
SL	75mM	84.15	45.90	98.15	52.25	105.21	10.26	0.88
	150mM	63.62	26.23	90.86	64.63	175.47	13.25	1.14
RL	75mM	73.03	44.00	91.18	47.18	86.39	9.29	0.80
	150mM	60.50	36.96	85.37	48.41	127.94	11.31	0.97
SFW	75mM	73.43	33.16	96.20	63.04	118.23	10.87	0.93
	150mM	47.19	12.61	82.61	70.00	159.90	12.65	1.08
SDW	75mM	76.85	40.20	96.50	56.30	94.88	9.74	0.84
	150mM	62.50	25.56	84.34	58.78	139.08	11.79	1.01
RDW	75mM	81.84	62.65	94.12	31.47	32.40	5.69	0.49
	150mM	70.39	52.94	88.75	35.81	51.29	7.16	0.61
PDW	75mM	79.16	53.51	92.61	39.10	38.25	6.18	0.53
	150mM	66.15	39.75	81.01	41.26	64.80	8.05	0.69
STI Mean	75mM	78.15	50.26	89.74	39.48	46.69	6.83	0.59
	150mM	61.82	33.72	81.10	47.38	84.53	9.19	0.79

SL: Shoot length (cm), RL: Root length (cm), SFW: Shoot fresh weight (g), SDW: Shoot dry weight(g), RDW: Root dry weight (g), PDW: Plant/seedling dry weight (g).

It is clearly evident from our results that increase in level of NaCl had negative effects on seedling biomass production. However, the tested genotypes showed wide range of genetic variability against salt

tolerance. Salt tolerant genotypes resulted increase in fresh and dry biomass than salt sensitive genotypes. Ahmadi and Ardekani, (2006) reported that wheat genotypes resulted higher plant biomass at the



seedling stage under salt treatment performed better against salinity at maturity. During the crop life cycle establishment of healthy and vigorous seedlings is an important parameter for plant growth. Significant resources and time can be saved by screening and selection against salt tolerance at the seedling stage.

In this study wheat genotypes with accession number 23, 897, 892, 80, 3, 44, 50, 33, 433, 605, 52, 551, 5, 593, 20, 866, 53, 906, Pasban-90, Shorawaki, and S-24 performed best and expressed higher plant fresh/dry biomass and root/shoot length and resulted lower growth reduction when exposed to 75 and 150mM NaCl with stress tolerance index STI ranges from 70-100% (Table 7, 8). The variation against the salt stress is due the diversity in the genetic makeup of genotypes.

Results obtained from this study clearly shows that the increase in the concentration of NaCl has detrimental effect on plant fresh and dry biomass production. However the wheat genotypes showed variations against salt tolerance because salt tolerant genotypes had minimum decrease in biomass than salt sensitive genotypes. In order to confirm these results the selected genotypes will be further investigated at reproductive and maturity stage for their tolerance against salinity in controlled greenhouse and natural field condition. The same germplasm is under molecular investigation by DNA based molecular markers in order to identify the promising and potential genomic regions associated with stress tolerance.

**Table 7.** Grouping of 136 wheat genotypes based on salt tolerance index (STI) at 75mM NaCl.

Category	STI	No. of genotypes	Accession No.
Tolerant	70-100%	122	23, 897, 892, Shorawaki, 80, 3, 44, Pasban-90, 50, 33, 433, 605, 52, 551, 5, S-24, 593, 20, 866, 53, 906, 614, 595, 57, 854, 97, 781, 594, 224, 861, 622, 782, 640, 419, 909, 1010, 923, 993, 895, 47, 17, 74, 96, 452, 32, 599, 479, 251, 187, 823, 919, 888, 318, 485, 573, 440, 483, 607, 1008, 240, 515, 918, 887, 59, 448, 261, 449, 921, 517, 610, 572, 867, 962, 148, 855, 889, 37, 596, 875, 884, 804, 955, D-23, 578, 894, 12, 903, 34, 25, 446, 250, 516, 88, 166, 896, 908, 590, 825, 26, 927, 584, 429, 48, 260, 786, 673, 450, 223, 899, 603, D67.2, 803, 454, 608, 186, 655, 460, 511, 865, 853, 847, 30, 930
Moderately Tolerant	60-70%	8	771, 885, 600, 477, 464, 64, 785, 8
Moderately susceptible	50-60%	6	CETA, ALTAR, PDW-34, 49, 513

**Table 8.** Grouping of 136 wheat genotypes based on salt tolerance index (STI) at 150mM NaCl.

Category	STI	No. of genotypes	Accession No.
Tolerant	70-100%	21	23, 897, 892, Shorawaki, 80, 3, 44, Pasban-90, 50, 33, 433, 605, 52, 551, 5, S-24, 593, 20, 866, 53, 906
Moderately Tolerant	60-70%	58	614, 595, 57, 854, 97, 781, 594, 224, 861, 622, 782, 640, 419, 909, 1010, 923, 993, 895, 47, 17, 74, 96, 452, 32, 599, 479, 251, 187, 823, 919, 888, 318, 485, 573, 440, 483, 607, 1008, 240, 515, 918, 887, 59, 448, 261, 449, 921, 517, 610, 572, 867, 962, 148, 855, 889, 37, 596, 875
Moderately susceptible	50-60%	40	884, 804, 955, D-23, 578, 894, 12, 903, 34, 25, 446, 250, 516, 88, 166, 896, 908, 590, 825, 26, 477, 927, 584, 429, 48, 260, 786, 673, 450, 223, 899, 464, 603, D67.2, 600, 803, 454, 608, 186, 885
Susceptible	Below 50%	17	511, 865, 853, 847, 8, 30, 930, CETA, 64, 785, ALTAR, 771, PDW-34, 460, 49, 655, 513

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