

Transcriptome profiling of Kentucky bluegrass (*Poa pratensis*) under salt stress

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Citation Report

#	ARTICLE	IF	CITATIONS
1	RNAseq analysis reveals pathways and candidate genes associated with salinity tolerance in a spaceflight-induced wheat mutant. <i>Scientific Reports</i> , 2017, 7, 2731.	3.3	63
2	Selection of Candidate Reference Genes for Gene Expression Analysis in Kentucky Bluegrass (<i>Poa</i>) Tj ETQq1 1 0.784314 rgBT /Overlo	3.6	47
3	Comparative transcriptomics with self-organizing map reveals cryptic photosynthetic differences between two accessions of North American Lake cress. <i>Scientific Reports</i> , 2018, 8, 3302.	3.3	19
4	Gene expression differs in codominant prairie grasses under drought. <i>Molecular Ecology Resources</i> , 2018, 18, 334-346.	4.8	6
6	Transcriptome analysis of salt-responsive genes and SSR marker exploration in <i>Carex rigescens</i> using RNA-seq. <i>Journal of Integrative Agriculture</i> , 2018, 17, 184-196.	3.5	8
7	Genomics Assisted Approaches for Improving Abiotic Stress Tolerance in Forage Grasses. <i>Sustainable Development and Biodiversity</i> , 2019, , 91-103.	1.7	0
8	Advances in Understanding the Physiological and Molecular Responses of Sugar Beet to Salt Stress. <i>Frontiers in Plant Science</i> , 2019, 10, 1431.	3.6	59
9	Biosynthesis and Signal Transduction of ABA, JA, and BRs in Response to Drought Stress of Kentucky Bluegrass. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1289.	4.1	59
10	Understanding salt tolerance mechanism using transcriptome profiling and de novo assembly of wild tomato <i>Solanum chilense</i> . <i>Scientific Reports</i> , 2020, 10, 15835.	3.3	35
11	Identification and Expression Analysis of the <i>SWEET</i> Gene Family from <i>Poa pratensis</i> Under Abiotic Stresses. <i>DNA and Cell Biology</i> , 2020, 39, 1606-1620.	1.9	16
12	Response to salt stress imposed on cultivars of three turfgrass species: <i>Poa pratensis</i> , <i>Lolium perenne</i> , and <i>Puccinellia distans</i> . <i>Crop Science</i> , 2020, 60, 1648-1659.	1.8	5
13	Biological mechanisms of cadmium accumulation in edible Amaranth (<i>Amaranthus mangostanus</i> L.) cultivars promoted by salinity: A transcriptome analysis. <i>Environmental Pollution</i> , 2020, 262, 114304.	7.5	20
14	Transcriptomic Profiling of Pomegranate Provides Insights into Salt Tolerance. <i>Agronomy</i> , 2020, 10, 44.	3.0	9
15	Antioxidant enzyme activity and microRNA are associated with growth of <i>Poa pratensis</i> callus under salt stress. <i>Plant Biotechnology Reports</i> , 2020, 14, 429-438.	1.5	9
16	Mechanisms of Environmental Stress Tolerance in Turfgrass. <i>Agronomy</i> , 2020, 10, 522.	3.0	29
17	Gene expression differences for drought stress response in three cool-season turfgrasses. <i>Itsrsj</i> , 0, , .	0.3	1
18	Transcriptome analysis of salt stress responsiveness in the seedlings of wild and cultivated <i>Ricinus communis</i> L. <i>Journal of Biotechnology</i> , 2021, 327, 106-116.	3.8	17
19	Transcriptomics and metabolomics reveal the induction of flavonoid biosynthesis pathway in the interaction of <i>Stylosanthes-Colletotrichum gloeosporioides</i> . <i>Genomics</i> , 2021, 113, 2702-2716.	2.9	23

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20	Nitrogen assimilation and gene regulation of two Kentucky bluegrass cultivars differing in response to nitrate supply. <i>Scientia Horticulturae</i> , 2021, 288, 110315.	3.6	7
21	The Full-Length Transcriptome of <i>Spartina alterniflora</i> Reveals the Complexity of High Salt Tolerance in Monocotyledonous Halophyte. <i>Plant and Cell Physiology</i> , 2020, 61, 882-896.	3.1	25
23	Transcriptomic characterization of candidate genes responsive to salt tolerance of <i>Miscanthus</i> energy crops. <i>GCB Bioenergy</i> , 2017, 9, 1222-1237.	5.6	13
24	Transcriptome analysis of creeping bentgrass exposed to drought stress and polyamine treatment. <i>PLoS ONE</i> , 2017, 12, e0175848.	2.5	22
25	Transcriptome and Metabolome Analyses Reveal Potential Salt Tolerance Mechanisms Contributing to Maintenance of Water Balance by the Halophytic Grass <i>Puccinellia nuttalliana</i> . <i>Frontiers in Plant Science</i> , 2021, 12, 760863.	3.6	11
26	Transcriptome Analysis Revealed a Positive Role of Ethephon on Chlorophyll Metabolism of <i>Zoysia japonica</i> under Cold Stress. <i>Plants</i> , 2022, 11, 442.	3.5	7
27	De novo assembly provides new insights into the evolution of <i>Elaeagnus angustifolia</i> L.. <i>Plant Methods</i> , 2022, 18, .	4.3	3
28	Transcriptome Analysis Reveals Molecular Mechanisms under Salt Stress in Leaves of Foxtail Millet (<i>Setaria italica</i> L.). <i>Plants</i> , 2022, 11, 1864.	3.5	6
29	Integrated metabolome, transcriptome analysis, and multi-flux full-length sequencing offer novel insights into the function of lignin biosynthesis as a <i>Sesuvium portulacastrum</i> response to salt stress. <i>International Journal of Biological Macromolecules</i> , 2023, 237, 124222.	7.5	4
30	Improving abiotic stress tolerance of forage grasses – prospects of using genome editing. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	7
31	Transcriptome Analysis of the Salt-Treated <i>Actinidia deliciosa</i> (A. Chev.) C. F. Liang and A. R. Ferguson Plantlets. <i>Current Issues in Molecular Biology</i> , 2023, 45, 3772-3786.	2.4	1
32	Mining of long non-coding RNAs with target genes in response to rust based on full-length transcriptome in Kentucky bluegrass. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	3
33	Transcriptomic profiling of <i>Poa pratensis</i> L. under treatment of various phytohormones. <i>Scientific Data</i> , 2024, 11, .	5.3	0