

Supplementary Table S1. Rice bioinformatic databases and tools for multiple omics analyses

Tools & Databases	Database description	Reference
RiceSRTFDB	Rice TFs	[1]
STIFDB2	Plant stress responsive genes	[2]
PSPDB	Plant stress related proteins	[3]
QlicRice	Rice abiotic stress responsive QTLs	[4]
RiceNetDB	Rice genome annotated information	[5]
RiceXPro	Gene expression profiles of tissues, organs and hormones	[6]
Stress2TF	Curated stress responsive TF informations	[7]
Plant ontology	Resource of plant anatomy, morphology, growth, and development to plant genomic data	[8]
Phytozome v10.2	Comparative genomic analysis	[9]
PlantPReS	Plant proteome response to stress	[10]
PtRFdb	Plant tRNA-derived fragments	[11]
GRASSIUS	TFs information	[12]
<i>O. sativa</i> genome DB –PlantGDB	EST, cDNA, PUT, and proteins.	[13]
BGI rice Database	Transcriptome analysis, smallRNA, sequence alignment, <i>de novo</i> genome assembly, functional annotation, evolutionary analysis.	[14]
Rice SNP seek Database	Information for rice genotype, phenotype and variety.	[15]
R-Oryzabase	DNA sequences, literature, phenotype description and classification of rice.	[16]
Integrated Genome Browser	Genomics analytic platform	[17]
Gramene	Comparative functional genomics	
Plant-Reactome Gramene Pathways	Analysis of plant pathways	[18]
Gramene QTL Database	QTL prediction	[19]
Expression Atlas	Annotated gene information	[20]
RAP-DB	Rice genome structure and function	[21]
KEGG	Pathway analysis	[22]
STRING	Protein- protein interaction and gene protein interaction	[23]
MCDRP	Curated rice proteins	[24]
Phospho Rice	Rice specific phosphorylation sites	[25]
funRiceGene	Comprehensive database of functionally characterized rice genes	[26]
PlantCARE and PLACE	cis-acting regulatory elements prediction	[27,28]
ExPASy - Protparam	Protein properties prediction	[29]
RiceFOX DB	Hormanome profile	[30]
PPDB	Plant proteomics	[31]
RIPP-DB	Plant phosphoproteome database	[32]
Oryza PG-DB	Rice proteogenomics database	[33]
GOEAST	Gene ontology annotation	[34]
Circos	Comparative genome visualization	[35]
Cytoscape web	Network visualization tool-modelled	[36]
PRIDE inspector	Visualize mass spectrometry (MS) proteomics data	[37]

Supplementary Table S2: Salinity stress responsive genes and its function

Gene	Gene description	Inducible to	Result	Reference
<i>Rab 16A</i>	LEA group of proteins	Drought, Salinity, Cold	Rice plants response to salinity tolerance	[38,39]
<i>GDH</i>	Glutamate dehydrogenase	Salinity, Drought, Cold	Abiotic stress tolerance	[40]
<i>OsNAC2</i>	TF	Salinity, Col d. Drought	Abiotic stress tolerance	[41]
<i>OsMYB6</i>	TF	Drought, Salinity	Salinity tolerance in rice	[42]
<i>P5CS</i>	Pyrroline carboxyl ate synthetase (proline synthesis)	Salinity	Accumulation of Proline in young cladodes	[43]
<i>Mn-SOD</i>	Superoxide dismutase	Salinity	Salinity tolerance	[44]
<i>GS2</i>	Glutamine synthetase (chloroplast)	Salinity, Cold	Salinity stress and chilling tolerance	[45]
<i>OsCDPK7</i>	TF (calcium-dependent protein kinase)	Salinity, Cold, Drought	Salinity, cold and drought stress tolerance	
<i>OsCDPK</i>			Positive regulation of the stress signaling pathways, increase in salinity, cold and drought tolerance	[46]
<i>Mt1D</i>	Manitol-1-phosphate dehydrogenase (mannitol synthesis)	Salinity	Salinity tolerance in rice	[47]
<i>codA</i>	Choline synthase (Betaine biosynthesis)	Salinity, Drought	Enhanced enhanced biomass production	[48]
<i>OsNAC5</i>	TF	Salinity, Col d, Drought	Detoxification, redox homeostasis, and macromolecule fortification	[49]
<i>SNAC1</i>	TF (Stress responsive NAC)	Salinity	Salinity tolerance	
<i>DREB1B/CBF1</i>		Salinity, Drought	Salinity and drought tolerance	[50]
<i>DREB1A/CBF3</i>	TF	Salinity	Salinity tolerance	[41]
<i>ZFP179</i>		Salinity	Salinity tolerance	[51]
<i>OsCDPK21</i>	TF (calcium-dependent protein kinase)	Salinity	Positive regulation of stress signaling pathways, increase in salinity tolerance and ABA	[52]
<i>MAPK5</i>	Mitogen-activated protein kinase	Salinity, Cold and Drought	Salinity, drought and cold stress tolerance	[53]
<i>MAPK44</i>		Salinity	Salinity tolerance	[54]
<i>SAPK4</i>	Serine-threonine protein kinase	Salinity	Salinity tolerance in rice	[55]
<i>OsNHX1</i>	Sodium/hydrogen exchanger	Salinity	Salinity tolerance, maintained growth at 200 mM NaCl and increased biomass production	[56,57]
<i>OsSIKI</i>	Stress-induced protein kinase gene 1 (Receptor-like kinases)	Drought, Salinity	Salinity and drought stress tolerance	[58]
<i>OsSIK2</i>	Stress-induced protein kinase gene 2 (Receptor-like kinases)	Drought, Salinity	Abiotic stress tolerance and early leaf development and senescence phenotype	[59]
<i>SOS2</i>	Salinity Overly Sensitive 2	Drought, Salinity	Exchange of Na^+/H^+ in plasma membrane of yeast (<i>Saccharomyces cerevisiae</i>) cells and reduced their	[60]

