

Supplementary Table 1. Summary of studies performed for the identification of QTLs under salinity stress in different crop plants.

Plant specie	Stress conditions	Approach/Linkage map	QTL/gene	No. of lines/accessions used	Chromosomal location	Key findings	References
Rice (<i>Oryza sativa</i>)	NaCl, CaCl ₂ , and MgSO ₄ in water with ECe ~ 40 mmol; till maturity	Joinmap and Win QTL cartographer software	39 QTLs	140 F ₂ population	All 12 chromosomes	<ul style="list-style-type: none"> ● 39 QTLs identified under salinity stress at reproductive stage ● qNaL-1.2, qNa/KL-1.3, qKR-1, and qNa/KL-1.2 were found in roots and leaves ● Novel QTL <i>qGY-2</i> was also identified for grain yield ● Four QTLs were found for Chl content 	[1]
Barley (<i>Hordeum vulgare</i>)	75, 90, 120 and 150 mM NaCl; 14d	MapQTL software, 350 Diversity Array Technology (DArT), and Multiple QTL model (MQM)	6 QTLs	103 DH lines, and 85 barley germplasm	1H, 3H, 4H	<ul style="list-style-type: none"> ● Identified 6 stable QTLs ● Shoot length (65.6% and 50.3%) was affected most among all phenotypic traits ● QTL on 3H detected more linked ● Chromosome 1H and 3H found to be studied 	[2]
Rice (<i>Oryza sativa</i>)	50 and 100 mM NaCl; 14d	MultiQTL package	38 QTLs	132 RILs	1, 2, 3, 4, 5, 6, 7 and 10	<ul style="list-style-type: none"> ● 21 out of 38 QTLs found stable ● <i>qSL7</i>, a novel major QTL for shoot length with a phenotypic variation of 7.5 and 6.8%, was identified 	[3]

Wheat (<i>Triticum aestivum</i>)	0.18% and 0.3% mM NaCl; 240d (whole growing season)	Wheat 55K SNP array, IciMapping, and MapChart	90 stable QTLs	F ₇ RIL population including 350 lines	All chromosomes except 4D, 6B, and 7D	<ul style="list-style-type: none"> ● 90 stable QTLs identified, out of which 8 were validated in a natural population ● <i>QPh-4B</i> was confirmed as an allele of <i>Rht-B1</i> 	[4]
Rice (<i>Oryza sativa</i>)	From 6 dSm ⁻¹ through 12 dSm ⁻¹ NaCl with 2 dSm ⁻¹ increments/day; 14d	qtlTools (Lovell) and R/qtl	14 QTLs	204 F _{2:3} families from <i>Horkuch</i> × <i>IR29</i>	1, 2, 3, 5, 7 and 10	<ul style="list-style-type: none"> ● 14 QTLs for 9 physiological and yield-related traits were found ● Cytoplasm effect on QTLs 	[5]
Wheat (<i>Triticum aestivum</i>)	1.2% (w/v) NaCl; 7 and 10d	IciMapping, and wheat 660K SNP array	91 QTLs	323 accessions and 150 DH lines	3D, 5B, 3B, 4D	<ul style="list-style-type: none"> ● Fourteen overlapped QTLs were identified with a phenotypic variation of 10% ● <i>TaRN1</i> and <i>TaRN2</i>, two novel candidate genes were identified against salt stress 	[6]
Chickpea (<i>Cicer arietinum</i>)	6 dS/m; 30, 60, and 90d	Axiom [®] <i>Cicer</i> SNP array, Join Map, and Windows QTL Cartographer	28 QTLs	201 RILs (F ₈)	All 8 chromosomes	<ul style="list-style-type: none"> ● 28 QTLs found with 28.40% of the phenotypic variance ● QTL clusters for yield and yield components were found on CaLG03 and CaLG06 	[7]
Wheat (<i>Triticum aestivum</i>)	100 mM NaCl; 13d	R/ASMap, WinQTLCart, genotyping by sequencing (GBS), and Illumina NextSeq500	9 QTLs	128 RILs	1A, 2A, 2B 3A, 5A, 7B and 2DS2	<ul style="list-style-type: none"> ● 9 QTLs were found ● Novel QTLs for shoot ion-independent tolerance (<i>QG(1-5).asl-</i> 	[8]

						7B), Cl ⁻ accumulation (<i>QCl.asl-3A</i>) and K ⁺ : Na ⁺ DW (<i>QK:Na.asl-2DS2</i>)	
Rice (<i>Oryza sativa</i>)	8 dSm ⁻¹ saline water; 40-45d	QTL IciMapping, and Graphical GenoTyping	7 QTLs	180 lines BC ₃ F ₅ generation	1, 2, 3, 4 and 11	<ul style="list-style-type: none"> ● 7 stable QTLs found for component traits ● <i>qDEG-S-2-1</i> and <i>qSSI-STE-2-1</i> QTLs were positively influenced by genotype × environment interactions QTLs	[9]

RIL, recombinant inbred lines; DH, double haploid.

