

**Table S1.** List of differentially expressed genes (DEGs) identified in *Betula spp.*, *Quercus spp.*, and *Populus spp.* under drought, PEG-mediated osmotic stress, and salt stress.

Process	DEG	Stress conditions	Species	Reference
<b>Drought stress</b>				
Iron homeostasis	ERF2	Drought stress, 120 h; 10 $\mu$ M Fe, 1 d	<i>Betula platyphylla</i> ; <i>Solanum lycopersicum</i>	[1,2]
Calcium signaling	ERF2	Drought stress, 120 h; Ca <sup>2+</sup> -deficient postharvested fruit	<i>B. platyphylla</i> ; <i>Malus domestica</i>	[2,3]
Chaperone activity	ERF2	Drought stress, 120 h; 20% PEG6000, 9 h	<i>B. platyphylla</i>	[2,4]
ROS-scavenging	ERF2	Drought stress, 120 h; 20% PEG6000, 9 h	<i>B. platyphylla</i>	[2,4]
Cell wall remodeling	ERF2	Drought stress, 120 h; 20% PEG6000, 9 h	<i>B. platyphylla</i>	[2,4]
Stomatal movement	HB7	Drought stress, 120h; 300 mM mannitol, drought stress, 21 d	<i>B. platyphylla</i> ; <i>A. thaliana</i>	[2,5]
Chaperone activity	MYB102	Drought stress, 120 h	<i>B. platyphylla</i>	[2]
ROS-scavenging	MYB102	Drought stress, 120 h	<i>B. platyphylla</i>	[2]
Pathogen response	PTI5	<i>Pseudomonas syringae</i> infiltration	<i>S. lycopersicum</i>	[6]
Pathogen response	PTI5	Drought stress, 120 h	<i>B. platyphylla</i>	[2]
Delay senescence	MYB102	200 mM NaCl treatment	<i>Arabidopsis thaliana</i>	[7]
Cell wall remodeling	WAT1	Drought stress, 124 d	<i>Quercus robur</i>	[8–11]
Root development	SPS4	Drought stress, 124d; Osmotic stress, mannitol -0.6 Mpa	<i>Q. robur</i> ; <i>A. thaliana</i>	[11,12]
Osmoprotection	SPS4	Drought stress, 124 d	<i>Q. robur</i>	[11]
Root growth suppression	DRIP1	Drought stress, 124 d	<i>Q. robur</i>	[11,13]
Negative regulation of putrescine biosynthesis	NAC72	Drought stress, 124 d; Drought stress, 120 h; ABA treatment; 150 mM NaCl, 36 h	<i>Q. robur</i> ; <i>B. platyphylla</i> ; <i>A. thaliana</i> ; <i>Populus spp.</i>	[5,11,14–16]
JA biosynthesis	LOX3.1 LOX3 LOX4	Drought stress, 124 d; Mechanical damage	<i>Quercus pubescens</i> ; <i>A. thaliana</i>	[11,17]
Pathogen response	AOS1	Drought stress, 124 d; <i>Rhizoctonia solani</i> infiltration	<i>Q. pubescens</i> ; <i>Oryza sativa</i>	[11,18]
Thermotolerance	HSFA4	Drought stress, 124 d; Heat stress 45°C, 1 h	<i>Q. pubescens</i> ; <i>Lilium longiflorum</i>	[11,19]
Pyruvate accumulation	HMG	Drought stress, 4 years	<i>Q. pubescens</i>	[20]
Stomatal movement	HMG	Drought stress, 3 weeks	<i>A. thaliana</i>	[21]
ROS-scavenging	FC	Drought stress, 4 years; Tetrapyrrole-mediated oxidative stress	<i>Q. pubescens</i> ; <i>Hordeum vulgare</i>	[20,22]
Root development	FC	Drought stress, 4 years; 400 mM NaCl, 12 h	<i>Q. pubescens</i> ; <i>A. thaliana</i>	[20,23]
Proline biosynthesis	FC	Drought stress, 4 years; 400 mM NaCl, 12 h	<i>Q. pubescens</i> ; <i>A. thaliana</i>	[20,23]
ROS-scavenging	UBP12	Drought stress, 13 d	<i>Nicotiana benthamiana</i>	[24]
Photosynthesis	UBP12	Drought stress, 13 d	<i>N. benthamiana</i>	[24]

