

Whole genome analysis of variety and expression of heat-shock protein encoding genes during desiccation stress in an anhydrobiotic midge *Polypedium vanderplanki*

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Heat shock proteins (HSP) are diverse group of molecular chaperones that involved in many normal cellular processes and response to stress conditions including desiccation stress. HSP are classified into families based on their molecular weight: small HSP, HSP40, HSP60, HSP70, HSP90, HSP100.

Recently we showed that at least several HSP are deeply involved in the anhydrobiosis in the sleeping chironomid. Here, we expand the analysis of expression of genes encoding HSP in different stages of desiccation stress using mRNA sequencing techniques using whole genome information. Identification of HSP families members are performed using MidgeBase Integrated genome database of chironomid [1] searching and manual results review. Totally 75 HSPs encoding genes are identified.

Expression analysis shows increasing transcription levels in substantial portion of HSPs genes, but the expression profiles are not identical among this genes. Most of genes encoding small HSPs demonstrate drastic increase of expression level in the last stage of desiccation stress, however significant up regulation in early desiccation stage indicated for sHSP 20 coding gene.

Different expression patterns are showed for HSP70 family genes also. In non stressed conditions only *hsc70* characterized by high transcription level, that increased to 4 fold change in last stage of desiccation. Expression of other *hsp70* – like genes in normal conditions substantially less and significantly increased in late stages. Members of both other families HSPs genes (HSP40 and HSP90) shows up-regulation under desiccation stress conditions too.

The work is performed according to the Russian Government Program of Competitive Growth of Kazan Federal University and supported by RFBR grant N 14-04-01657.

References:

1. <http://bertone.nises-f.affrc.go.jp/midgebase/>