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Carbohydrate and Nitrogen metabolism in wheat (*Triticum aestivum L.*)in response to salinity in laboratory and field condition. Jagriti Singh¹, Nawaz Ahmad Khan², Abhishek Kumar Verma³, Noah Nawaz Khan⁴ and Mubeen⁵

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Abstract

Article History Volume 6, Issue 13, 2024 Received: 18 June 2024 Accepted: 02 July 2024 doi: 10.48047/AFJBS.6.13.2024. 154-170 Wheat (*Triticum aestivum* L.) is second important crop being next only to rice and contributes about 33 percent of the total food grain production of this country, and salinity is one of the environmental factor that have acritical influen ceont hegermination of seeds and subsequent establishment of seedling in the soil. In order to investigate salinity stress on wheat germination indices, an experiment was carried out at A.N.D.U.A.T, (student instructional farm) and net house in department of MBB, (Kumarganj, Ayodhya) to create salinity stress at the level of T0(as control), 25, 75, 125 mM concentration of NaCl, and tenwheat (*TriticumaestivumL*.) cultivars FLW-11, DBW-303, DBW-71, DBW-129, FLW-3, DBW-187, FLW-8, KH-65, HD-2858, KRL-3-4 were tested. For each treatmentrate of germination percent, fresh weight of seedling, dry weight of seedling seedling length, number of tillers, panicle length, plant height, and number of grain per spike, testweight and other biochemical were compared. In conclusion it was observed the increase insalinity level, it hampers the plant growth and development. However, wheat productivity ity is adversely affected by salt stress, which is associated with a reduction ingermination,

growth, altered reproductive behavior andenzymatic activity, disruptedphotosynthesis,hormonalimbalance,oxidativestress,andyieldreductions. Thus,abet ter understanding of wheat (plant) behavior to salinity stress has essential implications todevise counter and alleviation measures to cope with salt stress. Different approachesincludingtheselectionofsuitablecultivars,conventionalbreeding,andmolecular techniquescanbeusedforfacingsaltstress

tolerance.Asrateofsalinityincreasethereweresignificantreductioninplantgrowth.Byinvestiga tion it was found that the most salinity tolerant variety is KH65, KRL3-4, DBW187, and least tolerant variety were HD2851, followed by FLW11 and other remainingvarietyaremoderatesalttolerant.

Keywords: oxidative stress; conventional breeding; salinity; enzymatic activity.

1. Introduction

In terms of production and consumption, wheat (Triticum aestivum L.) is the mostsignificantcerealcropglobally.Themajorityoftheworld'spopulationdependsonwheat tomeet their nutritional needs, and wheat-based foods like chapati, bread, biscuits, pasta, andfermenteditemsareeatenbypeopleeverywhere.Ahealthydietwithadequatecalories,well-balanced proteins, and micronutrients with minimal antinutrients is necessary for a person'snormal growth and development.

Wheat is the most important staple food forhumans and is farmed on more acreage than anyothercropusedforcommercialpurposes.WithIndiacontributing96millionmetrictonnes,orthesecond-

highestamountafterChina,the world's wheat production in 2017 was 754.1 million tonnes (USDA, 2017). Accordingto Curtis et al. (2002), wheat is traded more globally than all other crops combined.

With a higher protein concentration than other main cereals like maize or rice, wheat is the bestvegetableproteinsourceforhumanmealsworldwide(ArzaniandAshraf, 2017). According to Singh (2010), this crop provides over 50% of the calories needed by the people who eatit, which makes a significant contribution to the nation's food security. Much like othercrops, avariety of biotic and abiotic factors limit the amount of wheat that may be produced. Droug ht, extreme heat or cold, and salinity are examples of a biotic stress est hat impact crop qualityand globally. This is particularly true for emerging nations, where productivity thehighestpopulationgrowthwillplaceasignificantdemandonreliablefoodsources(Batesetal.,200 8). The issue of soil salinization in a griculture has become a global concern. Seawater and irrigation wat er, which have very littles odium chloride (NaCl) in them, are the primary sources of salt accumulation i nfarmedsoils(FlowersandYeo, 1995; TesterandDavenport, 2003). Soilsalinitylimitscropproducti oninabout20% of irrigated land (Flowers and Yeo, 1995). Wheat production is also affected severely due to salt stress. In India, 6.7 Mha landunder wheat cultivation is affected by salt including 3 Mha by salinity and 3.7 Mha bysodicity/alkalinity, distributed across 15 of the 28 of 15 states. Out these states, eightcontribute~97% of national wheat production and have~5.6 Mhaaffected by salt (Khokharet al., 2017; Lekshmy et al., 2016). About 10% of wheat cultivated area in the world isalreadysaltaffectedandispredictedtoincreaseinthefuture(Rajendranetal.,2009).

