

Table S1. Reports on some of the identified genomic regions linked with various agron-physiological, biochemical, root system architecture, and quality features in barley under salinity stress.

Characteristic	Marker	Reference	Characteristic	Marker	Reference
Days to heading	SSR/DArT	[72,80]	Root dry weight	SNP	[45,82]
Days to maturity	SSR/SNP	[72,80]	Seedling root dry weight	SNP	[45,82]
Relative water content	SSR	[72]	Salinity tolerance score	DArT	[73,86]
Chlorophyll content	SSR/SNP	[45,72]	Germination percentage	SSR/DArT/SNP	[64,66,74]
Plant height	SSR/DArT/SNP	[45,72,80,82]	Germination pace	SNP	[64]
Spike length	SSR/SNP	[72,83]	Seedling fresh weight	SSR/DArT/SNP	[45,64,85]
Biomass	SSR	[72]	Number of spike	SSR/DArT	[75,84]
Grain per spike	SSR/SNP	[72,83]	Number of spikelet	SNP	[83]
Thousand grain weight	SSR/DArT/SNP	[72,80,83]	Spike density	SNP	[83]
Grain yield	SSR/DArT/SNP	[72,79,84,82]	Number of tillers	DArT/SNP	[45,84]
Harvest index	SSR/DArT/SNP	[72,80,82]	O ₂ - mature zone	SNP/DArT	[78]
Biomass	SSR/ DArT/SNP	[72,79,80]	H ₂ O ₂ elongation zone	SNP/DArT	[78]
Na content	SSR/DArT/SNP	[45,72,84,82]	Leaf damage score	SNP/DArT	[87]
K content	SSR/DArT/SNP	[72,45,84,82]	Root and shoot Mg content	SNP	[45]
K/Na ratio	SSR/DArT/SNP	[45,72,84]	Root and shoot Ca content	SNP	[45]
Seedling leaf injury score	SNP	[85]	leaf temperature	SSR/DArT	[81]
Seedling shoot length	SNP	[64,77,85]	transpiration rate	SSR/DArT	[81]
Root length	SNP	[64,77,85]	leaf vapour pressure deficit	SSR/DArT	[81]
Number of leaves	SNP	[85]	stomatal conductance	SSR/DArT	[81]
Seedling shoot dry weight	SNP	[74,85]	intracellular CO ₂ concentration	SSR/DArT	[81]

Table S2. Reports on the identified genomic regions linked with various agronomic, physiological, biochemical, root system architecture, and quality features in barley under water deficit stress.

Characteristic	Marker	Reference	Characteristic	Marker	Reference
Germination pace	SNP	[113]	Fructose content	SNP	[114]
Germination percentage	SNP	[113]	Sucrose content	SNP	[114]
Shoot-to-root length ration	SNP	[108,113]	Raffinose content	SNP	[114]
Fresh weight	SNP	[113]	Maltose content	SNP	[114]
Reduction of germination pace	SNP	[113]	Ethylene content	SNP	[114]
Reduction of germination percentage	SNP	[113]	Superoxide dismutase activity	SNP	[114]
Reduction of root length	SNP	[113]	Catalase activity	SNP	[114]
Reduction of shoot length	SNP	[113]	Peroxidase activity	SNP	[114]
Reduction of fresh weight	SNP	[113]	γ -tocotrienol content	SNP	[114]
Root weight	SNP	[108]	α -tocotrienol content	SNP	[114]
Biomass	SNP	[108]	δ -tocopherol content	SNP	[114]
Number of main root	SNP	[108]	α -tocopherol content	SNP	[114]
Total root volume	SNP	[108]	β -carotene content	SNP	[114]
Total root length	SNP	[108]	Root features	SNP	[112,115]
Shoot length	SNP	[108]	Malting quality	SNP/DArT	[116]
Shoot dry weight	SNP	[108]	Days to heading	SNP/SSR/D ArT	[75,105,111,117, 118]
Free proline content	SNP	[110,114]	Grain filling period	SNP	[119]
Glucose content	SNP	[114]	Days to maturity	SNP	[105]
Grain protein	SNP	[117]	Intercellular CO_2 concentration	SNP/DArT	[104]
Polyphenol oxidase activity	SNP	[117]	Stomatal conductivity	SNP/DArT	[104]
Grain per spike	SNP	[118]	Quantum yield of CO_2 assimilation	SNP/DArT	[104]
Number of spikes	SNP	[106,118]	Water use efficiency	SNP/DArT	[104,109,114]
Thousand kernel weight	SNP/SSR	[105,111,118]	Water content	SNP/DArT	[33,104,114]
Performance index of energy trapped in PSII	SNP/DArT	[104]	Relative water content	SNP/DArT	[33,104,110,114]
Photochemical light energy quenching coefficient	SNP/DArT	[104]	Electrolyte leakage	SNP/DArT	[104,114]
Quantum yield of electron transport in PSII	SNP/DArT	[104]	Photosystem II efficiency	SNP	[33]
Fluxes in the energy absorbed by PSII antennae	SNP/DArT	[104]	Leaf greenness	SNP	[33]
Excited leaf cross section	SNP/DArT	[104]	Plant height	SNP/SSR	[120]
Excited leaf cross section	SNP/DArT	[104]	Peduncle length	SNP	[103]
Fluxes in the energy trapped in PSII reaction centers	SNP/DArT	[104]	Number of tillers	SNP	[33,107,110]
Fluxes in the energy used for electron transport	SNP/DArT	[104]	Biomass fresh	SNP	[33]
Fluxes in the energy dissipated from PSII	SNP/DArT	[104]	Biomass dry	SNP	[33,107,110,121]
The maximum number of active reaction centers	SNP/DArT	[104]	Harvest index	SNP	[103,106,110]
The overall PSII photochemical performance index for equal absorption	SNP/DArT	[104]	Kernal weight (KW) per spike	SNP	[103,106]
Transpiration rate	SNP/DArT	[104,110]	Spike length	SNP	[103]
Net photosynthesis rate	SNP/DArT	[104]	Grain yield	SNP/SSR/D ArT	[75,105,111,117, 120,121]