Reference

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Supplementary Table 2. Summary of key GWAS studies undertaken for mapping salinity stress in different crop plants.

Plant specie	Stress conditions	Approach	No. of QTLs/genes	No. of lines/accessions used	Chromosomal location	SNPs	Key findings	References
Rice (<i>Oryza sativa</i>)	100 mM NaCl; 14d	TASSEL software, MLM model and STRUCTURE software	151 MTAs	155	1, 2, 4, 6, 7, 8, 9, 10, 11, 12	33,000	<ul style="list-style-type: none"> ● 151 MTAs identified on 10 chromosomes ● Os01g0304100 was identified encoding a cation chloride cotransporter ● Os01g0624700 and Os01g0812000 encode a WRKY transcription factor ● Os02g0730300 identified as a high-affinity K⁺ transporter (HAK) 	[1]
Soybean (<i>Glycine max</i>)	200 mM NaCl; 24h	HMMER web server and EggNOG mapper, MEME server, I-TASSER, MapGene2Chromosome v2	9 NHX genes	Gujosoya-2 (sensitive) and MAUS-47 (tolerant)	3, 7, 8, 9, 10, 15, 17, 19, 20	-----	<ul style="list-style-type: none"> ● 9 putative NHX genes identified ● Identified NHXs predicted 75 miRNA candidates ● Identified NHXs act as ion transporters 	[2]
Wheat (<i>Triticum aestivum</i>)	1.2% (w/v) NaCl; 7 and 10d	PLINK 1.9, Mixed linear model (MLM), multi-locus GWAS on Farm CPU	91 QTLs	323 accessions and 150 DH lines	3D, 5B, 3B, 4D	395,675	<ul style="list-style-type: none"> ● Fourteen overlapped QTLs were identified with a phenotypic variation of 10% ● <i>TaRN1</i> and <i>TaRN2</i>, two novel candidate genes were identified against salt stress 	[3]

Cotton (<i>Gossypium hirsutum</i>)	200 mM NaCl; 14d	GSNAP software, Illumina HiSeq 2500, and GAPIT software	23 QTLs	550 RILs (MAGIC population)	A01, A03, A08, A11, A12, A13, D01, D03, D05, D06, D08, D09, D12, D13	473,516	<ul style="list-style-type: none"> ● 23 QTLs identified against salt stress ● 9 out of 23 were common with that for drought stress ● QTLs covered plant height (PH) and dry shoot weight (DSW) under salt stress ● 53 candidate genes identified across these QTL regions 	[4]
Barley (<i>Hordeum vulgare</i>)	150 mM NaCl; 2-4d	Illumina HiSeq4000 DArTseq platform, and TASSEL software	19 QTLs	350 diverse accessions	H1, H2, H3, H4, H5, H6, H7	~24,000	<ul style="list-style-type: none"> ● 19 QTLs with 52 salt tolerance associated markers were identified ● L6H495910722, L6H286731484, and L7H614807240 marker alleles have a positive phenotypic effect 	[5]
Wheat (<i>Triticum aestivum</i>)	0.2, 0.4, 0.6, 0.8, and 1 salt solution (standard concentration of seawater (SCS); 7d	660 K SNP array, and Affymetrix Genotyping Console (GTC) software	3 QTLs	307 accessions	1A, 3B, 6B	402,176	<ul style="list-style-type: none"> ● <i>QSt.nwafu-6B</i> identified as a novel QTL ● 53 genes were found to be regulating salt tolerance 	[6]
Rice (<i>Oryza sativa</i>)	NaCl, Na ₂ SO ₄ and CaCl ₂ in 7:1:2; from tillering till maturity	Structure 2.3.4 program, Tassel and GGT software	28 MTAs	180	All 12 chromosomes	127	<ul style="list-style-type: none"> ● Eight marker-trait associations (MTA) found novel out of twenty-eight for 7 different traits under salt stress ● Higher allelic variation was found for one or more traits ● Candidate genes are closely related to transcription factors, membrane transporters, and signal transducers 	[7]