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Salt only reduces vield but also impairs a number of physiostress not chemicalprocessesinplants, including membranestability, iontoxicity, cell turgor, and the buildup of toxic metabolites (Kumar et al., 2017; Arzani and Ashraf, 2016). Breeders have made progress in creating salt-tolerant lines for numerouscrops thanks to recent advances in our understanding of how plants respond to salt (Kumarand Singh, 2016; Kumar et al., 2017). In addition to identifying the genes responsible forsalttoleranceandproducingnewbreedingmaterials, understanding the biochemical, physiologic al. and molecular components of salt tolerance will be useful in screeninggermplasmforbreedinginsaline circumstances(Sairametal.,2002).

Therefore, the greatest challenge for the coming decades will be increasing the wheatproduction from the salt affected lands. Understanding abiotic stress and signaling can be very helpful in improving wheat's genetic resistance to abiotic stress.

2.Materials and Methods

Ten genotypes of saline wheatviz.., FLW -11, DBW-303, DBWW-71, DBW-129,FLW-3,DBW-187,FLW-8,KHARCHIA-65,HD-2851,KRL-3-4.Kharchia-65isthecheck varietyused as the study's experimental materials, At the Acharya Narendra Deva UniversityofAgricultureandTechnology,locatedinKumarganj,Ayodhya,thesegenotypeswereproduc ed using a collection of genetic stock kept in the Wheat division of the Department ofPlant Molecular Biology and Genetics Engineering. This experiment is totally based on salineconditionsofwheatgenotype.

3.Results and discussions

Wheat is a staple food and a source of carbohydrate and calories for the majority ofpeople across the globe. However, wheat productivity is adversely affected by salt stresswhich is associated with reductioning remination, growth , altered reproductive behavior and enzymatic activity, disrupted photosynthesis, harmonal imbalance, oxidative stress and yield reducti on. Thus a better understanding of wheat (plant) behavior to salinity stress has essential implications to devise counter all alleviation measure to cope with the salt stress,

The production of salt-tolerant plant genotypes in salt-affected areas requires a thoroughunderstanding of how plants respond to salinity stress at different levels as well as an

integratedstrategy that combines molecular tools with physiological and biochemical procedures. At themolecular, cellular, metabolic, and physiological levels, recent research has revealed avarietyofadaptiveresponsesto salinity stress.

3.1)

Responseofwheatgenotypesduringgerminationunderdifferentregimeofsalinitytreatment Tencontrastinggenotypesofwheatviz.,FLW-11,DBW-303,DBW-71,DBW-129,FLW-3,DBW-

187,FLW-8,KH-65,HD-2858,KRL-3-4weresubjectedtogerminationunder fourregimes of salinity control(T_0), 25, 75 , 125 mM concentration of NaCl T_1 , T_2 , T_3 respectively by putting their seeds on top of the filter paper in petriplates. Thefollowing observation were recorded during germination of different parameters i.e:-

3.1) Germination Percent :-

It is expressed in percent and it was found that there was no difference ingermination among all genotypes at control treatment. A slight decrease germinationpercent in all genotypes except KH-65 ,and KRL-3-4,where germination was notsignificantlydecreasedevenat125mMNaClconcentrationofsalt.Themaximum reductionwasrecordedinFLW11,FLW8andHD2851.

