LANDI et al., 2019 - HSP70 Barley upon abiotic stresses

SUPPLEMENTARY FILES

Supplementary Table S1

Co-expression analysis of Arabidopsis HSP70S orthologous, obtained using the ATTED-II database. The first 15 co-expressed genes were selected for the table.

Co-expression degree was estimated as Mutual Rank, as described in [54].

At5g02500	**At5g02490**	**At3g09440**	**At3g12580**	**At1g16030**
DNAJ homologue 3	Heat shock protein 70	heat shock protein 81-2	heat shock protein 90.1	HSP20-like chaperones
heat shock protein 81-2	DNAJ homologue 2	PPPDE putative thiol peptidase	DNAJ heat shock family protein	BCL-2-associated athanogene 6
Heat shock protein 70	heat shock protein 81-2	DNAJ homologue 3	heat shock protein 101	HSP20-like chaperones superfamily protein
heat shock protein 60	heat shock protein 90.1	Heat shock protein 70	stress-inducible protein, putative	heat shock protein 17.4
DNAJ homologue 2	DNAJ homologue 3	DNAJ homologue 2	ATPase, AAA-type, CDC48 protein	heat shock protein 17.6A
ABC transporter family protein	mitochondrial HSO70 2	serine/threonine phosphatase 2A	HSP20-like chaperones	heat-shock protein 70T-2
Heat shock protein 70	Fes1A	heat shock cognate protein 70-1	multiprotein bridging factor 1C	17.6 kDa class II heat shock protein
S-adenosyl-L-homocysteine hydrolase	heat shock protein 70	mitochondrial HSO70 2	FKBP-type peptidyl-prolyl cis-trans isomerase	mitochondrial small heat shock protein 23.6
mitochondrial HSO70 2	PPPDE putative thiol peptidase	rotamase FKBP 1	Fes1A	HSP20-like chaperones
Aha1 domain-containing protein	Aha1 domain-containing protein	Chaperone DnaJ-domain	SERINE-ARGININE PROTEIN 30	heat shock protein 21
MIF4G domain-containing protein	heat shock cognate protein 70-1	stress-inducible protein, putative	PPPDE putative thiol peptidase family protein	At3g07150
Ribosomal protein S5	pyridoxine biosynthesis 1.2	DNAJ heat shock family protein	heat shock transcription factor A2	P-loop nucleoside triphosphate hydrolases
DEAD box RNA helicase (PRH75)	DNAJ heat shock	Fes1A	RNA-binding (RRM/RBD/RNP motifs)	heat shock protein 101
HSP20-like chaperones	Argonaute family protein	heat shock protein 70	TIN1	HSP20-like chaperones superfamily protein
pyridoxine biosynthesis 1.2	non-ATPase subunit 9	Aha1 domain-containing protein	Cytochrome bd ubiquinol oxidase	Chaperone DnaJ-domain superfamily protein
At4g24280	**At5g49910**	**At2g32120**	**At4g37910**	**At5g09590**
chaperonin-60alpha	TCP-1/cpn60 chaperonin	heat shock protein 101	heat shock protein 60-2	rotamase FKBP 1
TCP-1/cpn60 chaperonin	At2g43630	HSP20-like chaperones	nucleoside triphosphate hydrolases	ankyrin repeat family protein
Chaperone protein htpG	DNAJ heat shock	HSP20-like chaperones	hydroxyproline-rich glycoprotein	heat shock protein 81-2
chaperonin 60 beta	chaperonin-60alpha	heat shock protein 70B	elongation factor family protein	HEAT SHOCK PROTEIN 89.1
translocon at membrane of chloroplasts 11	chloroplast heat shock protein 70-1	gravitropism-deficient-yellow-green-like 3	lon protease 1	heat shock protein 60
chloroplast heat shock protein 70-2	Chaperone protein htpG	HSP20-like chaperones	Haloacid dehalogenase-like hydrolase (HAD)	HSP20-like chaperones superfamily protein
RNI-like superfamily protein	heat shock protein 81-2	heat shock protein 17.6A	GTP binding Elongation factor	Heat shock protein 70 (Hsp 70) family protein
FTSH protease 12	glycyl-tRNA synthetase	stress-inducible protein, putative	heat shock protein 60	casein lytic proteinase B4