Process	DEG	Stress conditions	Species	Reference
Stomatal movement	UBP12	Drought stress, 13 d	<i>N. benthamiana</i>	[24]
Thermotolerance	ClpB1	Drought stress, 17 and 24 d; Heat stress 42°C, 2 and 6 h	<i>Quercus ilex</i> ; <i>Nicotiana tobaccum</i>	[25]
Photosynthesis	ClpB1	Drought stress, 17 and 24 d; Heat stress 42°C, 2 and 6 h	<i>Q. ilex</i> ; <i>N. tobaccum</i>	[25]
ROS-scavenging	ClpB1	Drought stress, 17 and 24 d; Heat stress 42°C, 2 and 6 h	<i>Q. ilex</i> ; <i>N. tobaccum</i>	[25]
Thermotolerance	Hsp22	Drought stress, 17 and 24 d; Heat stress 43.5°C, 1 h	<i>Q. ilex</i> ; <i>A. thaliana</i>	[25,26]
Heat memory	FtsH6	Drought stress, 17 and 24 d; Heat stress 44°C, 1.5 h	<i>Q. ilex</i> ; <i>A. thaliana</i>	[25,27]
Epigenetic regulation	DRD1	Drought stress, 124 d	<i>Q. ilex</i> ; <i>A. thaliana</i>	[11,28]
DNA repair	CUL1	Drought stress, 124 d	<i>Q. ilex</i>	[11,29]
Stomatal movement	CUL1	Drought stress, 124 d	<i>Q. ilex</i>	[11,29]
ABA signaling	CUL1	Drought stress, 124 d	<i>Q. ilex</i>	[11,29]
ROS-scavenging	NADH3	Drought stress, 124 d; 150 mM NaCl, 200 mM mannitol	<i>Q. ilex</i> ; <i>A. thaliana</i>	[11,30]
Cell wall remodeling	CSLE6	Drought stress, 17 and 24 d; 250 mM NaCl, cold stress 3°C, 20% PEG6000	<i>Quercus ilex</i> ; <i>Elymus sibiricus</i>	[25,31]
Cell wall remodeling	ARAD1	Drought stress, 17 and 24 d; Mechanical damage	<i>Quercus ilex</i> ; <i>A. thaliana</i>	[25,32]
Growth and development	WAK1, WAK5	Drought stress, 17 and 24 d	<i>Quercus ilex</i>	[25,33]
Cell wall remodeling	ExPA1	Drought stress, 17 and 24 d; Drought stress, 15 d	<i>Quercus ilex</i> ; <i>Saccharum sp.</i>	[25,34]
Pathogen response	WAK1, WAK5	Drought stress, 17 and 24 d; <i>Erwinia amylovora</i> and <i>Pseudomonas syringae</i> infiltration	<i>Quercus ilex</i> ; <i>A. thaliana</i>	[25,35]
<b>PEG-mediated osmotic stress</b>				
Cell wall remodeling	ERF017	20% PEG6000, 9 h	<i>B. platyphylla</i>	[4,36]
Heavy metal response	ERF017	20% PEG6000, 9 h; 16 mg Pb/kg	<i>B. platyphylla</i> ; <i>Lycopersicon esculentum</i>	[4,37]
Growth and development	AGL61	20% PEG6000, 9 h	<i>B. platyphylla</i>	[4,38,39]
Negative regulator of stomatal movement	WRKY6	20% PEG6000, 9 h; 400 mM NaCl, 15% PEG6000, 36 h	<i>B. platyphylla</i> ; <i>A. thaliana</i>	[4,40]
Proline biosynthesis	HOX2	9% PEG6000, 25 d	<i>B. platyphylla</i>	[41,42]
Auxin signaling	ERF114	9% PEG6000, 25 d; Mechanical damage	<i>B. platyphylla</i> ; <i>A. thaliana</i>	[41,43]
Negative regulator of stomatal movement	WRKY29	9% PEG6000, 25 d; 30% PEG6000, 3d	<i>B. platyphylla</i> ; Apple rootstocks	[41,44]
ROS-scavenging	TGA5	9% PEG6000, 25 d; UV-B stress, 24 h	<i>B. platyphylla</i> ; <i>A. thaliana</i>	[41,45]
Negative regulator of stomatal movement	PP2C	6% PEG, 120 h; 0.4% NaCl, 12 d	<i>P. ussuriensis</i> ; <i>B. platyphylla</i>	[46,47]
Anthocyanin biosynthesis	NAC35	6% PEG, 120 h	<i>Populus ussuriensis</i>	[46,48]
Pathogen response	NAC35	6% PEG, 120 h; <i>Puccinia</i>	<i>P. ussuriensis</i> ;	[46,49]

