

Table S1. Candidate genes involved in the salinity tolerance in quinoa

Genes	Varieties evaluated and annotations	Salt concentration	Reference
Salt Overly Sensitive 1 (CqSOS1a, CqSOS1b)	Sal variety 'Ollague', up-regulated in leaves but not in roots	300 mM NaCl	[173]
	Sea-level varieties 'PRJ', 'PRP', 'UDEC9', and 'B078'. In shoots strongly up-regulated than in roots	450 mM NaCl	[133]
	Valley variety 'Cica' and the salares varieties 'Ollague', and 'Chipaya'; up-regulated in leaves	450 mM NaCl	[174]
Na ⁺ /H ⁺ exchanger 1 (CqNHX1)	Sea-level varieties 'PRJ', 'PRP', 'UDEC9', and 'B078'; up-regulated in shoots and roots	450 mM NaCl	[133]
	'Valley variety 'Cica' and the salares varieties 'Ollague', and 'Chipaya'; up-regulation in leaves and shoots	300 mM NaCl	[174]
Betaine aldehyde dehydrogenase (BADH)	'Valley variety 'Cica' and the salares varieties 'Ollague', and 'Chipaya'; up-regulated in leaves	450 mM NaCl	[174]

<p><i>ABA-related:</i> 9-cis-epoxycarotenoid dioxygenase (NCED) ABA-binding factors (ABF3) Pyrabactin resistant (PYR, PYL) β-glucosidase homologues (BG1) Polyamine-related Arginine decarboxylase (ADC1, ADC2) Spermidine synthase (SPDS1) S-adenosylmethionine decarboxylase (SAMDC) Spermine synthase (SPMS) Diamine oxidase (DAO) Ion homeostasis-related CqSOS1a CqNHX K⁺ transporter (HKT)</p> <p><i>Growth:</i> Cyclin D3 (CycD3) B-Expansion (βEXP1) Stress-related genes Responsive to desiccation 22 (RD22) Pyrroline-5-carboxylate (P5CS) Transcription factors Dehydration-responsive element-binding protein 2A (DREB2a)</p>	<p>Salar variety 'R49' and sea-level variety 'Villarica'</p>	<p>300 mM NaCl 0 – 120 hours</p>	<p>[122]</p>
<p>CqSOS1a CqNHX K⁺ transporter (HKT)</p>	<p>Salar variety 'R49', early up-regulated of ion homeostasis genes and polyamine related genes</p>		
<p>Sea-level variety 'Villarica' highly expression on NCED, RD22, and DREB2a</p>	<p>Sea-level variety 'Villarica' highly expression on NCED, RD22, and DREB2a</p>		
<p>Pyrabactin resistant (PYR, PYL) Serine/threonine kinases (SnRK2)</p>	<p>Inbred quinoa accession 'Kd'. Two phylogenetically similar genes of PYR and two of SnRK2 were observed in quinoa</p>	<p>300 mM NaCl</p>	<p>[167]</p>

<p><i>Copy number of main genes in salinity conditions:</i></p> <p>9-cis-epoxycarotenoid dioxygenase (NCED), 11 genes</p> <p>Neoxanthin synthase (NSY), 7 genes ABA4, 2 genes</p> <p>Short-chain dehydrogenases/reductases (SDRs), 37 genes</p> <p>Pyrabactin resistant (PYL) family, 22 genes</p> <p>Na⁺/H⁺ exchanger, 11 genes</p> <p>ABC transports group (ABCGs), 81 genes</p> <p>Zeaxanthin epoxidase (ZEP), 2 genes</p> <p>Violaxanthin de-epoxidase (VDE), 2 genes</p> <p>Cell anion channels (SLAH), 6 genes</p> <p>Nitrate transporter (NRT), 12 genes</p> <p>Chloride channel protein (C1C), 10 genes</p> <p>Hemoglobin family (HB), 8 genes</p> <p>H⁺ ATPase (AHA), 20 genes</p> <p>Glucose transporter (GLUT), 68 genes</p>	<p>Salar variety 'Quinoa Real' (genome and mRNA sequencing)</p>	<p>100 mM NaCl</p>	<p>[151]</p>
	<p>Quinoa variety 5020 (mRNA sequencing in EBCs)</p>		
	<p>EBC is a photosynthetically inactive tissue and has a strong activity in ion transportation, cell wall and wax synthesis</p>		

<p><i>Transmembrane domains genes:</i> WAKL8 Wall-associated receptor kinase-like 8 (AUR62006689) (AUR62029668) At1g21890 WAT1-related protein At1g21890 (AUR62039756) At1g67300 Probable plastidic glucose transporter 2 (AUR62021463) CYP75B1 Flavonoid 3'-monooxygenase (AUR62007451) psbD Photosystem II D2 protein (AUR62039871) CER1: Protein ECERIFERUM (AUR62043781) (AUR62043583) AAP6 Amino acid permease 6 (AUR62034957) SULTR1;1 Sulfate transporter 1.1 (AUR62011984) SULTR3;4 Probable sulfate transporter 3.4 (AUR62021522) SULTR3;4 Probable sulfate transporter 3.4 (AUR62016440) CNGC7 Putative cyclic nucleotide-gated ion channel 7 (AUR62004478) DTX14 Protein DETOXIFICATION 14 (AUR62002768) TMK1 Receptor protein kinase 1 (AUR62041961)</p>	<p>14 quinoas (6 sea-level, 4 altiplano, 2 valley, and 2 salares varieties) 5 <i>C. berlandieri</i> and 2 <i>C. hircinum</i> accessions</p>	<p>300 mM NaCl</p>	<p>[118]</p>
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