	Germination %						
			Treatment				
S. No.	Genotype	T ₀ (Control)	T1(25mM)	T₂(75mM	T₃(125mM)	Mean	
1	FLW11	98.00	95.00	90.00	89.25	93.06	
2	DBW303	99.00	98.00	98.00	90.00	96.25	
3	DBW71	98.00	98.00	95.00	95.00	96.50	
4	DBW129	97.00	98.00	97.00	92.00	96.00	
5	FLW3	100.00	100.00	95.00	90.00	96.25	
6	DBW187	100.00	100.00	90.00	90.00	95.00	

7	FLW8	97.00	96.00	92.00	90.00	93.75
8	KH 65	100.00	100.00	100.00	100.00	100.00
9	HD2851	100.00	100.00	90.00	90.00	95.00
10	KRL3-4	100.00	100.00	99.90	99.00	99.73
	Mean	98.90	98.50	94.69	92.53	
	Factors	SE(d)	SE(m)	C.D.		
	Treatment(T)	1.01	0.714	2.014		
	Variety(V)	1.597	1.129	3.185		
	T xV	3.193	2.258	N/A		

3.2) Length of seedling:-

Seedlinglength werecalculatedbybyrootandshootoflengthofindividualseedling and summing up by selecting three random seedling from each replication.the mean value is taken from three seedling from each treatment. seedling lengthwas significantly reduced in all genotype with all sanity treatment.table no.(4.2)The maximum reduction was seen in DBW71 followed by HD2851 and least inKH65and KRL3-4.

	Lengthof seedling(cm)							
	Treatmen							
			1	t				
S. No.	Genotype	T ₀ (Control)	T₁(25mM)	T ₂ (75mM)	T₃(125mM)	Mea n		
1	FLW11	7	6	6	5	6.00		
2	DBW303	6	5.5	5	4	5.13		
3	DBW71	6	4.5	4.5	4.15	4.79		
4	DBW129	6	4	6	5	5.25		
5	FLW3	6	5	4.75	4.25	5.00		
6	DBW187	6.75	6	6	5	5.94		
7	FLW8	6	6	5	4	5.25		
8	KH 65	8	7	6.5	5.75	6.81		
9	HD2851	5.75	5	5	4.25	5.00		
10	KRL3-4	7	7	6.5	5	6.38		
	Mean	6.25	5.60	5.53	4.64			
	Factors	SE(d)	SE(m)	C.D.				
	Treatment(T)	0.062	0.044	0.124				
	Variety(V)	0.098	0.069	0.196				
	T xV	0.196	0.139	0.392				

		F	resh wt.ofs	eedling (gm)			
			Treatmen				
				t			
S. No.	Genotype	T ₀ (Control)	T₁(25mM)	T ₂ (75mM)	T₃(125mM	Mean	
)		
1	FLW11	2.55	2.71	0.98	0.92	1.79	
2	DBW303	1.99	1.68	1.38	1.32	1.5925	
3	DBW71	2.46	1.26	1.47	1.09	1.57	
4	DBW129	2.16	2.0351	2.15	2.01	2.08877	
						5	
5	FLW3	2.52	2.05	1.98	1.68	2.0575	
6	DBW187	2.81	2.72	1.64	0.9	2.0175	
7	FLW8	1.0921	2.55	1.38	2.7	1.93052	
8	KH 65	2.85	2.71	1.9	1.3	2.19	
9	HD2851	1.95	1.04	0.89	0.34	1.055	
10	KRL3-4	2.68	1.95	0.95	0.91	1.6225	
	Mean	2.30621	2.07051	1.472	1.317		

3.3) Fresh weight of seedling

Itwascalculatedbyaddingfreshweightofrootandshoot.Therewassignificantreduction in fresh weight of all genotypes with increase in salinity. The maximumreductionwasobservedinHD2851followedbyDBW71andleastinKH65.