			Na^+ content	
<i>SDIR1</i>	Salinity- and drought-induced ring finger 1	Drought an d Salinity	Decrease water loss likely due to their enhanced stomata response	[61]
<i>DSR2</i>	DUF966 stress-repressive gene 2	Drought, Col d, Salinity, Hea t, Oxidative	Salinity and drought stress tolerance and decreased ABA sensitivity	[62]
<i>OsNCED3</i>	9-cisEpoxyxcarotenoid dioxygenase (rice stress-inducible promoter)	Drought, Salinity	ABA biosynthesis, roots and leaves enhancement under drought and salinity conditions	[63]
<i>OsCYP2</i>	Cyclophilin 2	Salinity	Controls ROS level, involved in PEG, heat, cold, or ABA signal pathways	[64]
<i>OsPYL/RCA R5</i>	Pyrabactin Resistance 1 Like/Regulatory Components of ABA receptors	Drought, Salinity	Abiotic stress tolerance in rice, inhibits plant growth, and modulates gene expression	[65]
<i>OsLEA3-2</i>	Late embryogenesis abundant proteins	Drought, Salinity	Elevated growth performance under salinity/osmotic stress conditions	[66]
<i>OsOAT</i>	Ornithine δ -amino-transferase)	Drought, Salinity, Oxidative	Involved in proline (Pro) and arginine (Arg) metabolism, increased δ -OAT activity, glutathione (GSH) and ROS content	[67]
<i>OsSAP</i>	Stress associated Protein	Multiple abiotic stresses including salinity	Induces the ubiquitination, ROS scavenging activities, redox sensing and hormone metabolism	[68,69]

Supplementary Table S3: Salinity stress responsive TFs and their functions

TF Family	Genes	Function	Abiotic tolerance	Reference
bZIP	bZIP23, bZIP71	Increase sensitivity to exogenous ABA at both germination and post-germination stages, improving the stress resistance of crops	Drought, salinity	[70,71]
	bZIP4	Regulates the ABA synthesis development	Salinity	[72]
	bZIP110	Regulating absorption of Na ⁺ nd oline accumulation	a pr Salinity	[73]
	ABF2	Function in osmotic stress signaling	Salinity	
	ABF3		Salinity	
	ABF4	Participate in multiple stress responses	Drought, Salinity, Cold	
	bZIP44,62,78	Differentially regulate expressions of ABA and stress- responsive genes	Drought, Salinity, Cold	[75]
	bZIP132	Reduce ABA sensitivity, increased water loss	Salinity, Drought	[76]
	ABI5	Regulation of adaptive stress response	Salinity	[77]
	NAC29	Improve physiological traits, reduced H ₂ O ₂ accumulation	salinity, drought	[78]
NAC	NAC022	Na ⁺ accumulation is less in roots and shoots, increases proline and soluble sugar contents	Salinity, drought, and ABA	[79]
	NAC2	Lateral root development and stress tolerance	Salinity	[80]
	NAC019,055,072	Upregulation of stress inducible	Drought, Salinity	[81]
	NAC4	Regulation of plant stresses	Drought, salinity, Cold	[82]
	NAC6	Root system development and yield, regulates the stress tolerance	Drought, salinity	[83-85]
bHLH	NAC066	Increases proline and soluble sugar contents	Salinity, H ₂ O ₂	[86]
	NAC2	Stress tolerance	Salinity, Drought	[87]
	NAC4,11,13,24,29,30, 37,47,51, 52,59,69,76,80,86,87,112	Playe a role in abiotic stress tolerance, signal transduction pathway regulation	Salinity, Drought, metal, cold, temperature, UV, flooding	[88]
	NAC032	Promotes senescence and accumulation of H ₂ O ₂ , stress tolerance	Salinity, mannitol	[89]
	bHLH035	Mediates seed germination and seedling recovery	Salinity	[90]
	bHLH22	Increase osmotic potential and accumulation of secondary metabolites	Salinity, Drought	[91]
	bHLH26,87,94,105, 110,116,127,129	Multiple abiotic stress tolerance and transduction signal pathway regulation	Salinity, Drought, metal, cold, temperature, UV, flooding	[88]
	bHLH38	Regulate osmotic balance, stress-induced oxidation damage	Salinity, Drought	[92]
	MYC2	Regulate proline biosynthesis	Salinity	[93]
	MYB6	Elevated CAT and SOD activities,	Salinity, Drought	[94]

		salt stress tolerance		
MYB	MYB91	Rice tolerance to abiotic stress	Salinity	[95]
	MYB15	Enhanced ABA sensitivity, reduced water loss rate, increased ABA biosynthesis	Drought, Salinity	[96]
	MYB76		Salinity	
	MYB92	Stress tolerance and plant physiology processes	Salinity, Cold	[97]
	MYB117		Drought, Salinity	
	MYB76	Response to ionic stresses, improve stress resistance	Salinity	[98]
	MYB3R-2	Increased tolerance to Salt	Freezing, Drought, and Salinity	[99]
	MYB48-1	Increase Salinity tolerance	Salinity, Drought	[100]
CBF/DREB	MYB118	Regulate osmotic stress	Salinity, Drought	[101]
	DREB2	Salinity and dehydration stress in roots and stems, transcript accumulation and alternative splicing regulation	Drought, Salinity, Cold	[102]
	DREB1F, DREB2A, DREB5A & DREB6B	Increased the number of transcripts in roots and stem	Salinity, Cold, Dehydration and ABA	[103]
	DREB1A	Produce transgenic monocots that are tolerant abiotic stress	Cold, Salinity	
	DREB1C		Drought, Salinity, Cold	[104]
	DREB2C	Negative impact of several ABA/stress-responsive genes, involve physical interaction	Cold, Salinity	[105]
	DREB1F	Regulation of ABA-dependent pathway, Stress tolerance	Drought, Salinity,	[106]
	ERF3	Enhanced resistance to high salinity and dehydration stresses	Salinity, Drought	[107]
AP2/ERF	EREBP1,9,10,11,36,39,49,75, 87,104,132,145,147	Multiple abiotic stress tolerance mechanisms and signal transduction pathway regulation	Salinity, Drought, metal, cold, temperature, UV, flooding	[88]
	WRKY30	Higher antioxidant activities and lower ROS contents, increases soluble sugar and proline contents	Salinity	[108]
	WRKY93	Increase stress tolerance, maintain membrane stability and played a major role superior agricultural trait of SR3 through promoting root development	Salinity	[109]
	WRKY13,54	Abiotic stress response and root development	Drought, Salinity	[110]
	WRKY83	Alterations in physiological parameters such as proline, malondialdehyde (MDA) and electrolyte leakage after stress treatments, increase proline accumulation	Salinity	[111]
	WRKY4,20,25,31,53,68, 76, 79,90,103,104	Multiple abiotic stress tolerance mechanisms and signal transduction pathway regulation	Salinity, Drought, metal, cold, temperature, UV, flooding	[88]
	WRKY33	Improved Salinity stress tolerance than the wild type under abiotic stress condition.	Salinity	[112]
	SAP1, 2, 5, 6, 7, 8, 9, 11,	Developmental regulation, signal transduction,	Salinity, Drought, metal, cold, temperature, UV,	[69]