Class II aaRS and biotin synthetases	Heat shock protein 70	heat shock protein 17.4	lysyl-tRNA synthetase 1	stress-inducible protein, putative
Octicosapeptide/Phox/Bem1p (PB1)	SWIB/MDM2 domain;Plus-3;GYF	At4g23493	Ribosome recycling factor	DNAJ homologue 3
RNA-binding CRS1 / YhbY	rotamase FKBP 1	mitochondrial small heat shock protein 23.6	Glutathione S-transferase	Phosphoglycerate mutase
plastid transcriptionally active 12	arogenate dehydratase 1	17.6 kDa class II heat shock protein	prohibitin 2	DNAJ homologue 2
presequence protease 1	zinc finger (Ran-binding)	HSP20-like chaperones	translocon at outer membrane of chloroplasts 6	Glutathione S-transferase family protein
glycine-tRNA ligases	plastidial pyruvate kinase 3	galactinol synthase 1	voltage dependent anion channel 3	RNA-binding (RRM/RBD/RNP motifs)
elongation factor Ts family protein	aspartate kinase-homoserine dehydrogenase ii	heat shock protein 70	heat shock protein 60-3°	SGS domain-containing protein
At1g09080	**At1g11660**	**At4g16660**	**At1g56410**	
DNAJ heat shock N-terminal	Chaperone protein htpG	Chaperone protein htpG family protein	At4g07720	
Preprotein translocase Sec	DNAJ heat shock family protein	DNAJ heat shock family protein	At4g16090	
cysteine-rich RLK	glutamine-fructose-6-phosphate transaminasi	glutamine-fructose-6-phosphate transaminase	UDP-Glycosyltransferase superfamily	
UDP-Glycosyltransferase	calnexin 1	calnexin 1	Cysteine proteinases superfamily protein	
endoplasmic reticulum oxidoreductins 1	PDI-like 1-2	PDI-like 1-2	F-box domains protein	
TIN1	Vps51/Vps67	At4g29520	At5g38400	
RECEPTOR-like protein kinase n36	Coatomer, beta' subunit	Coatomer, beta' subunit	zinc ion binding;nucleic acid binding	
receptor like protein 41	calreticulin 1°	calreticulin 1a	transposable element gene	
nucleoside triphosphate hydrolases	calreticulin 1b	calreticulin 1b	transposable element gene	
wall associated kinase 3	DnaJ / Sec63 Brl domains-containing protein	DnaJ / Sec63 Brl domains-containing protein	transposable element gene	
UDP-galactose transporter 1	PDI-like 1-1	PDI-like 1-1	glycine-rich protein	
receptor like protein 23	UDP-galactose transporter 3	UDP-galactose transporter 3	At3g50250	
2-oxoglutarate (2OG) oxygenase	stromal cell-derived factor 2-like precursor	stromal cell-derived factor 2-like protein precursor	Galactose oxidase/kelch repeat superfamily protein	
PDI-like 1-2	PDI-like 2-2	PDI-like 2-2	At2g11010	
cysteine-rich RLK 37	UDP-galactose transporter 1	UDP-galactose transporter 1	Plant EC metallothionein-like protein, family 15	

[54] Aoki Y.; Okamura Y.;, Tadaka S.; Kinoshita K.; Obayashi T. ATTED-II in 2016: A plant co-expression database towards lineage-specific co-expression. *Plant Cell Physiol* **2016** *57*, e5(1–9). doi: 10.1093/pcp/pcv165

Supplementary Table S2 – Expression rate of selected loci MLOC_67581 and MLOC_50972 measured by qRT-PCR analysis in barley Batinì and Icarda 20 vs Barley Nure under control conditions. The expression rate in barley Nure has been arbitrarily assigned as 1, and expression ratios with respect to other varieties calculated accordingly.

LOCUS	**Name**	**Nure (reference)**	**Batinì (fold-change)**	**Icarda 20 (fold-change)**
MLOC_67581	HSP70 Cyt	1	**3.43**	**7.66**
MLOC_50972	HSP70 Mito	1	**1.26**	**0.56**

Supplementary Table S3 – List of selected genotypes of barley (*Hordeum vulgare*) utilized in this study.

Barley variety	**Crossing**	**Variety**	**Production**	**Landrace/genotype from**
Nure	(FIOR+40+x+ALPHA2+) x BARAKA	Two-Row	Seeds + Forage	Italy
Aiace	FO+1078+x+FO+1638	Two-Row	Seeds + Forage	Italy
Cometa	PO202.169x+F2FO3356 (Amillis x+Fior2377)	Two-Row	Forage	Italy
Batinì	Traditional landrace	Six-Row	Seeds	Oman
Suihili	Traditional landrace	Six-Row	Seeds + Forage	Tunisia
Medenine	Traditional landrace	Six-Row	Seeds + Forage	ICARDA/Tunisia
Icarda20	Improved	Six-Row	Seeds + Forage	ICARDA

Supplementary Table S4 – List of primers used for qRT-PCR analysis.

For/Rev	Sequences	Description
Forward	CTCCATGATGGCCAAGTGTGA	Alfa-tub
Reverse	ATGTCGCTTGGTCTTGATGGT	
Forward	CCTTGGTTGCTCCTCCAGTA	MLOC_67581
Reverse	TGCTGAAAAACACTCGCAGC	
Forward	AGCAGCATCAGCCGTGATAA	MLOC_50972
Reverse	TCTGCAAAGGTTGCGTGAAG	
Forward	CTACCAGCAGCAGGGATCTG	MLOC_55086
Reverse	CACCATCGCCTGTCTTCTCA	
Forward	TAAGGCTTGCCCTCCTTGTT	MLOC_55999
Reverse	ACGTCAAGCGTCTCATTGGA	
Forward	CCTCAGCTGCAAACTGCTTC	MLOC_53941
Reverse	CTGTGGCCATTCAAGGTTGT	