

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. S1 Maize inbred lines used in annotation of microarray probes

Inbred line	Reference
B73	Schnable et al. (2009)
W22	Lai et al. (2004)
Han21	Jia et al. (2006)
Various	Alexandrov et al. (2008)
Mo17	Rokhsar et al. (2009)
B73	Soderlund et al. (2009)
<i>Palomero Toluqueño</i>	Vielle-Calzada et al. (2009)
Zheng58, 5003, 478, 178, Chang7-2, Mo17	Lai et al. (2010)

Probe sequences were aligned to cDNA sequences from ten maize inbred lines (Tab. S1) using BLAST (Altschul et al. 1990). Only matches with perfect alignment of ≥ 20 bp were retained. For each microarray probe the best cDNA match was chosen according to e-value and percent identity. When more than one best hit was found (i.e., to different cDNAs), one nearest to the 3' end was chosen as less susceptible to degradation (MAQC Consortium 2006). Alignments to cDNA from the best annotated B73 and Mo17 inbred lines were preferred. Our procedure allowed many-to-one probe-cDNA alignments. We annotated successfully 80% (34,548 out of 43,405) unique probes.

Alexandrov NN, Brover VV, Freidin S, Troukhan ME, Tatarinova TV, Zhang H, Swaller TJ, Lu Y-P, Bouck J, Flavell RB, Feldmann KA (2009) Insights into corn genes derived from large-scale cDNA sequencing. *Plant Mol Biol* 69:179–194

Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ (1990) Basic local alignment search tool. *J Mol Biol* 215:403–410.

Jia J, Fu J, Zheng J, Zhou X, Huai J, Wang J, Wang M, Zhang Y, Chen X, Zhang J, Zhao J, Su Z, Lv Y, Wang G (2006) Annotation and expression profile analysis of 2073 full-length cDNAs from stress-induced maize (*Zea mays* L.) seedlings. *Plant J* 48:710–727

Lai J, Dey N, Kim C-S, Bharti AK, Rudd S, Mayer KFX, Larkins BA, Becraft P, Messing J (2004) Characterization of the maize endosperm transcriptome and its comparison to the rice genome. *Genome Res* 14:1932–1937

Lai J, Li R, Xu X, Jin W, Xu M, Zhao H, Xiang Z, Song W, Ying K, Zhang M, undefined others (2010) Genome-wide patterns of genetic variation among elite maize inbred lines. *Nat Genet* 42:1027–1030

MAQC Consortium (2006) The MicroArray Quality Control (MAQC) project shows inter- and intraplatform reproducibility of gene expression measurements. *Nat Biotechnol* 24:1151–1161.

Rokhsar D, Chapman J, Mitros T, Goodstein D (2009) Update on the Mo17 genome sequencing project. In: *Maize Genetics Conference Abstracts*. 51:T13, <http://maizegdb.org/cgi-bin/displayrefrecord.cgi?id=1232822>

Schnable PS, Ware D, Fulton RS et al (2009) The B73 maize genome: complexity, diversity, and dynamics. *Science* 326:1112–1115

Soderlund C, Descour A, Kudrna D, Bomhoff M, Boyd L, Currie J, Angelova A, Collura K, Wissotski M, Ashley E, Morrow D, Fernandes J, Walbot V, Yu Y (2009) Sequencing, mapping, and analysis of 27,455 maize full-length cDNAs. *PLoS Genet* 5:e1000740

Vielle-Calzada J-P, Martinez de la Vega O, Hernandez-Guzman G, Ibarra-Laclette E, Alvarez-Mejia C, Vega-Arreguin JC, Jimenez-Moraila B, Fernandez-Cortes A, Corona-Armenta G, Herrera-Estrella L, Herrera-Estrella A (2009) The Palomero genome suggests metal effects on domestication. *Science* 326:1078–1078