	17	translation, biosynthesis of amino acids, energy metabolism	flooding	
ZF-HD	Zat7	Salinity stress tolerance to transgenic plants, defense response	Salinity	[113]
	CaZF	Potential plant salt-tolerance and osmotolerance determinant	Salinity	[114]
	ZHD10,12,14	Multiple abiotic stress tolerance mechanisms and signal transduction pathway regulation, plant differentiation	Salinity, Drought, metal, cold, temperature, UV, flooding	[88]
HSF	HSF1-25	Transcriptional, post-transcriptional, translational and post-translational activators of abiotic stressors, regulate hormonal signal transduction	Salinity, Drought, metal, cold, heat, UV, flooding	[115]
Others	HARDY	Improves water use efficiency, increase in leaf biomass and bundle sheath cells, stress tolerance	Drought, Salinity	[116]

References

1. Priya, P. and Jain, M., 2013a. RiceSRTFDB: a database of rice transcription factors containing comprehensive expression, cis-regulatory element and mutant information to facilitate gene function analysis. *Database*, 2013.
2. Naika, M., Shameer, K., Mathew, O.K., Gowda, R. and Sowdhamini, R., 2013. STIFDB2: an updated version of plant stress-responsive transcription factor database with additional stress signals, stress-responsive transcription factor binding sites and stress-responsive genes in Arabidopsis and rice. *Plant and Cell Physiology*, 54(2), pp.e8-e8.
3. Kumar, S.A., Kumari, P.H., Sundararajan, V.S., Suravajhala, P., Kanagasabai, R. and Kishor, P.K., 2014. PSPDB: plant stress protein database. *Plant molecular biology reporter*, 32(4), pp.940-942.
4. Smita, S., Lenka, S.K., Katiyar, A., Jaiswal, P., Preece, J. and Bansal, K.C., 2011. QlicRice: a web interface for abiotic stress responsive QTL and loci interaction channels in rice. *Database*, 2011.
5. Liu, L. et al. An integrative bioinformatics framework for genome-scale multiple level network reconstruction of rice. *Journal of integrative bioinformatics*. 10, 94-102 (2013).
6. Sato, Y. et al. RiceXPro Version 3.0: expanding the informatics resource for rice transcriptome. *Nucleic Acids Res.* 41, D1206–D1213 (2013b).
7. Zhang, X., Yao, C., Fu, S., Xuan, H., Wen, S., Liu, C., Li, F., Liu, A., Bi, S., Zhang, S. and Li, S., 2018. Stress2TF: a manually curated database of TF regulation in plant response to stress. *Gene*, 638, pp.36-40.
8. Cooper, L. and Jaiswal, P., 2016. The plant ontology: a tool for plant genomics. In *Plant Bioinformatics* (pp. 89-114). Humana Press, New York, NY.
9. Goodstein, D. M. et al. Phytozome: a comparative platform for green plant genomics. *Nucleic Acid Res.* 40, D1178–D1186 (2012).
10. Mousavi, S.A., Pouya, F.M., Ghaffari, M.R., Mirzaei, M., Ghaffari, A., Alikhani, M., Ghareyazie, M., Komatsu, S., Haynes, P.A. and Salekdeh, G.H., 2016. PlantPReS: A database for plant proteome response to stress. *Journal of proteomics*, 143, pp.69-72.
11. Gupta, N., Singh, A., Zahra, S. and Kumar, S., 2018. PtRFdb: a database for plant transfer RNA-derived fragments. *Database*, 2018.
12. Yilmaz, A. et al. GRASSIUS: a platform for comparative regulatory genomics across the grasses. *Plant Physiol.* 149, 171–180 (2009).
13. Duvick, J. et al. PlantGDB: a resource for comparative plant genomics. *Nucleic Acids Res.* 36, D959–D965 (2008).
14. Zhao, W. et al. BGI-RIS: an integrated information resource and comparative analysis workbench for rice genomics. *Nucleic Acids Res.* 32, D377–D382 (2003).
15. Alexandrov, N., Tai, S., Wang, W., Mansueto, L., Palis, K., Fuentes, R.R., Ulat, V.J., Chebotarov, D., Zhang, G., Li, Z. and Mauleon, R., 2014. SNP-Seek database of SNPs derived from 3000 rice genomes. *Nucleic acids research*, 43(D1), pp.D1023-D1027.
16. Kurata, N. & Yamazaki, Y. Oryzabase. An Integrated Biological and Genome Information Database for Rice. *Plant Physiol.* 140 (2006).
17. Freese, N.H., Norris, D.C. and Loraine, A.E., 2016. Integrated genome browser: visual analytics platform for genomics. *Bioinformatics*, 32(14), pp.2089-2095.
18. Tello-Ruiz, M. K. et al. Gramene 2016: comparative plant genomics and pathway resources. *Nucleic Acids Res.* 44, 1133–1140 (2016).
19. Ni, J. et al. Gramene QTL database: development, content and applications. *Database*, Article ID bap005 (2009).
20. Petryszak, R. et al. Expression Atlas update - an integrated database of gene and protein expression in humans, animals and plants. *Nucleic Acids Res.* 44, 746–752 (2016).
21. Sakai, H. et al. Rice Annotation Project Database (RAP-DB): An Integrative and Interactive Database for Rice Genomics. *Plant Cell Physiol.* 54, 1–11 (2012).
22. Kanehisa M, Goto S. KEGG: Kyoto Encyclopedia of Genes and Genomes. *Nucleic Acids Res.* 2000;28(1):27–30. PMID: 10592173.
23. Szklarczyk, D. et al. The STRING database in 2017: quality-controlled protein–protein association networks, made broadly accessible. *Nucleic Acids Res.* 45, D362–D368 (2017).
24. Raghuvanshi, S., Gour, P. & Joseph, S.V. Manually Curated Database of Rice Proteins (MCDRP), a database of digitized experimental data on rice. *Current Plant Biol.* 8, 26–30 (2016).
25. Que, S. et al. PhosphoRice: a meta-predictor of rice specific phosphorylation sites. *Plant Methods*. 8, 5(2012).
26. Yao, W., Li, G., Yu, Y. & Ouyang, Y. funRiceGenes dataset for comprehensive understanding and application of rice functional genes. *Giga Sci.* 7, gix119 (2017).
27. Higo, K., Ugawa, Y., Iwamoto, M. & Korenaga, T. Plant cis-acting regulatory DNA elements (PLACE) database: 1999. *Nucleic Acid Res.* 27, 297–300 (1999).
28. Lescot, M. et al. PlantCARE, a database of plant cis-acting regulatory elements and a portal to tools for in silico analysis of promoter sequences. *Nucleic Acid Res.* 30, 325–327 (2002).
29. Gasteiger, E. et al. Protein Identification and Analysis Tools on the ExPASy Server. In Walker, J. M. (ed), *The Proteomics Protocols Handbook*, Springer, New York, pp. 571–607 (2005).