Factors	SE(d)	SE(m)	C.D.	
TreatmentT	0.020	0.014	0.041	
Variety(V)	0.032	0.023	0.064	
T xV	0.064	0.046	0.128	

3.4)Dry weight of seedling:-

Seedling dry weight was calculated by adding root and shoot dry weight of individualseedling by selecting random seedling from treatment. Seedling dry weightis decreased significantly with increasing salinity in all genotypes. Again maximum eduction was observed in HD2851, followed by DBW71. And least in KH65 and DBW129, given below in table

	Drywt.ofseedling(g)							
			Treatment					
S.								
No.	Genotype	T ₀ (Control)	T ₁ (25mM)	T ₂ (75mM)	T₃(125mM)	Mean		
1	FLW11	0.261	0.155	0.146	0.144	0.1765		
2	DBW303	0.257	0.171	0.15	0.121	0.17475		
3	DBW71	0.214	0.152	0.132	0.125	0.15575		
4	DBW129	0.242	0.155	0.129	0.107	0.15825		
5	FLW3	0.17	0.144	0.134	0.139	0.14675		
6	DBW187	0.181	0.171	0.153	0.139	0.161		
7	FLW8	0.192	0.141	0.137	0.118	0.147		
8	KH 65	0.295	0.177	0.148	0.142	0.1905		
9	HD2851	0.185	0.145	0.132	0.131	0.14825		
10	KRL3-4	0.275	0.152	0.122	0.125	0.1685		
	Mean	0.2272	0.1563	0.1383	0.1291			
	Factors	SE(d)	SE(m)	C.D.				
	Treatment(T)	0.002	0.001	0.003				
	Variety(V)	0.003	0.002	0.005				
	T xV	0.005	0.004	0.011				

3.5)Number of Tiller:-

The following record we retaken during vegetative phase of plant. Three plants we reselected randomly from each treatment from each variety. There we renot somuch difference observed, but the maximum number of tillers bearing plants are observed from KH65 and least in HD2851

	No.oftillers(Reproductive stage)								
			Treatment						
S.									
No.	Genotype	T₀(Control)	T1(25mM)	T₂(75mM)	T₃(125mM)	Mean			
1	FLW11	6	6	6	5	5.75			
2	DBW303	7	7	5	3	5.5			
3	DBW71	6	5	4	4	4.75			
4	DBW129	6	6	4	4	5			
5	FLW3	6	4	5	4	4.75			
6	DBW187	6	6	4	4	5			
7	FLW8	5	5	4	4	4.5			
8	KH 65	7	6	6	6	6.25			
9	HD2851	5	5	4	3	4.25			
10	KRL3-4	7	6	6	5	6			
	Mean	6.1	5.6	4.8	4.2				
	Factors	SE(d)	SE(m)	C.D.					
	Treatment(T)	0.055	0.039	0.109					
	Variety(V)	0.086	0.061	0.172					
	ΤxV	0.173	0.122	0.344					

3.6) Spikelet/panicle length:-

spikelet length were measured, and following observation The the were made. In which the spikelet length decreased mostly in HD2851 followed by FLW3. And minimum the spikelet length decreased mostly in HD2851 followed by FLW3. And minimum the spikelet length decreased mostly in HD2851 followed by FLW3. And minimum the spikelet length decreased mostly in HD2851 followed by FLW3. And minimum the spikelet length decreased mostly in HD2851 followed by FLW3. And minimum the spikelet length decreased mostly in HD2851 followed by FLW3. And minimum the spikelet length decreased mostly in HD2851 followed by FLW3. And minimum the spikelet length decreased mostly in HD2851 followed by FLW3. And minimum the spikelet length decreased mostly in HD2851 followed by FLW3. And minimum the spikelet length decreased mostly in HD2851 followed by FLW3. And minimum the spikelet length decreased mostly in HD2851 followed by FLW3. And minimum the spikelet length decreased mostly in HD2851 followed by FLW3. And minimum the spikelet length decreased mostly in HD2851 followed by FLW3. And minimum the spikelet length decreased mostly in HD2851 followed by FLW3. And minimum the spikelet length decreased mostly in HD2851 followed by FLW3. And minimum the spikelet length decreased mostly in HD2851 followed by FLW3. And minimum the spikelet length decreased mostly in HD2851 followed by FLW3. And minimum the spikelet length decreased mostly in HD2851 followed by FLW3. And minimum the spikelet length decreased mostly in HD2851 followed by FLW3. And minimum the spikelet length decreased mostly in HD2851 followed by FLW3. And minimum the spikelet length decreased mostly in HD2851 followed by FLW3. And minimum the spikelet length decreased mostly in HD2851 followed by FLW3. And minimum the spikelet length decreased mostly in HD2851 followed by FLW3. And minimum the spikelet length decreased mostly in HD2851 followed by FLW3. And minimum the spikelet length decreased mostly in HD2851 followed by FLW3. And minimum the spikelet length decreased mostly in HD2851 followed by FLW3. And minimum the spikelet length decreasKH65, DBW187, reduction observed in other were and remainingvarietieshaveaverageandnearly samespikeletlength.

