

Supplementary Information

Table S1. Crops with reduced genetic diversity proven by whole genome sequencing studies.

Crop	Materials	Methods	Genetic diversity indicators	Values	Reference
Barley	Barley cultivar (cv.) Morex (as <i>de novo</i> reference) 4 Barley cultivars (“Bowman”, “Barke, Igri” and “Haruna Nijo”) 1 <i>Hordeum vulgare</i> ssp. <i>spontaneum</i> (wild progenitor of cultivated barley)	Mapping sequence reads of 4 barley cultivars and <i>H. spontaneum</i> accession to the Morex reference genome to identify single nucleotide variation (SNV)	Single nucleotide variation compared with the reference	Bowman: 3,112,520 Barke: 3,651,330 Haruna Nijao: 948,722 Igri: 3,257,946 <i>H. spontaneum</i> : 6,191,10	[19]
Maize	35 improved maize lines 23 traditional landraces 17 wild relatives (14 <i>parviglumis</i> ; 2 <i>Zea mays</i> ssp. <i>Mexicana</i> , 1 <i>Tripsacum dactyloides</i> var. <i>meridionale</i>)	Mapping of re-sequencing read to the maize reference genome (release 4a.53)	LOWESS curves of nucleotide diversity (π)		[42]
Rice	40 cultivated rice accessions (<i>Oryza sativa</i>) 10 wild progenitors (<i>Oryza rufipogon</i> and <i>Oryza nivara</i>)	Mapping of re-sequencing reads to IRGSP v4 rice genome	π per kb θ_w per kb	Cultivated rice: 5.4 Wilde rice: 7.7 Cultivated rice: 6.6 Wilde rice: 11.5	[41]
Soybean	17 wild soybeans 14 cultivated soybeans	Mapping re-sequencing reads of the 31 accessions to the Williams 82 reference genome	Whole genome θ_π values	Cultivated: 1.89×10^{-3} Wild: 2.97×10^{-3}	[40]

Table S2. Recent genome-wide identification of gene families.

Species	Gene family	No. of gene	Search strategy	Tools/databases	Reference
Viridiplantae	Annexin Superfamily	149 *	Keyword	SUPERFAMILY database; Plaza database; Phytozome database	[238]
<i>Cucumis sativus</i>	NBS-encoding genes	57	Pattern	TBLASTN; BLASTN; FGENESH; GENSCAN	[239]
	ERF	103	Pattern	TBLASTN; Pfam; SMART	[240]
	R2R3MYB family	55	Pattern	BLASTP; Pfam; SMART	[241]
	WRKY	55	Pattern	BLASTP; HMMER; Pfam	[242]
<i>Glycine max</i>	NB-LRR	319	Pfam ID		[243]
	MYB	244	Pattern	BLASTN; BLASTP; SMART;	[244]
	NAC	152	Other	SoyDB; PlantTFDB; TMHMM	[245]
	trihelix-GT	63	Pattern	BLASTP; SMART; MEME; TBLASTN	[246]
	bHLH	45	Pattern	BLASTP; SMART; MEME; TBLASTN	[246]
	NAC	31	Pattern	TBLASTN	[247]
	WRKY	58	Pattern	BLAST	[248]
<i>Malus domestica</i>	Dehydrin	12	Pattern	Pfam; HMMER	[249]
	DREB	68	Pattern	BLASTP; Pfam; SMART	[250]
<i>Oryza sativa</i>	HD-Zip	30	Pattern	BLAST; GENSCAN	[251]
	C2H2 zinc finger	189	Keyword and Pattern	HMMER; PROSITE; INTERPRO	[252]
	HAK Potassium transporter gene	26	Pattern	BLAST; GENSCAN; GenomeScan; FGENESH; GeneMark.hmm; GrailEXP	[253]
	SOT family	35	Pattern	BLAST; SMART; Pfam	[254]
	BURP domain-containing genes	17	Pattern	BLAST; Pfam; SMART	[255]
	FKBP	29	Keyword and Pattern	TBLASTN	[256]
	Ankyrin repeat containing proteins	158	Pattern	BLASTP; TBLASTN; Pfam; hmmer	[257]
<i>Oryza sativa</i>	Homeobox	107	Pattern	Pfam; SMART; TIGR; BLAST	[258]
	Ribosome-inactivating proteins	31	Keyword and Pattern	TBLASTN; BLASTP; Pfam	[259]
	NAC	151	Keyword and Pattern	BLASTP; TBLASTN; Pfam; SMART	[260]
	Thioredoxin gene	61	Other	HomoloGene	[261]
	Hsp20	39	Pattern	Pfam; BlastP; SMART	[262]
	AP2/EREBP	163	Keyword and Pattern	BLASTP; TBLASTN; SMART; Pfam	[87]
	Receptor-like cytoplasmic kinase	379	Pattern	HMMER; SMART; InterProScan; TMMH2; KOME	[263]
	CCCH-type zinc finger	67	Pattern	SMART; Pfam; BLASTP; TBLASTN	[264]
	Amino acid transporter	85	Keyword and Pattern	BLASTP; Pfam; InterProScan	[265]

