

Drying without dying: multi-omics analysis of mechanisms of anhydrobiosis in the sleeping chironomid *Polypedilum vanderplanki* (Diptera)

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The sleeping chironomid *Polypedilum vanderplanki* (*Chironomidae*, *Diptera*) is a unique example of evolution of resistance to excess of the environmental stresses in a single species of insects. Larvae of this midge inhabit temporary water pools formed during raining seasons in semi-arid regions in Africa and enter an ametabolic state – anhydrobiosis – decreasing the water content in the body to less than 3% when dry season comes. The desiccated larvae maintain ability to revive and restore metabolism soon after next rehydration after decades in the dry state (Gusev, et.al, 2010; Cornette and Kikawada, 2011).

In order to uncover molecular background of anhydrobiosis we conducted NGS-based comparative analysis of genomes of two chironomid midges from the same genus, but different their ability to resist complete desiccation: *P. vanderplanki* and desiccation sensitive *P. nubifer*. Primary genomes analysis was further followed by intensive transcriptome and metabolome analysis of the larvae of two species under desiccation stress. Key findings include identification in the sleeping chironomid genome the rapid expansion of several groups of genes involved in protection against the oxidative stress and amino acid aging; involvement and rapid expansion the set of intrinsically disordered proteins. Some of the

newly evolved and expanded clusters shared features of horizontally transferred genes. In contrast, genome of the desiccation-sensitive *P. nubifer* showed none of these features and shared general similarity with other dipteran insect species sequences up to date. We have further noticed that while general features (genes number, GO distribution, etc.) of the two genomes are similar, mRNA expression profile and metabolites dynamics in response to desiccation were different in two chironomids. Interestingly, the expanded in the sleeping chironomid groups of gene were highly expressed specifically in response to desiccation. Newly developed genome resources advance the sleeping chironomid for genetic research targeted on the uncovering mechanisms underlying complete desiccation resistance in higher eukaryotes. In addition, its provides an effective tool and knowledge to use whole genome comparative analysis for understanding micro-evolutionary processes leading to evolvement of unique survival abilities in a single eukaryotic species .

1. O. Gusev, R. Cornette, T. Kikawada, and T. Okuda. (2011) Expression of heat shock proteins associated with anhydrobiosis in an African chironomid *Polypedilum vanderplanki*. *Cell Stress & Chaperones*. **16**: 81-90.
2. R. Cornette and T. Kikawada. (2011) The induction of anhydrobiosis in the sleeping chironomid: current status of our knowledge. *IUBMB Life* **63**: 419–429.

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