Table S3. List of studies that identified genomic regions linked with various agronomic, physiological, biochemical, root system architecture, and quality features in barley under low temperature stress.

Characteristic	Marker type	Temperature	References
Days to flowering	SNP	High	[144]
Chlorophyll content	SNP	High	[144]
Quantum yield of PS	SNP/ STS	Low	[145–147]
Electrolyte Leakage	SNP	Low	[145,148]
Biomass yield	SNP	High	[149]
Grain yield	SNP	High	[144,149]
Leaf water content	SNP	High	[144,149]
Quantum yield of PS	SNP	High	[149]
Straw biomass	SNP	High	[149]
leaf temperature	SNP	High	[149]
relative leaf water content	SNP	High	[149]
Glutathione	SNP	High	[149]
Starch	SNP	High	[144,149]
Succinate	SNP	High	[149]
Glycine	SNP	High	[149]
% α -Tocopherol	SNP	High	[149]
γ -Tocopherol	SNP	High	[149]
Stay-green	DArT	High	[126]
Proline content	SNP	High	[144]
Amino acids	SNP	High	[144]
Vernalization response	SNP/EST	Low	[142,143]
Final leaf number	SNP	Low	[150]
Flowering time	SNP	Low	[150]
Freezing tolerance test	SNP	Low	[143,144,150]

Table S4. List of reports that identified genomic regions linked with various agronomic, physiological, biochemical, root system architecture, and quality features in barley under waterlogging stress.

Characteristic	Marker type	References
Tolerance score	DArT/SNP	[78,173–176]
Root porosity	DArT	[173]
Aerenchyma formation	DArT/SNP	[173,177]
Root fresh and dry weights	DArT/SSR	[174]
Shoot fresh and dry weights	DArT/SSR	[174]
Number of tillers	DArT/SSR	[174,177]
Root length	DArT/SSR	[174]
Leaf chlorosis	DArT/SSR	[172]
Plant biomass	DArT/SSR/SNP	[172,176]
Plant survival	DArT/SSR	[172,178]
Plant healthiness	DArT/SSR/SNP	[172,178]
Plant height	DArT/SNP	[176,177]
Grain yield	DArT/SNP	[177]
Number of spikes	SNP	[176]
Number of grains	SNP	[176]
Grain weight	SNP	[176]
Chlorophyll content	SNP	[176]
Carotenoid content	SNP	[176]
ROS formation	SNP	[78]

Table S5. List of reports that identified genomic regions linked with various agronomic, physiological, biochemical, root system architecture, and quality features in barley under heavy metal stress.

Trait	Marker type	Metal	References
Cd in roots (solution)	SNP	Cd	[198]
Cd in shoots (solution)	SNP	Cd	[198]
Cd translocation (solution)	SNP	Cd	[198]
Cd in shoots (soil)	SNP	Cd	[198]
Leaf chlorosis	DArT/SSR	Mn	[199]
Plant height	DArT/SSR/AFLP	Mn	[199,200]
Plant survival	DArT/SSR	Mn	[199]
Chlorophyll content	DArT/SSR	Mn	[199]
Root tolerance index	EST	Al	[201]
Zn in grain	SNP	Zn	[202]
Cd in grain	SNP	Cd	[202]
Fe in grain	SNP	Fe	[202]
Spike length	SSR/AFLP	Mn	[200]
Awen length	SSR/AFLP	Mn	[200]
Chlorophyll content	GSB/SSR	Mn/Cd	[1]
Root length	GSB/SSR	Mn/Cd	[1]
Leaf POD	GSB/SSR	Mn/Cd	[1]
Root POD	GSB/SSR	Mn/Cd	[1]
Leaf APX	GSB/SSR	Mn/Cd	[1]
Plant height	GSB/SSR	Mn/Cd	[1]
Cd in root	GSB/SSR	Mn/Cd	[1]
Mn in root	GSB/SSR	Mn/Cd	[1]
Cd in shoot	GSB/SSR	Mn/Cd	[1,197]
Leaf chlorosis and necrosis	SNP/RNAseq	Cd	[197]