30. Sakurai, T. et al. RiceFOX: a database of Arabidopsis mutant lines overexpressing rice full-length cDNA that contains a wide range of trait information to facilitate analysis of gene function. *Plant and cell physiol.* 52, 265-273 (2010).
31. Sun, Q. et al. PPDB, the plant proteomics database at Cornell. *Nuclieic Acid. Res.* 37, D969-D974 (2008).
32. Nakagami, H. et al. Large scale comparative phosphoproteomics identifies conserved phosphorylation sites in plants. *Plant Physiol.* 153, 1161-1174 (2010).
33. Helmy, M., Tomita, M. & Ishihama, Y. OryzaPG-DB: rice proteome database based on shotgun proteogenomics. *BMC Plant Biol.* 11, 63 (2011).
34. Zheng, Q. & Wang, X. J. GOEAST: a web-based software toolkit for Gene Ontology enrichment analysis. *Nucleic Acids Res.* 36, W358-W363 (2008).
35. Krzywinski, M., Schein, J., Birol, I., Connors, J., Gascoyne, R., Horsman, D., Jones, S.J. and Marra, M.A., 2009. Circos: an information aesthetic for comparative genomics. *Genome research*, 19(9), pp.1639-1645.
36. Lopes, C.T., Franz, M., Kazi, F., Donaldson, S.L., Morris, Q. and Bader, G.D., 2010. Cytoscape Web: an interactive web-based network browser. *Bioinformatics*, 26(18), pp.2347-2348.
37. Wang, R., Fabregat, A., Ríos, D., Ovelleiro, D., Foster, J.M., Côté, R.G., Griss, J., Csordas, A., Perez-Riverol, Y., Reisinger, F. and Hermjakob, H., 2012. PRIDE Inspector: a tool to visualize and validate MS proteomics data. *Nature biotechnology*, 30(2), pp.135-137.
38. Ganguly, M., Datta, K., Roychoudhury, A., Gayen, D., Sengupta, D.N. and Datta, S.K., 2012. Overexpression of Rab16A gene in indica rice variety for generating enhanced Salinity tolerance. *Plant signaling & behavior*, 7(4), pp.502-509.
39. Basu, S. and Roychoudhury, A., 2014. Expression profiling of abiotic stress-inducible genes in response to multiple stresses in rice (*Oryza sativa L.*) varieties with contrasting level of stress tolerance. *BioMed research international*, 2014.
40. Skopelitis, D.S., Paranychianakis, N.V., Paschalidis, K.A., Pliakonis, E.D., Delis, I.D., Yakoumakis, D.I., Kouvarakis, A., Papadakis, A.K., Stephanou, E.G. and Roubelakis- Angelakis, K.A., 2006. Abiotic stress generates ROS that signal expression of anionic glutamate dehydrogenases to form glutamate for proline synthesis in tobacco and grapevine. *The Plant Cell*, 18(10), pp.2767-2781.
41. Hu, H., Dai, M., Yao, J., Xiao, B., Li, X., Zhang, Q. and Xiong, L., 2006. Overexpressing a NAM, ATAF, and CUC (NAC) transcription factor enhances drought resistance and Salinity tolerance in rice. *Proceedings of the National Academy of Sciences*, 103(35), pp.12987-12992.
42. Liu, C., Chen, K., Zhao, X., Wang, X., Shen, C., Zhu, Y., Dai, M., Qiu, X., Yang, R., Xing, D. and Pang, Y., 2019. Identification of genes for salt tolerance and yield-related traits in rice plants grown hydroponically and under saline field conditions by genome- wide association study. *Rice*, 12(1), p.88.
