Supplementary Table S1: Differentially expressed target genes under salt stress.

Turfgrass species	Accession/unigene number	Responsive gene/signal compound	Downstream genes	Related function/description	Up/down regulation	Tissue	Study	Reference
Festuca arundinacea (Schreb.)	CL8335.Contig1_All	*GAPC* (Glyceraldehyde-3-Phosphate Dehydrogenase)	*GAPCp2* (Plastidic GAPDH), *ENO1* (Enolase 1)	Enzyme in glycolysis, photosystem repair, and salt tolerance	Up	leaf	qPCR	[15]
	CL342.Contig3_All	*CAT1*	*GPX2* (Glutathione Peroxidase 2), *RBOHD* (Respiratory Burst Oxidase Homolog D)	Reducing hydrogen peroxide in oxidative stress				
	CL16806.Contig2_All/CL16806.Contig2_All	*APX1/2*	*GPX2, RBOHD*	Reducing hydrogen peroxide in oxidative stress				
	Unigene27613_All	*PFK6* (Phosphofructokinase 6)	*SUS1* (Sucrose Synthase 1), *PFP* (Pyrophosphate-Dependent Phosphofructokinase)	Fructose 6-phosphate metabolic process				
	Unigene12326_All	*VAR3*	–	Chloroplast RNA editing				
	CL1733.Contig12_All	*WhAB1.6*	–	Chlorophyll a/b binding protein (Cab) in light-harvesting complex				
	CL1733.Contig11_All)	*CAB1*	–	Chlorophyll a/b binding protein (Cab)				
	CL1333.Contig4_All	*ACS* (Acetyl-CoA Synthetase)	*ACL* (ATP-Citrate Lyase)	Acetyl-CoA synthetase				
	–	*ATK5*	–	Protein kinase, metabolism, cell survival				
	–	*PTR4*	*AAP1* (Amino Acid Permease 1), *NRT1.1* (Nitrate Transporter 1.1)	Peptide transporters				
	–	*EXPA4* (Expansin A4)	*XTH18* (Xyloglucan Endotransglucosylase/Hydrolase 18), *PME41* (Pectin Methylesterase 41)	Salt and drought tolerance				
Agropyron elongatum L.	AY848951.1/AY357107.2	*NHX1/2*	*CML18, EXPA5, VHA-A*	Cation/H$^+$ transporters, cell expansion, K$^+$ homeostasis	Up	Leaf and root	qPCR	[34]
	KF956112.1	*HKT1;4*	*SOS1*	Na$^+$ transporters				
Lolium arundinaceum / Festuca arundinacea		*SOS1*	–	Ion homeostasis	Up	Leaf	qPCR	[1]
		FaCYP707A1	–	ABA signaling				
Cynodon dactylon (L.) Pers.		*JAZ1*	*JAZ1*, MYC2 TF	Jasmonate signal transduction, plant defense	Up	Root	RNA-seq	[38]
		AOC4	*JA-Ile* (bioactive JA)	Allene oxide cyclase in jasmonate biosynthesis				
		AOS1	*OPDA* (JA precursor)	Allene oxide synthase in jasmonate biosynthesis				
		NIP	*ABA/MAPK2*	Nodulin26-like intrinsic proteins for water homeostasis				
		PIP	SnRK2s	Plasma membrane intrinsic protein for water homeostasis				
		NCED	Xanthoxin	ABA biosynthesis and signal transduction				
		PP2C	*SnRK2s*	ABA signal transduction				
		PMCA	CDPK/SOS3 signaling	Ca^{2+} transporting ATPase transporters				
	cluster-342,212.2695	*MAPK2*	Phosphorylates *ABF2/4, PIPs, RBOHF*	Mitogen-activated protein kinase (homolog of At2g43790)				
Agrostis scabra	AY158077	*CDPK*	*SOS1, PIP2;1, RBOHF*	Abiotic stress-responsive TFs/Na$^+$ exclusion; water uptake; ROS signaling	Up	Root	qPCR	[29]
	AAW33875.	*SOS1*	*HKT1/4, SKOR, HAK5*	Ion homeostasis/Leaf Na$^+$ reduction; K$^+$ retention				
	BAA83337.1/AAQ63678.1	*NHX1/2*	*TST1, VHA-A* (Vacuolar H$^+$-ATPase)	Ion homeostasis/Osmolyte accumulation/ pH regulation				
Cynodon dactylon	XP_002463483.1	*GA20ox*	GA$_1$/GA$_4$	GA 20-oxidases in GA biosynthesis	Down	Root	qPCR	[31]
	XP_004953177.1	*GA2ox*	GA catabolites (e.g., GA$_8$, GA$_{34}$)	Deactivates active GAs				
	XP_002455113/PAN21149.1	*TAA/UCCA*	ARF5, ARF7	Converts tryptophan (Trp) into indole-3-acetic acid (IAA)	Up			
	OQU80479.1	*CYP735A*	*tZ*-type cytokinins	Catalyzes biosynthesis of trans-zeatin (tZ)				
Panicum virgatum	Pavir.4KG320705	*SOS2/CIPK24*	*SOS2-SOS3, GORK, HAK5, PIN3*	SOS pathway, protein kinase superfamily protein/K$^+$ circulation; osmotic adjustment	Down	Leaf	RNA-seq	[35]
	Pavir.3NG258073	*SOS3/CBL4*	*SOS2-SOS3, GORK, HAK5, PIN3*	SOS pathway, calcium-binding EF-hand family protein/PSII repair; NPQ activation				
	Pavir.3KG576900	*SOS1/NHX7*	*HKT1/4* Synergy/ *PIP2/1*	Na$^+$/H$^+$ antiporter, recruits HKT1/4 for xylem Na$^+$ unloading in stems	Up			
	Pavir.5NG438600	*SCaBP8/CBL10*	*NHX1/2, ATHB-7*	Ca^{2+} signaling pathway				
	Pavir.9NG489800	*MPK6*	*ABF2/4, RBOHF*	Osmotic stability via MKKK20-MPK6 cascades, phosphorylates ABF2/4 to activate osmoprotectant genes				
	Pavir.1KG331900	*SnRK2.10*	*PIP2/1, P5CS2, P5CR*	Sucrose non-fermenting 2-protein kinase/↑ Root hydraulic conductivity/Activates RD29A, RAB18				
	Pavir.5NG597428	*P5CS2*	*SOD2, CAT1/2, APX1/2, GSH*	ROS pathway induced by high salt, dehydration, and ABA				
	*	*P5CR*	*SOD2, CAT1/2, APX1/2, GSH*	Proline production under salt and drought stress				
	Pavir.4NG337300	*CAT1/2*	–	Reduces hydrogen peroxide in oxidative stress				
	Pavir.3KG126500	*GSH*	–	Glutathione S-transferase gene				
	*	*SOD2*	–	Reduces hydrogen peroxide in oxidative stress				
	*	*APX1/2*	–	Reduces hydrogen peroxide in oxidative stress				

