

## **Molecular basics of different mechanisms of desiccation tolerance in *Chironomidae* midges**

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Many species of chironomids are known for their ability to successfully combat desiccation during larval stage of development (Frouz et al., 2003). *Polipedyllum vanderplanki* from Africa and *Paraborniola tonnoiri* from Australia are considered to be among the most adaptable to extremely dry conditions *Chironomidae* species. However, their mechanisms of surviving during partial desiccation are different: if in case of *P. vanderplanki* it is cryptobiotic strategy, expressed in complete drying and termination of life functions, then in larvae of *P. tonnoiri* we have hypometabolic strategy, expressed in deceleration of internal processes and using the minimum amount of stored water (Nakahara et al., 2008).

In order to understand and compare molecular mechanisms of *P. vanderplanki* and *P. tonnoiri* in detail, we performed whole-genome analysis of mRNA expression properties in control and partially desiccated groups of their larvae. The first stage of research for *P. tonnoiri* was raw transcriptome assembly with Trinity, that gave us 24 741 ORFs with minimal protein size equal to 50 amino acids, while the gene model set of *P. vanderplanki* contains 17 137 sequences (Gusev et al., 2014). As a result of differential expression analysis, performed for *P. tonnoiri* larvae, we revealed 1459 gene models with significantly increasing and 195 gene models with significantly decreasing expression in case of desiccation. During the given research, more than threefold increase or decrease of expression level measured in FPKM and FPKM value > 10 for the higher value were used as the criteria for calling the corresponding gene model of either midge differentially expressed.

In order to find orthologous gene groups from *P. vanderplanki* and *P. tonnoiri* data, we performed cross tBlastX-search, which revealed 9756 putative orthologous gene models in total. Focusing on this group of genes revealed different expression properties in response to

partial desiccation: for instance, 53 gene models up-regulated in *P. tonnoiri* but down-regulated in *P. vanderplanki* were found during comparison. According to GO annotation, the most common molecular function of this gene group was serine-type endopeptidase activity. Gene enrichment analysis, performed for the differentially expressed groups of genes in *P. tonnoiri* and followed by comparing the obtained information with *P. vanderplanki* data, showed that these two species have different mechanisms of adaptation towards desiccation not only on behavioral, but also on molecular level.

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1. J. Frouz et al. (2003) Survival strategies of chironomids (Diptera: Chironomidae) living in temporary habitats: a review, *Eur. J. Entomol*, **100**: 459-465.
2. O. Gusev et al. (2014) Comparative genome sequencing reveals genomic signature of extreme desiccation tolerance in the anhydrobiotic midge, *Nat commun.*, **5**: 4784
3. Y. Nakahara et al. (2008) Effects of dehydration rate on physiological responses and survival after rehydration in larvae of the anhydrobiotic chironomid, *Journal of Insect Physiology*, **54**: 1220-1225