43. Silva-Ortega, C.O., Ochoa-Alfaro, A.E., Reyes-Agüero, J.A., Aguado-Santacruz, G.A. and Jiménez-Bremont, J.F., 2008. Salinity stress increases the expression of p5cs gene and induces proline accumulation in cactus pear. *Plant Physiology and Biochemistry*, 46(1), pp.82-92.
44. Eyidoğan, F.I., Öktem, H.A. and Yücel, M., 2003. Superoxide dismutase activity in Salinity stressed wheat seedlings. *Acta physiologiae plantarum*, 25(3), pp.263-269.
45. Hoshida, H., Tanaka, Y., Hibino, T., Hayashi, Y., Tanaka, A., Takabe, T. and Takabe, T., 2000. Enhanced tolerance to Salinity stress in transgenic rice that overexpresses chloroplast glutamine synthetase. *Plant molecular biology*, 43(1), pp.103-111.
46. Saijo, Y., Hata, S., Kyozuka, J., Shimamoto, K. and Izui, K., 2000. Over- expression of a single Ca²⁺- dependent protein kinase confers both cold and Salinity/drought tolerance on rice plants. *The Plant Journal*, 23(3), pp.319-327.
47. Li, Z.C., X.C. Zhang, L. Zhang, B.C. Thuang, C.L. hang, G.Y. Wang and Y.C. Fu, 2004. Expression of MtD1 gene in transgenic rice leads to enhanced Salinity tolerance. *J. china Agric. Univ*, 9: 38-43
48. Li, H., Wang, Z., Ke, Q., Ji, C.Y., Jeong, J.C., Lee, H.S., Lim, Y.P., Xu, B., Deng, X.P. and Kwak, S.S., 2014. Overexpression of codA gene confers enhanced tolerance to abiotic stresses in alfalfa. *Plant Physiology and Biochemistry*, 85, pp.31-40.
49. Hu, H., You, J., Fang, Y., Zhu, X., Qi, Z. and Xiong, L., 2008. Characterization of transcription factor gene SNAC2 conferring cold and Salinity tolerance in rice. *Plant molecular biology*, 67(1-2), pp.169-181.
50. Oh, S.J., Song, S.I., Kim, Y.S., Jang, H.J., Kim, S.Y., Kim, M., Kim, Y.K., Nahm, B.H. and Kim, J.K., 2005. Arabidopsis CBF3/DREB1A and ABF3 in transgenic rice increased tolerance to abiotic stress without stunting growth. *Plant physiology*, 138(1), pp.341-351.
51. Sun, S.J., Guo, S.Q., Yang, X., Bao, Y.M., Tang, H.J., Sun, H., Huang, J. and Zhang, H.S., 2010. Functional analysis of a novel Cys2/His2-type zinc finger protein involved in Salinity tolerance in rice. *Journal of experimental botany*, 61(10), pp.2807-2818.
52. Asano, T., Hakata, M., Nakamura, H., Aoki, N., Komatsu, S., Ichikawa, H., Hirochika, H. and Ohsugi, R., 2011. Functional characterisation of OsCPK21, a calcium-dependent protein kinase that confers Salinity tolerance in rice. *Plant molecular biology*, 75(1-2), pp.179-191.
53. Xiong, L. and Yang, Y., 2003. Disease resistance and abiotic stress tolerance in rice are inversely modulated by an abscisic acid-inducible mitogen-activated protein kinase. *The Plant Cell*, 15(3), pp.745-759.
54. Jeong, M.J., Lee, S.K., Kim, B.G., Kwon, T.R., Cho, W.S., Park, Y.T., Lee, J.O., Kwon, H.B., Byun, M.O. and Park, S.C., 2006. A rice (*Oryza sativa L.*) MAP kinase gene, OsMAPK44, is involved in response to abiotic stresses. *Plant Cell, Tissue and Organ Culture*, 85(2), pp.151-160.
55. Diédhiou, C.J., Popova, O.V., Dietz, K.J. and Golldack, D., 2008. The SNF1-type serine- threonine protein kinase SAPK4 regulates stress-responsive gene expression in rice. *BMC plant biology*, 8(1), pp.1-13.