Table S2. Cont.

Species	Gene family	No. of gene	Search strategy	Tools/databases	Reference
<i>Solanaceae sp.</i>	Aux/IAA gene	26 + 27	Keyword and Pattern	TBLASTN; DNASTAR; FGENSESH	[266]
<i>Solanum lycopersicum</i>	Dicer-like	7	Pattern	Pfam; HMMER; BLAST	[267]
	Argonaute	15	Pattern	Pfam; HMMER; BLAST	[267]
	RNA-dependent RNA polymerase	6	Pattern	Pfam; HMMER; BLAST	[267]
	WRKY	81	Pattern	Pfam; HMMER; SMART	[268]
	MAP Kinase	16	Pattern	SOL Genomics Network; tomato plant GDB database	[269]
<i>Sorghum vulgare</i>	BURP domain-containing genes	11	Pattern	Pfam; SMART: BLASTP	[270]
<i>Vitis vinifera</i>	Stilbene synthase multigenic family	48	Pattern	BLAST; GAZE; JIGSAW; Genoscope	[271]
	AP2/ERF	132	Pattern	BLASTP; PSI-BLAST	[272]
<i>Zea mays</i>	NBS-encoding gene	109	Pattern	Pfam; DNATOOLS; SMART	[273]
	BURP domain-containing genes	15	Pattern	Pfam; SMART: BLASTP	[270]
	beta-glucosidase	26	Pattern	BLAST	[274]
	Heat shock transcription factor	25	Pattern	BLASTP; Pfam; SMART	[275]
	CCCH-type zinc finger	68	Pattern	BLASTP; DNATOOLS software; Pfam; SMART	[276]
	immunophilin FKBP	30	Keyword and Pattern	BLASTP; Pfam	[277]
	WRKY	119	Pattern	BLASTP	[278]
	HAK potassium transporter gene	27	Pattern	BLASTP	[279]
	Galactinol synthase	53	Pattern	MaizeGDB; Maize Sequence Search; Pfam	[280]
	RS and stachyose synthase	10	Pattern	MaizeGDB; Maize Sequence Search; Pfam	[280]
alpha-galactosidase	5	Pattern	MaizeGDB; Maize Sequence Search; Pfam	[280]	
beta-fructofuranosidase	11	Pattern	MaizeGDB; Maize Sequence Search; Pfam	[280]	

* Total number of genes identified from multiple Viridiplantae species.

Table S3. Proteomics studies related to crop stresses reported in 2012.

Species	Stress	Analysis methods	Reference
Barley	Drought	2D DIGE + MALDI-TOF MS	[281]
	Salt	2D PAGE + MALDI-TOF-TOF MS	[282]
Canola	<i>Pseudomonas putida</i> + Salt	2D DIGE + Q-TOF, LC-MS/MS	[283]
Carrot	<i>Mycocentrospora acerina</i>	2D PAGE + MALDI-TOF-TOF MS	[284]
Cotton	Drought	2D PAGE + MALDI-TOF-TOF MS	[285]
	Low temperature	2D PAGE + MALDI-TOF MS, MALDI-TOF-TOF MS	[286]
	Nitrogen stress	2D PAGE + MALDI-TOF MS, MALDI-TOF-TOF MS	[287]
Cucumber	Hypoxic stress	2D PAGE + MALDI-TOF MS, MALDI-TOF-TOF MS	[288]
Grapevine	Downy mildew	Eight-plex + LC-MS/MS	[289]
	GA3	2D PAGE + MALDI-TOF MS, MALDI-TOF-TOF MS	[290]
Kiwifruit	Ozone	SDS PAGE + LC-MS/MS	[291]
Maize	Desiccation	2D PAGE + MALDI-TOF-TOF MS	[292]
	Drought	iTRAQ + LC-MALDI	[293]
	Low light	SDS PAGE (ProQ Diamond staining for phosphoprotein or Western blot with antibody against phosphothreonine) LC-MS/MS, thylakoid proteins	[294]
Mungbean	Cd-induced oxidative stress	2D PAGE + LC-MS/MS	[295]
Papaya	Papaya meleira virus	SDS PAGE + LC-MS/MS	[296]
Rapeseed	Drought	2D PAGE + LTQ XL Orbitrap MS/MS	[297]
	Methyl Jasmonate	eight-plex + QSTAR, LC-TOF/TOF, LC-TripleTOF	[298]