	Spikeletlength(cm)(Flowering/Reproductiv e)							
		Treatment						
S.								
No.	Genotype	T ₀ (Control)	T ₁ (25mM)	T₂(75mM)	T₃(125mM)	Mean		
1	FLW11	9	10	9	7	8.75		
2	DBW303	9	9	7	8	8.25		
3	DBW71	9	9	8	8	8.5		

4	DBW129	9	9.5	9	8	8.875
5	FLW3	9	9	7.5	7	8.125
6	DBW187	10	9	8	9.5	9.125
7	FLW8	9	9.5	8	9	8.875
8	KH 65	10.25	10	9.75	8	9.1875
9	HD2851	9	8	8	7	8
10	KRL3-4	10	9	8	8	8.75
	Mean	9.3	9.1	8.225	7.95	
	Factors	SE(d)	SE(m)	C.D.		
	Treatment(T)	0.090	0.064	0.179		
	Variety(V)	0.142	0.100	0.283		
	T xV	0.284	0.201	0.567		

3.7)Plant height:-

Height of plant is significantly changes due to change in salt concentration of different genotypes. The maximum plant height was noted in KRL 3 -4, followed byKH65. And the least plant height was observed in HD2851 and DBW 187. But theheight of plant donot effect overall yield. Some varieties with dwarf shoot characters, yieldmore then the genotype shaving more plant height.

Plantheight (Physical maturity)(cm)							
			Trea	tmen			
S.				ι 			
No.	Genotype	T₀(Control)	T1(25mM)	T ₂ (75mM)	T₃(125mM)	Mean	
1	FLW11	81	73	70	71	75.25	
2	DBW303	75	70	70	70	71.25	
3	DBW71	74	74	72	70	72.5	
4	DBW129	88	90	87	85	87.5	
5	FLW3	88 89 84 87					
6	DBW187	68	70	70	65	68.25	

7	FLW8	91	87	88	77	85.75
8	KH65	85	91	88	81	86.25
9	HD2851	66	61	57	57	60.25
10	KRL3-4	99	90	88	85	90.5
	Mean	82.2	79.5	77.4	75.5	
	Factors	SE(d)	SE(m)	C.D.		
	Treatment(T)	0.807	0.571	1.609		
	Variety(V)	1.276	0.902	2.545		
	T xV	2.551	1.804	5.089		

Estimation of enzyme alpha amylase and isoenzyme of peroxidase:-

3.9) Alpha amylase activity:-

The estimation of enzymatic activity were done in wheat seedling (7DAS) inpetri dish (in vitro) of different salt concentration of each genotypes. The yellowcolouredcomplex wasformed.TheminimumalphaamylaseactivitywasobservedinDBW303,HD2851,DBW12andFL W11.TheminimumreductionwasobservedinKRL3-4,FLW8followedbyKH65.

		α - amylase		
S. No.	Genotype	Maltose released µg/g Fresh wt. (control)	Treatment	mean
1	FLW 11	454.2	301.25	377.725
2	DBW 303	370.12	310.17	340.145
3	DBW 71	385.25	372.76	379.005
4	DBW 129	426.36	317.78	372.07
5	FLW 3	476.34	327.15	401.745
6	DBW 187	435.21	387.92	411.565
7	FLW 8	521.02	352.66	436.84
8	KH 65	456.27	395.21	425.74
9	HD 2851	436.49	300.04	368.265
10	KRL 3-4	495.75	390	442.875
	mean	445.701	345.494	
	Factors	SE(d)	SE(m)	C.D.
	Treatment(T)	3.27	2.32	6.65
	Variety(V)	7.32	5.18	14.88
	TxV	10.35	7.32	21.04

3.10) Isoenzymeofperoxidase

The peroxidaseactivitywas measuredinwheatseedlingfrom rootandshoot(7DAS). The peroxidase activity was found be maximum in salt treated condition to inKH65followedbyKRL3-4,DBW187,DBW129.LeastperoxidaseactivitywasfoundinHD2851 ANDFLW11.