56. Fukuda, A., Nakamura, A., Tagiri, A., Tanaka, H., Miyao, A., Hirochika, H. and Tanaka, Y., 2004. Function, intracellular localization and the importance in Salinity tolerance of a vacuolar Na⁺/H⁺ antiporter from rice. *Plant and cell physiology*, 45(2), pp.146-159.
57. Chen, M., Chen, Q., Niu, X., Zhang, R., Lin, H., Xu, C., Wang, X., Wang, G. and Chen, J., 2007. Expression of OsNHX1 gene in maize confers Salinity tolerance and promotes plant growth in the field. *Plant Soil and Environment*, 53(11), p.490.
58. Ouyang, S. Q., Liu, Y. F., Liu, P., Lei, G., He, S. J., Ma, B., et al. (2010). Receptor-like kinase OsSIK1 improves drought and Salinity stress tolerance in rice (*Oryza sativa*) plants. *Plant J.* 62: 316–329.
59. Chen, L. J., Wuriyanghan, H., Zhang, Y. Q., Duan, K. X., Chen, H. W., Li, Q. T., et al. (2013). An S-domain receptor-like kinase, OsSIK2, confers abiotic stress tolerance and delays dark-induced leaf senescence in rice. *Plant Physiol.* 163: 1752–1765.
60. Martinez-Atienza, J., Jiang, X., Garciadeblas, B., Mendoza, I., Zhu, J. K., Pardo, J. M. and Quintero, F. J. (2007). Conservation of the Salinity Overly Sensitive Pathway in Rice. *Plant Physiol.* 143(2): 1001-1012.
61. Gao, T., Wu, Y., Zhang, Y., Liu, L., Ning, Y., Wang, D., Tong, H., Chen, S., Chu, C., Xie, Q. (2011). OsSDIR1 overexpression greatly improves drought tolerance in transgenic rice. *Plant Mol Biol* 76: 145–156.
62. Luo, C., Guo, C., Wang, W., Wang, L., Chen, L. (2013). Overexpression of a new stress- repressive gene OsDSR2 encoding a protein with a DUF966 domain increases Salinity and simulated drought stress sensitivities and reduces ABA sensitivity in rice. *Plant Cell Rep* 33: 323–336.
63. Bang, S. W., Park, S. H., Jeong, J. S., Kim, Y. S., Jung, H., Ha, S. H., Kim, J. K. (2013). Characterization of the stress-inducible OsNCED3 promoter in different transgenic rice organs and over three homozygous generations. *Planta* 237(1):211-24.
64. Ruan, S. L., Ma, H. S., Wang, S. H., Fu, Y. P., Xin, Y., Liu, W. Z., Wang, F., Tong, J. X., Wang, S. Z., Chen, H. Z. (2011). Proteomic identification of OsCYP2, a rice cyclophilin that confers Salinity tolerance in rice (*Oryza sativa* L.) seedlings when overexpressed. *BMC Plant Biology*. 11.
65. Kim, H., Lee, K., Hwang, H., Bhatnagar, N., Kim, D.-Y., Yoon, I. S., et al. (2014). Over expression of PYL5 in rice enhances drought tolerance, inhibits growth, and modulates gene expression. *J. Exp. Bot.* 65: 453–464.
66. Duan, J., and Cai, W. (2012). OsLEA3-2, an abiotic stress induced gene of rice plays a key role in Salinity and drought tolerance. *PLoS ONE* 7: e45117.
67. You, J., Hu, H., and Xiong, L. (2012). An ornithine δ-aminotransferase gene OsOAT confers drought and oxidative stress tolerance in rice. *Plant Sci* 197: 59–69.
68. Krishnan, S. R., Muthuramalingam, P., Mohan, C., & Ramesh, M. (2018). Emerging Trends Of A20/An1 Zinc-Finger Proteins In Improving Rice Productivity Under Abiotic Stress. *Rice Science: Biotechnological and Molecular Advancements*, 1.
69. Muthuramalingam, P., Jeyasri, R., Selvaraj, A., Kalaiyarasi, D., Aruni, W., Pandian, S.T. K., & Ramesh, M. (2020b). Global transcriptome analysis of novel stress associated protein (SAP) genes expression dynamism of combined abiotic stresses in *Oryza sativa* (L.). *Journal of Biomolecular Structure and Dynamics*, 1-12.
70. Xiang, Y., Tang, N., Du, H., Ye, H. and Xiong, L., 2008. Characterization of OsbZIP23 as a key player of the basic leucine zipper transcription factor family for conferring abscisic acid sensitivity and salinity and drought tolerance in rice. *Plant physiology*, 148(4), pp.1938-1952.
71. Liu, C., Mao, B., Ou, S., Wang, W., Liu, L., Wu, Y., Chu, C. and Wang, X., 2014. OsbZIP71, a bZIP transcription factor, confers salinity and drought tolerance in rice. *Plant molecular biology*, 84(1-2), pp.19-36.
72. Ma, H., Liu, C., Li, Z., Ran, Q., Xie, G., Wang, B., Fang, S., Chu, J. and Zhang, J., 2018. ZmbZIP4 contributes to stress resistance in maize by regulating ABA synthesis and root development. *Plant physiology*, 178(2), pp.753-770.
73. Xu, Z., Ali, Z., Xu, L., He, X., Huang, Y., Yi, J., Shao, H., Ma, H. and Zhang, D., 2016. The nuclear protein GmbZIP110 has transcription activation activity and plays important roles in the response to salinity stress in soybean. *Scientific reports*, 6, p.20366.
74. Choi, H.I., Hong, J.H., Ha, J.O., Kang, J.Y. and Kim, S.Y., 2000. ABFs, a family of ABA- responsive element binding factors. *Journal of Biological Chemistry*, 275(3), pp.1723-1730.
75. Liao, Y., Zou, H.F., Wei, W., Hao, Y.J., Tian, A.G., Huang, J., Liu, Y.F., Zhang, J.S. and Chen, S.Y., 2008a. Soybean GmbZIP44, GmbZIP62 and GmbZIP78 genes function as negative regulator of ABA signaling and confer salt and freezing tolerance in transgenic Arabidopsis. *Planta*, 228(2), pp.225-240.
76. Liao, Y., Zhang, J.S., Chen, S.Y. and Zhang, W.K., 2008b. Role of soybean GmbZIP132 under abscisic acid and salt stresses. *Journal of Integrative Plant Biology*, 50(2), pp.221-230
77. Zou, M., Guan, Y., Ren, H., Zhang, F. and Chen, F., 2008. A bZIP transcription factor, OsABI5, is involved in rice fertility and stress tolerance. *Plant molecular biology*, 66(6), pp.675-683.
78. Xu, Z., Wang, C., Xue, F., Zhang, H. and Ji, W., 2015. Wheat NAC transcription factor TaNAC29 is involved in response to salt stress. *Plant Physiology and Biochemistry*, 96, pp.356-363.
79. Hong, Y., Zhang, H., Huang, L., Li, D. and Song, F., 2016. Overexpression of a stress- responsive NAC transcription factor gene ONAC022 improves drought and salt tolerance in rice. *Frontiers in Plant Science*, 7, p.4.
80. He, X.J., Mu, R.L., Cao, W.H., Zhang, Z.G., Zhang, J.S. and Chen, S.Y., 2005. AtNAC2, a transcription factor downstream of ethylene and auxin signaling pathways, is involved in salt stress response and lateral root development. *The Plant Journal*, 44(6), pp.903-916.

