Antioxidant system of desiccation-tolerant insect Polypedilum vanderplanki

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Polypedilum vanderplanki is a small African chironomid able to revive after almost full desiccation at a larva stage. Despite of its relatively small size (around 7 mm), larva of this insect is the most complex desiccation-tolerant organism known at the date. Such an extreme adaptation implies an ability to cope with a severe damage of cell interior including protein aggregation and denaturation, perturbation of membranes and DNA damage. Comparative analysis of genome and transcriptome of *P. vanderplanki* and congeneric desiccation-sensitive chironomid *P. nubifer* help us to reveal genes and proteins that ensure desiccation tolerance. Particularly, *P. vanderplanki* genome contain an extended set of genes encoding proteins involved in antioxidant defense.

An empowering of *P. vanderplanki* antioxidant system is closely related to an elevation of oxidative stress during water loss and in a desiccated state. Such an elevation is mediated by disruptions of the mitochondrial electron transport chain, reduction of the hydrating shell of macromolecules, an increase of ionic strength and pH change [1]. The number of antioxidant system genes in *P. vanderplanki* (54) is considerably higher than in *P. nubifer* and even higher than in the genome of the honey bee (38) whereas the latter is characterized far more higher metabolic rates [2].

The increase of a number of antioxidant genes in *P. vanderplanki* is not only a result of gene duplication and diversification. Molecular evolution of *P. vanderplanki* resulted also in an acquisition of new genes. Such new genes include two *P. vanderplanki* specific superoxide dismutases (SOD) that are not related to SOD's of *P. nubifer* based on another location and low sequence similarity. These *P. vanderplanki* specific enzymes become highly upregulated during anhydrobiosis cycle. *P. vanderplanki* genome contain the sole gene of manganese-containing mitochondrial SOD which belongs to a classic insect enzymes. Its

expression is not increased in desiccation despite of the fact that mitochondria are obviously the main source of reactive oxygen species (ROS). Unique SOD genes of *P. vanderplanki* that are upregulated in anhydrobiosis encode copper/zinc-containing dismutases that are usually considered as cytosolic/extracellular enzymes. Recently reported controllable process of localization of CuZn SOD into intramembrane space of mitochondria in human macrophages suggests that typical specialization of two types of SOD in the case of *P. vanderplanki* should be also revised [3].

An absence of gene encoding glutathione reductase suggests that *P. vanderplanki* antioxidant system glutathione does not serve as a main mediator of ROS scavenge and is at least partially substituted by thioredoxins. Such a substitution was already reported for *Drosophila melanogaster*. However, *P. vanderplanki* larva express 12 splice variants of glutathione peroxidase (GPx). Similarly to *D. melanogaster* they are expected to be thioredoxin-specific [4]. Among different variants of *P. vanderplanki* GPx eight are typical enzymes with three catalytic amino acid residues and highly conserved residues in proximal regions. However, in four variants catalytic glutamine is replaced by glycine and proximal downstream region is disturbed.

In addition to an increase in the gene number (54 versus 27 in *P. nubifer*) some of antioxidant genes are upregulated in *P. vanderplanki* intrinsically or become upregulated during desiccation cycle. Transcriptomic data provides us interesting examples of differential expression of genes that are specific for *P. vanderplanki* and genes that are analogous to *P. nubifer*. During desiccation cycle in *P. vanderplanki* larva genes encoding catalase and glutaredoxin become upregulated in 2.5 and 6 times, accordingly. Expression of analogous genes of *P. nubifer* during desiccation cycle does not change. Taken together with well-known ability of *P. vanderplanki* to start a huge accumulation of trehalose at the onset of desiccation, these data demonstrate a presence of specific desiccation-sensitive system of differential gene regulation in *P. vanderplanki*.

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