Table S3. Cont.

Species	Stress	Analysis methods	Reference
Rice	Cold	2D PAGE (ProQ diamond staining for phosphoprotein) + MALDI-TOF-TOF MS	[299]
	Drought	2D PAGE + MALDI-TOF MS	[300]
	Drought	2D PAGE + LTQ-XL Orbitrap MS	[301]
	<i>Magnaporthe oryza</i>	2D PAGE + MALDI-TOF MS	[302]
	<i>Magnaporthe oryza</i>	2D PAGE + MALDI-MS/MS	[303]
	Nitrogen stress	2D PAGE + MALDI-TOF MS	[304]
	Ozone	2D PAGE + LTQ XL Orbitrap MS	[305]
	Selenium	2D PAGE + MALDI-TOF-TOF MS	[306]
	<i>Xanthomonas campestris pv. Oryicola</i>	2D PAGE + MALDI-TOF-MS	[307]
Sorghum	Salt	2D PAGE + MALDI-TOF-TOF MS	[308]
Soybean	Cadmium stress	Microsomal proteins 2D PAGE + LTQ XL Orbitrap MS	[125]
	Cadmium stress	2D PAGE + LTQ XL Orbitrap MS	[309]
	Drought	2D PAGE + LTQ XL Orbitrap MS	[310]
	Flooding	2D PAGE + MALDI-TOF MS, LTQ XL Orbitrap MS	[311]
	Flooding	Proteolysis proteomics 2D PAGE + LTQ XL Orbitrap MS	[312]
	Flooding + <i>Bradyrhizobium japonicum</i>	2D PAGE + MALDI TOF MS/NanoLC MS/MS	[313]
	High temperature and humidity	2D PAGE + MALDI-TOF	[314]
	Ozone	Thio-labeling for redox proteome 2D + LC-MS/MS	[127]

Table S3. Cont.

Species	Stress	Analysis methods	Reference
Soybean	<i>Phakopora pachyrhizi</i>	2D PAGE + MALDI-TOF/TO	[315]
	Salt	2D PAGE + MALDI-TOF-TOF MS	[316]
	Flooding	2D PAGE + LTQ XL Orbitrap MS	[317]
	Flooding	Total protein or enriched phosphoprotein LTQ XL Orbitrap	[318]
	Flooding or low oxygen	2D PAGE + MALDI TOF MS/NanoLC MS/MS	[319]
Strawberry	Cold	2D PAGE + LC-MS/MS	[320]
	<i>Colletorichum fragariae</i>	2D PAGE + MALDI-TOF-TOF MS/MS	[321]
Sugarcane	Osmotic stress	2D PAGE + MALDI-TOF-MS	[322]
Tomato	<i>Botrytis cinerea</i>	2D PAGE + LC-MS/MS	[323]
Wheat	Drought	2D PAGE + MALDI-TOF MS, MALDI-TOF-TOF MS	[324]
	Drought	2D PAGE + MALDI TOF/TOF MS	[325]
	Frost	2D PAGE + MALDI-TOF MS, MALDI-TOF-TOF MS	[326]
	<i>Fusarium graminearum</i>	2D PAGE + LC-LTQ-Qrbitrap	[327]
	<i>Fusarium verticillioides</i>	SDS PAGE + LC-MS/MS	[328]
	Salt	2D PAGE + LTQ-FTICR-MS Chloroplastic proteins	[124]
	Salt	2D PAGE + MALDI TOF/TOF MS	[329]