3.11) Estimationoftotalsolublesugar

The total soluble carbohydrate was estimated in leaf and grain by phenol sulphuricacid method. The amount of total soluble was greater in grain as compare leaves.Itwasrecorded to be maximum in KH65,(195mg/ml) and KRL (187.87mg/ml) 3-4, and found

tobeminimuminFLW3,DBW129,DBW303,DBW71,FollowedbyFLW11.

		TSS			
S.No.	Genotype	D-glucose released(mg/ml)	D-glucose released(mg/ml)	mean	
		Freshwt, control	Freshwt, treatment		
1	FLW11	180	150	165	
2	DBW303	170	70	120	
3	DBW71	122	207	164.5	
4	DBW129	166	67	116.5	
5	FLW3	165	50	107.5	
6	DBW187	150	160	155	
7	FLW8	180	175	177.5	3.12)
8	KH 65	200	190	195	, , , , , , , , , , , , , , , , , , ,
9	HD2851	195	180	187.5	Estimationof
10	KRL3-4	202	167	184.5	proteinbyfoli
	mean	173	141.6		
	Factors	SE(d)	SE(m)	C.D.	nlowry'smet
	Treatment(T)	1.383	0.978	2.81	hod
	Variety(V)	3.092	2.186	6.283	
	T xV	4.372	3.092	8.885	True protein
content	t in wheat	t leaves present	ted in table	no. (4.1	3) It was

observed that the highest protein content was found in KH65, followed by KRL3-

4.andminimuminDBW303,DBW129followed byHD2851.

S.No.	Genotyp e	Protein cont. mg/gFreshwt. control	Protein mg/g Fresh wt.treatment	mean
1	FLW11	46.78	37.21	41.995
2	DBW303	38	36.62	37.31
3	DBW71	45	39.21	42.105
4	DBW129	42	33	37.5
5	FLW3	44	32.43	38.215
6	DBW187	41	44.24	42.62
7	FLW8	40	41.73	40.865
8	KH 65	44	48.92	46.46
9	HD2851	43	32.2	37.6
10	KRL3-4	43	46.23	44.615
	Mean	42.67 8	39.17 9	
		CE(-I)		
	Factors	SE(d)	SE(m)	C.D.
	Treatment(T)	0.286	0.202	0.581
	Variety(V)	0.639	0.452	1.299
	T xV	0.904	0.639	1.837

To estimate nitrate reductase (NR) and nitrite reductase (NiR)enzymeactivityinleavesin response o NaClsalinity

3.13) Nitratereductase(NR)

The nitrate reductase activity was assayed from wheat leaves of ten different genotypes ,and it was observed that the nitrate was found to be maximum in KH65 in treatment of differentsaltconcentrationfollowedby KRL3-

4andleastinDBW129,FLW11,HD2851andDBW303.

Nitratereductase				
S.No.	Genotype	Nitrate con. (n molesNO₂/gfreshwt. /hr)control	Nitrate con. (n molesNO2/gfreshwt. /hr)treatment	mean
1	FLW11	934.32	770	852.16
2	DBW303	917.02	801.28	859.15
3	DBW71	931.71	817.32	874.515
4	DBW129	926.24	772.312	849.276
5	FLW3	919.51	820.71	870.11
6	DBW187	901.72	849.29	875.505
7	FLW8	905.27	841.73	873.5
8	KH 65	912.71	872.63	892.67
9	HD2851	915.26	800.23	857.745
10	KRL3-4	907	870	888.5
	mean	917.076	821.5502	
	Factors	SE(d)	SE(m)	C.D.
	Treatment(T)	2.42	1.71	4.914
	Variety(V)	5.41	3.82	10.989
	T xV	7.65	5.41	15.541

3.14) Nitrite reductase activity

The estimation of nitrite reductase activity was done by wheat leaves, from tendifferent wheat genotypes. There was maximum nitrite concentration was found in KH65and KRL3-4 in treatment and least in FLW11 and HD2851, while it was also observed that the nitrite reductase activity was maximum in FLW11(596.21nmol) in control.

