

# Meta-analysis of heat-stressed transcriptomes using public gene expression database for human, mouse and rice

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## Background

Heat stress is an environmental stress characterized by exposure to abnormally high temperatures. Previous research has focused on response systems involving heat shock factors (HSFs) and heat shock proteins (HSPs). However, further studies of genes that have yet to be well-focused on previous research are necessary to understand how organisms respond to heat stress. Additionally, a comprehensive analysis that includes these genes is required. In this study, novel heat stress response genes were discovered through meta-analysis of numerous gene expression data from humans and mice (doi: 10.3390/ijms241713444). In addition, rice exposed to heat stress was compared with human and mouse results to analyze common functional genes.

## - Flowchart of the meta-analysis -