81. Tran, L.S.P., Nakashima, K., Sakuma, Y., Simpson, S.D., Fujita, Y., Maruyama, K., Fujita, M., Seki, M., Shinozaki, K. and Yamaguchi-Shinozaki, K., 2004. Isolation and functional analysis of *Arabidopsis* stress-inducible NAC transcription factors that bind to a drought-responsive cis- element in the early responsive to dehydration stress 1 promoter. *The Plant Cell*, 16(9), pp.2481-2498.
82. Meng, C., Cai, C., Zhang, T. and Guo, W., 2009. Characterization of six novel NAC genes and their responses to abiotic stresses in *Gossypium hirsutum* L. *Plant Science*, 176(3), pp.352-359.
83. Nakashima, K., Tran, L.S.P., Van Nguyen, D., Fujita, M., Maruyama, K., Todaka, D., Ito, Y., Hayashi, N., Shinozaki, K. and Yamaguchi- Shinozaki, K., 2007. Functional analysis of a NAC- type transcription factor OsNAC6 involved in abiotic and biotic stress- responsive gene expression in rice. *The Plant Journal*, 51(4), pp.617-630.
84. Lee, D.K., Chung, P.J., Jeong, J.S., Jang, G., Bang, S.W., Jung, H., Kim, Y.S., Ha, S.H., Choi, Y.D. and Kim, J.K., 2017. The rice Os NAC 6 transcription factor orchestrates multiple molecular mechanisms involving root structural adaptions and nicotianamine biosynthesis for drought tolerance. *Plant Biotechnology Journal*, 15(6), pp.754-764.
85. Chung, P.J., Jung, H., Do Choi, Y. and Kim, J.K., 2018. Genome-wide analyses of direct target genes of four rice NAC-domain transcription factors involved in drought tolerance. *BMC genomics*, 19(1), p.40.
86. Yuan, X., Wang, H., Cai, J., Bi, Y., Li, D. and Song, F., 2019. Rice NAC transcription factor ONAC066 functions as a positive regulator of drought and oxidative stress response. *BMC plant biology*, 19(1), p.278.
87. Shen, J., Lv, B., Luo, L., He, J., Mao, C., Xi, D. and Ming, F., 2017. The NAC-type transcription factor OsNAC2 regulates ABA-dependent genes and abiotic stress tolerance in rice. *Scientific reports*, 7, p.40641.
88. Muthuramalingam, P., Krishnan, S. R., Saravanan, K., Mareeswaran, N., Kumar, R., & Ramesh, M. (2018a). Genome-wide identification of major transcription factor superfamilies in rice identifies key candidates involved in abiotic stress dynamism. *Journal of Plant Biochemistry and Biotechnology*, 27(3), 300-317.
89. Mahmood, K., El-Kereamy, A., Kim, S.H., Nambara, E. and Rothstein, S.J., 2016. ANAC032 positively regulates age-dependent and stress-induced senescence in *Arabidopsis thaliana*. *Plant and Cell Physiology*, 57(10), pp.2029-2046.
90. Chen, H.C., Cheng, W.H., Hong, C.Y., Chang, Y.S. and Chang, M.C., 2018. The transcription factor OsbHLH035 mediates seed germination and enables seedling recovery from Salinity stress through ABA-dependent and ABA-independent pathways, respectively. *Rice*, 11(1), p.50.
91. Waseem, M. and Li, Z., 2019. Dissecting the Role of a Basic Helix-Loop-Helix Transcription Factor, SlbHLH22, Under Salinity and Drought Stresses in Transgenic *Solanum lycopersicum* L. *Frontiers in plant science*, 10, p.734.
92. Qiu, J.R., Huang, Z., Xiang, X.Y., Xu, W.X., Wang, J.T., Chen, J., Song, L., Xiao, Y., Li, X., Ma, J. and Cai, S.Z., 2020. MfbHLH38, a *Myrothamnus flabellifolia* bHLH transcription factor, confers tolerance to drought and salinity stresses in *Arabidopsis*. *BMC Plant Biology*, 20(1), pp.1-14.
93. Verma, D., Jalmi, S.K., Bhagat, P.K., Verma, N. and Sinha, A.K., 2019. A bHLH transcription factor, MYC2, imparts Salinity intolerance by regulating proline biosynthesis in *Arabidopsis*. *The FEBS Journal*.
94. Tang, Y., Bao, X., Zhi, Y., Wu, Q., Guo, Y., Yin, X., Zeng, L., Li, J., Zhang, J., He, W. and Liu, W., 2019. Overexpression of a MYB family gene, OsMYB6, increases drought and salinity stress tolerance in transgenic rice. *Frontiers in plant science*, 10, p.168.
95. Zhu, N., Cheng, S., Liu, X., Du, H., Dai, M., Zhou, D.X., Yang, W. and Zhao, Y., 2015. The R2R3-type MYB gene OsMYB91 has a function in coordinating plant growth and Salinity stress tolerance in rice. *Plant Science*, 236, pp.146-156.
96. Ding, Z., Li, S., An, X., Liu, X., Qin, H. and Wang, D., 2009. Transgenic expression of MYB15 confers enhanced sensitivity to abscisic acid and improved drought tolerance in *Arabidopsis thaliana*. *Journal of Genetics and Genomics*, 36(1), pp.17-29.
97. Liao, Y., Zou, H.F., Wang, H.W., Zhang, W.K., Ma, B., Zhang, J.S. and Chen, S.Y., 2008c. Soybean GmMYB76, GmMYB92, and GmMYB177 genes confer stress tolerance in transgenic *Arabidopsis* plants. *Cell research*, 18(10), pp.1047-1060.
98. He, Y., Li, W., Lv, J., Jia, Y., Wang, M. and Xia, G., 2012. Ectopic expression of a wheat MYB transcription factor gene, TaMYB73, improves salinity stress tolerance in *Arabidopsis thaliana*. *Journal of Experimental Botany*, 63(3), pp.1511-1522.
99. Dai, X., Xu, Y., Ma, Q., Xu, W., Wang, T., Xue, Y. and Chong, K., 2007. Overexpression of an R1R2R3 MYB gene, OsMYB3R-2, increases tolerance to freezing, drought, and salt stress in transgenic *Arabidopsis*. *Plant physiology*, 143(4), pp.1739-1751.
100. Xiong, H., Li, J., Liu, P., Duan, J., Zhao, Y., Guo, X., Li, Y., Zhang, H., Ali, J. and Li, Z., 2014. Overexpression of OsMYB48-1, a novel MYB-related transcription factor, enhances drought and salinity tolerance in rice. *PloS one*, 9(3), p.e92913.
101. Du, Y.T., Zhao, M.J., Wang, C.T., Gao, Y., Wang, Y.X., Liu, Y.W., Chen, M., Chen, J., Zhou, Y.B., Xu, Z.S. and Ma, Y.Z., 2018. Identification and characterization of GmMYB118 responses to drought and Salinity stress. *BMC plant biology*, 18(1), pp.1-18.
102. Egawa, C., Kobayashi, F., Ishibashi, M., Nakamura, T., Nakamura, C. and Takumi, S., 2006. Differential regulation of transcript accumulation and alternative splicing of a DREB2 homolog under abiotic stress conditions in common wheat. *Genes & genetic systems*, 81(2), pp.77-91.
103. Konzen, E.R., Recchia, G.H., Cassieri, F., Caldas, D.G.G., Berny Mier y Teran, J.C., Gepts, P. and Tsai, S.M., 2019. DREB genes from common bean (*Phaseolus vulgaris* L.) show broad to specific abiotic stress responses and distinct levels of nucleotide diversity. *International journal of genomics*, 2019.