Nitritereductase				
S.No.	Genotype	Control	Treatment	mean
1	FLW11	596.21	301	448.605
2	DBW303	570.14	312	441.07
3	DBW71	507.92	365.79	436.855
4	DBW129	495.51	361.28	428.395
5	FLW3	513.24	340.85	427.045
6	DBW187	466.91	366.71	416.81
7	FLW8	502.17	345.44	423.805
8	KH 65	547.79	385.34	466.565
9	HD2851	401.37	309	355.185
10	KRL3-4	522.24	379.47	450.86

mean	501.35	346.688	
Factors	SE(d)	SE(m)	C.D.
Treatment(T)	3.08	2.18	6.25
Variety(V)	6.88	4.86	13.98
T xV	9.73	6.88	19.77

3.15) Estimation of proline

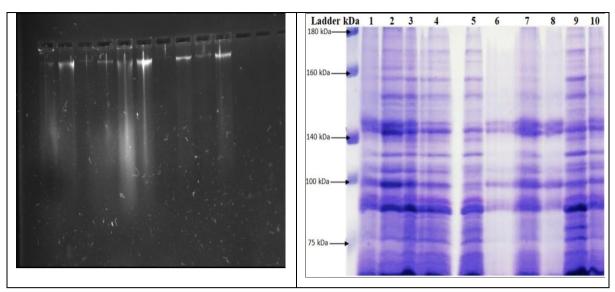
Proline was measured in both root and shoot at vegetative stage and result are presented in figure.

Initial proline content was found to be higher in leaf than in root. Salinity treatmentwas resultinincreaseinprolineconcentrationinbothrootandshoot. Howeverincreasewas more in leaf then root. The maximum accumulation of proline was recorded in KH 65and followed by KRL3-4, DBW187 in treatment. And least in FLW 11, HD2851 ,followedby DBW303.

		Proline			
S.No.	Genotype	Proline releasedµg/ mlcontrol	Proline released µg/mltreatme nt	mean	
1	FLW11	6	13	9.5	
2	DBW303	5.45	13.45	9.45	
3	DBW71	6	15	10.5	
4	DBW129	6.12	15.75	10.935	
5	FLW3	5.75	16	10.875	
6	DBW187	5.9	19	12.45	
7	FLW8	5.75	16	10.875	
8	KH 65	7	24	15.5	
9	HD2851	7	13	10	
10	KRL3-4	9	20	14.5	
	mean	6.39	16.52		
					l l
	Factors	SE(d)	SE(m)	C.D.]
	Treatment(T)	0.079	0.056	0.161	
	Variety(V)	0.177	0.125	0.360	
	ΤxV	0.250	0.177	0.509	

SDS-PAGE of

Protein



DNA

SDS-PAGE of Protein

Conclusion

Soil salinity has become of the limiting environmental factors for crop productivity in many parts of India. It severly hampers the response of standing crops by altering its physiological attributes. Hence, for sustaining crop production, it is imperative to understand the physiological and biochemical adaptations, imparting tolerance to crops towards abiotic stress like salt. Salt stress negatively affects seed germination, plant growth, photosynthesis, ATP production, water relationships, nutrient uptake and yield because of a salt-induced oxidative stress and ionic and hormonal imbalances. Wheat crop shows a wide range of morphological, physiological, and molecular responses under salinity stress. The physiological and molecular mechanisms are very important because they can help the breeders to develop salt tolerance in wheat. These mechanisms against salinity stress are well understood in wheat. However, a better understanding is still needed in many fields, especially in understanding the physiological basis of assimilate partitioning from plant sources to sinks. Additionally, more studies are needed to study the response of roots to salinity stress involving the root-shoot signaling and corresponding impacts on the nutrient and water uptake. Genetic manipulation of salt-tolerant traits is also an important approach to improve salinity tolerance in wheat crops.

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