Wheat (<i>Triticum aestivum</i>)	0.18% and 0.3% mM NaCl; till maturity	Wheat 660K SNP array, SAS and TASSEL software, and mixed linear model (MLM)	11 QTLs	191	1B, 3B, 4A, 4D, 5A, 5B, 7A	389	<ul style="list-style-type: none"> ● 11 loci were identified for different traits under salinity stress ● Three out of 14 KASP marker loci were confirmed against yield-related traits 	[8]
Cotton (<i>Gossypium hirsutum</i>)	400 mM NaCl; 3, 6, and 12h	Phytozome v11, MEGA and iTOL	25 NHX genes	4	A01, A02, A03, A06, A08, A09, A11, A12, D01, D02, D04, D05, D06, D07, D08, D09, D10, D11, D12 and D13	----	<ul style="list-style-type: none"> ● Identified 25 NHX genes under salinity stress ● <i>Cis</i>-acting elements were found in promoter regions ● <i>GbNHX7</i> was identified as involved in CBL-CIPK protein pathway 	[9]
Alfalfa (<i>Medicago sativa</i>)	7.4 dS m ⁻¹ ; till maturity	NGSEP software and GWASpoly	27 QTLs	304	2, 3, 4, 6, 8	27	<ul style="list-style-type: none"> ● Six out of 27 QTLs were sturdily associated with salinity tolerance ● Identified marker loci and candidate genes for salt tolerance ● Optimized 2 genome selection (GS) models for further alfalfa breeding 	[10]

RIL, recombinant inbred lines; DH, double haploid.

References

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Supplementary Table 3. Some examples of transgenic plants with improved salinity tolerance. Abbreviations are explained in the main text.

Host plant	Source plant	Stress conditions	Targeted gene	Key improvement	References
<i>Arabidopsis thaliana</i>	Wheat (<i>Triticum aestivum</i>)	50 mM NaCl; 7d	<i>TaHSP17.6</i>	<ul style="list-style-type: none"> • Increased number of lateral roots • Higher accumulation of proline • Boosted the activity of the POD enzyme 	[1]
<i>Arabidopsis thaliana</i>	Barrelclover (<i>Medicago truncatula</i>)	200 mM NaCl; 0, 2, 4, 8, 12 and 24h	<i>MtDof32</i>	<ul style="list-style-type: none"> • Enhanced tolerance for osmotic and salt stresses • Increased rosette number • Enlarged flower and leaf organs 	[2]
<i>Arabidopsis thaliana</i>	Indian Winter cherry (<i>Withania somnifera</i>)	150 mM NaCl; 2, 4, 8, 16, and 24h	<i>SGT</i> gene (<i>WssgtL3.1</i>)	<ul style="list-style-type: none"> • Higher germination rate • Decreased H₂O₂ and MDA accumulation • Defensive role against salt stress with firm membrane integrity 	[3]
<i>Arabidopsis thaliana</i>	Sweet potato (<i>Ipomoea batatas</i>)	100 mM NaCl; 7 and 14d	<i>IbATL38</i>	<ul style="list-style-type: none"> • Enhanced salt tolerance • Reduced H₂O₂ contents • Upregulates genes responsible for scavenging systems against ROS 	[4]
<i>Arabidopsis thaliana</i>	Maize (<i>Zea mays</i>)	100 and 150 mM NaCl; 3, 7 and 14d	<i>ZmEREB20</i>	<ul style="list-style-type: none"> • Increased survival rate • Enhanced ROS scavenging systems • Maintained ion homeostasis • Improved root hair growth 	[5]
Indian mustard (<i>Brassica juncea</i>)	<i>Arabidopsis thaliana</i>	200 mM NaCl; 10d	<i>AtApx1</i>	<ul style="list-style-type: none"> • Decreased H₂O₂ levels • Lesser membrane damage • Enhanced proline accumulation and Chl stability index • Improved antioxidative enzyme activities 	[6]
<i>Arabidopsis thaliana</i>	Siberian crabapple (<i>Malus baccata</i>)	200 mM NaCl; 1, 3, 6, 12, 24 and 48h	<i>MbNAC25</i>	<ul style="list-style-type: none"> • Higher survival rate • Significant increase in Chl and proline contents • Increased the activities of SOD, POD and CAT enzymes • A decrease in MDA contents 	[7]
<i>Arabidopsis thaliana</i>	Rice (<i>Oryza sativa</i>)	50 mM NaCl; 7 and 14d	<i>OsMT-3a</i>	<ul style="list-style-type: none"> • Enhanced seed germination and seedling growth • Reduced H₂O₂ and Na⁺ levels • Increased activity of CAT and APX enzymes 	[8]

Key lime (<i>Citrus aurantifolia</i>)	<i>Arabidopsis thaliana</i>	100 mM NaCl; 24h	<i>CBF3</i>	<ul style="list-style-type: none"> • Tolerant transgenic lines against saline stress • Increased Chl content • Less accumulation of ROS species 	[9]
Rice (<i>Oryza sativa</i>) and <i>Arabidopsis thaliana</i>	Rice (<i>Oryza sativa</i>)	200 or 300 mM NaCl; 7d	<i>OsACBP4</i>	<ul style="list-style-type: none"> • Regulate lipid metabolism • Transgenic rice was tolerant to salinity stress than non-transgenic rice 	[10]

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