[1] Esmailpourmoghadam E, Salehi H, Moshtaghi N. 2024. Differential gene expression responses to salt and drought stress in tall fescue (*Festuca arundinacea* Schreb.). *Molecular Biotechnology* 66:2481–2496.

[15] Amombo E, Li X, Wang G, An S, Wang W, et al. 2018. Comprehensive transcriptome profiling and identification of potential genes responsible for salt tolerance in tall fescue leaves under salinity stress. *Genes* 9:466.

[29] Liu T, Zhuang L, Huang B. 2019. Metabolic adjustment and gene expression for root sodium transport and calcium signaling contribute to salt tolerance in *Agrostis* grass species. *Plant and Soil* 443:219–232.

[31] Yang Y, Wassie M, Liu NF, Deng H, Zeng YB, et al. 2022. Genotypic-specific hormonal reprogramming and crosstalk are crucial for root growth and salt tolerance in bermudagrass (*Cynodon dactylon*). *Frontiers in Plant Science* 13:956410.

[34] Sheikh-Mohamadi MH, Etemadi N, Aalifar M, Pessarakli M. 2022. Salt stress triggers augmented levels of Na$^+$, K$^+$ and ROS alters salt-related gene expression in leaves and roots of tall wheatgrass (*Agropyron elongatum*). *Plant Physiology and Biochemistry* 183:9–22.

[38] Shao A, Xu X, Amombo E, Wang W, Fan S, et al. 2023. CdWRKY2 transcription factor modulates salt oversensitivity in bermudagrass [*Cynodon dactylon* (L.) Pers.]. *Frontiers in Plant Science* 14:1164534.