

Global analysis of gene expression in maize leaves treated with low temperature. II. Combined effect of severe cold (8 °C) and circadian rhythm. Plant Molecular Biology. Jończyk M., Sobkowiak A., Trzcinska-Danielewicz J., Skoneczny M., Solecka D., Fronk J., Sowiński P. Faculty of Biology, University of Warsaw, pawes@biol.uw.edu.pl

Tab. S2 Microarray data used for meta-analysis

inbred line	growth stage ^a / age (days)	stress conditions / sampling time (dpi ^b)	microarray database accession ^c	reference ^c
Severe cold				
B73	7	10 °C, 16 h, light 10 °C, 8 h, dark	MOAP ^d , 1.3, 57k. GPL1992 i GPL1993 (GEO)	Fernandes et al. (2008) GSE9453 (GEO)
CM109	V3	8 °C, 4 h, light 6 °C, 10 h, dark	MOAP, 1, 46k, A-MEXP-2054 (AE)	This work
CM109	V3	6 °C, 10 h, dark 8 °C, 3.5 h, light	MOAP, 1, 46k, A-MEXP-2054 (AE)	This work
CM109	V3	6 °C, 10 h, dark 8 °C, 7 h, light	MOAP, 1, 46k, A-MEXP-2054 (AE)	This work
CM109	V3	6 °C, 10 h, dark 8 °C, 10.5 h, light	MOAP, 1, 46k, A-MEXP-2054 (AE)	This work
CM109	V3	6 °C, 10 h, dark 8 °C, 14 h, light	MOAP, 1, 46k, A-MEXP-2054 (AE)	This work
ETH-DL	V3	6 °C, 10 h, dark 8 °C, 4 h, light	MOAP, 1, 46k, A-MEXP-2054 (AE)	Sobkowiak et al. (2014) E-MTAB-1315
Moderate chilling				
CM109	V3	14 °C 14 h, light 12 °C 10 h, dark 14 °C 4 h, light	MOAP, 1.13, 57k, A-MEXP-1419 A-MEXP-1427	Trzcińska-Danielewicz et al. (2009), E-MEXP-1865
CM109	V3	14 °C 10 h, dark 14 °C 4 h, light	MOAP, 1, 46k, A-MEXP-2054	Jończyk, unpublished data
S160, S50676	V3	12 °C 10 h, dark 14 °C 14 h, light 12 °C 10 h, dark 14 °C 4 h, light	MOAP, 1, 46k, A-MEXP-2054	Sobkowiak et al. (2016) E-MTAB-1315
Fungal infection				
Early Golden Bantam	8-10	1, 2, 4	Affymetrix GeneChip Maize Genome Array, GPL4032	Doehlemann et al. (2008), GSE10023
Nathan	14	1.5, 4	Affymetrix GeneChip Maize Genome Array, GPL4032	Voll et al. (2011), GSE31188

W23	8	1, 3	Agilent/WalbotLab Zea mays + Ustilago maydis (dual organism) 4×44K array, GPL9997	Skibbe et al. (2010), GSE20130
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^a Growth stages according to Elmore and Abendroth (2011).

^b Days post infection.

^c Identifiers from Gene Expression Omnibus (GEO, www.ncbi.nlm.nih.gov/geo/) or ArrayExpress (AE, www.ebi.ac.uk/arrayexpress/) database.

^d Maize Oligonucleotide Array Project (www.maizearray.org/).

Data normalization

Severe cold and moderate chilling

Data was normalized in limma R package (Smyth 2004). For within-array normalization print-tip loess method was used (Cleveland et al. 1991; Smyth and Speed 2003), for between-array normalization Aquantile method. After normalization, control probes were removed. Fluorescence value (log2 fluorescence) for each gene and variant was standardized by subtracting median value computed for all data for this gene and dividing by corresponding standard deviation.

Fungal infection

Agilent data was normalized as for low temperature, except within-array normalization. Since Agilent arrays are not divided in blocks global loess instead of print-tip loess normalization was performed. Affymetrix data (raw CEL files) was quality-controlled, normalized and summarized by GCRMA method (GeneChip Robust Multiarray Analysis, Wu et al. 2004) using affy (Irizarry et al. 2003) and simpleaffy (Wilson and Miller 2005) R packages.

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