104. Dubouzet, J.G., Sakuma, Y., Ito, Y., Kasuga, M., Dubouzet, E.G., Miura, S., Seki, M., Shinozaki, K. and Yamaguchi-Shinozaki, K., 2003. OsDREB genes in rice, *Oryza sativa* L., encode transcription activators that function in drought-, high- salt- and cold- responsive gene expression. *The Plant Journal*, 33(4), pp.751-763.
105. Lee, S.J., Kang, J.Y., Park, H.J., Kim, M.D., Bae, M.S., Choi, H.I. and Kim, S.Y., 2010. DREB2C interacts with ABF2, a bZIP protein regulating abscisic acid-responsive gene expression, and its overexpression affects abscisic acid sensitivity. *Plant physiology*, 153(2), pp.716-727.
106. Wang, Q., Guan, Y., Wu, Y., Chen, H., Chen, F. and Chu, C., 2008. Overexpression of a rice OsDREB1F gene increases salt, drought, and low temperature tolerance in both *Arabidopsis* and rice. *Plant molecular biology*, 67(6), pp.589-602.
107. Zhang, G., Chen, M., Li, L., Xu, Z., Chen, X., Guo, J. and Ma, Y., 2009. Overexpression of the soybean GmERF3 gene, an AP2/ERF type transcription factor for increased tolerances to Salinity, drought, and diseases in transgenic tobacco. *Journal of experimental botany*, 60(13), pp.3781-3796.
108. Zhu, D., Hou, L., Xiao, P., Guo, Y., Deyholos, M.K. and Liu, X., 2019. VvWRKY30, a grape WRKY transcription factor, plays a positive regulatory role under salinity stress. *Plant Science*, 280, pp.132-142.
109. Qin, Y., Tian, Y. and Liu, X., 2015. A wheat salinity-induced WRKY transcription factor TaWRKY93 confers multiple abiotic stress tolerance in *Arabidopsis thaliana*. *Biochemical and biophysical research communications*, 464(2), pp.428-433.
110. Zhou, Q.Y., Tian, A.G., Zou, H.F., Xie, Z.M., Lei, G., Huang, J., Wang, C.M., Wang, H.W., Zhang, J.S. and Chen, S.Y., 2008. Soybean WRKY- type transcription factor genes, GmWRKY13, GmWRKY21, and GmWRKY54, confer differential tolerance to abiotic stresses in transgenic *Arabidopsis* plants. *Plant biotechnology journal*, 6(5), pp.486-503.
111. Wu, M., Liu, H., Han, G., Cai, R., Pan, F. and Xiang, Y., 2017. A moso bamboo WRKY gene PeWRKY83 confers salinity tolerance in transgenic *Arabidopsis* plants. *Scientific reports*, 7(1), pp.1-16.
112. Li, H., Gao, Y., Xu, H., Dai, Y., Deng, D. and Chen, J., 2013. ZmWRKY33, a WRKY maize transcription factor conferring enhanced Salinity stress tolerances in *Arabidopsis*. *Plant Growth Regulation*, 70(3), pp.207-216.
113. Ciftci-Yilmaz, S., Morsy, M.R., Song, L., Coutu, A., Krizek, B.A., Lewis, M.W., Warren, D., Cushman, J., Connolly, E.L. and Mittler, R., 2007. The EAR-motif of the Cys2/His2-type zinc finger protein Zat7 plays a key role in the defense response of *Arabidopsis* to salinity stress. *Journal of Biological Chemistry*, 282(12), pp.9260-9268.
114. Jain, D., Roy, N. and Chattopadhyay, D., 2009. CaZF, a plant transcription factor functions through and parallel to HOG and calcineurin pathways in *Saccharomyces cerevisiae* to provide osmotolerance. *PloS one*, 4(4), p.e5154.
115. Muthuramalingam, P., Jeyasri, R., Bharathi, R. K. A. S., Suba, V., Pandian, S. T. K., & Ramesh, M. (2020a). Global integrated omics expression analyses of abiotic stress signaling HSF transcription factor genes in *Oryza sativa* L.: An in silico approach. *Genomics*, 112(1), 908-918.
116. Karaba, A., Dixit, S., Greco, R., Aharoni, A., Trijatmiko, K.R., Marsch-Martinez, N., Krishnan, A., Nataraja, K.N., Udayakumar, M. and Pereira, A., 2007. Improvement of water use efficiency in rice by expression of HARDY, an *Arabidopsis* drought and salt tolerance gene. *Proceedings of the National Academy of Sciences*, 104(39), pp.15270-15275.