Process	DEG	Stress conditions	Species	Reference
		<i>triticina</i> infiltarion	<i>Triticum sp.</i>	
Growth and development	ZAT11	6% PEG, 120 h	<i>P. ussuriensis</i>	[46,50]
Growth and development	WRKY33	6% PEG, 120 h; Pi-deficiency growth	<i>P. ussuriensis</i> ; <i>A. thaliana</i>	[46,51]
Iron homeostasis	WRKY33	6% PEG, 120 h; Pi-deficiency growth	<i>P. ussuriensis</i> ; <i>A. thaliana</i>	[46,51]
Iron homeostasis	MYB58	6% PEG, 120 h; Fe-deficiency growth	<i>P. ussuriensis</i> ; <i>A. thaliana</i>	[46]
Stomatal movement	HB7	6% PEG, 120 h; Drought stress 120, h; 300 mM mannitol, 24 h	<i>P. ussuriensis</i> ; <i>B. platyphylla</i> ; <i>A. thaliana</i>	[2,5,46]
Growth and development	HB7	6% PEG, 120 h	<i>P. ussuriensis</i>	[15,46]
Premature senescence	WRKY75	6% PEG, 120 h; ABA treatment	<i>P. ussuriensis</i> ; <i>A. thaliana</i>	[46,52]
<b>Salt stress</b>				
JA biosynthesis	ERF15	150 mM NaCl, 36 h; <i>Helicoverpa armigera</i> infiltration	<i>Populus simonii</i> × <i>Populus nigra</i> ; <i>S. lycopersicum</i>	[16,53–55]
Hormone response	GH3	150 mM NaCl, 36 h; ABA and MetJA treatment	<i>P. simonii</i> × <i>P. nigra</i> ; <i>Saccharum spontaneum</i>	[16,54,56]
Pathogen response	GH3	150 mM NaCl, 36 h; <i>Fusarium solani</i> var. <i>coeruleum</i> infiltration	<i>P. simonii</i> × <i>P. nigra</i> ; <i>N. benthamiana</i>	[16,54,56]
Chaperone activity	ERF76	150 mM NaCl, 36 h	<i>P. simonii</i> × <i>P. nigra</i>	[16]
Growth and development	ERF76	150 mM NaCl, 36 h	<i>P. simonii</i> × <i>P. nigra</i>	[16]
ROS-scavenging	ERF76	150 mM NaCl, 36 h	<i>P. simonii</i> × <i>P. nigra</i>	[16]
Antioxidant activity	ERF76	150 mM NaCl, 36 h	<i>P. simonii</i> × <i>P. nigra</i>	[16,57]
Proline biosynthesis	ERF76	150 mM NaCl, 36 h	<i>P. simonii</i> × <i>P. nigra</i>	[16,57]
Iron homeostasis	MYB308	150 mM NaCl, 36 h	<i>P. simonii</i> × <i>P. nigra</i>	[16,58]
Growth and development	NAC4	150 mM NaCl, 36 h	<i>P. simonii</i> × <i>P. nigra</i> ; <i>A. thaliana</i>	[16,59]
Premature senescence	NAC42	150 mM NaCl, 36 h	<i>P. simonii</i> × <i>P. nigra</i>	[16,60]
Lignin biosynthesis	NAC17	150 mM NaCl, 36 h; Drought stress	<i>P. simonii</i> × <i>P. nigra</i> ; <i>O. sativa</i>	[16,61]
Glutathione biosynthesis	NAC2	150 mM NaCl, 36 h; 200 mM NaCl	<i>P. simonii</i> × <i>P. nigra</i> ; <i>A. thaliana</i>	[16,62]
Proline biosynthesis	NAC2	200 mM NaCl; Drought stress, 21 d	<i>A. thaliana</i> ; <i>N. tabacum</i>	[62,63]
JA biosynthesis	WRKY30	200 mM NaCl, 12 h; <i>Magnaporthe grisea</i> infiltration	<i>Populus. davidiana</i> × <i>Populus bolleana</i> ; <i>O. sativa</i>	[18,64]
Cell wall remodeling	MYB4	200 mM NaCl, 12 h	<i>P. davidiana</i> × <i>P. bolleana</i>	[64,65]
Proline biosynthesis	MYB4	200 mM NaCl, 12 h; 200 mM NaCl, 48; 300 mM mannitol, 48 h	<i>P. davidiana</i> × <i>P. bolleana</i> ; <i>B. platyphylla</i>	[64,66]
Iron homeostasis	MYB4	200 mM NaCl, 12 h; Fe-	<i>P. davidiana</i> × <i>P.</i>	[64,67]

Process	DEG	Stress conditions	Species	Reference
		deficiency growth	<i>bolleana</i> ; <i>A. thaliana</i>	
Premature senescence	CRF6	200 mM NaCl, 48 h	<i>P. davidiana</i> × <i>P. bolleana</i>	[64,68]
ABA biosynthesis	bZIP4	200 mM NaCl, 48 h	<i>P. davidiana</i> × <i>P. bolleana</i>	[64,69,70]

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