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Cooption of heat shock regulatory system for anhydrobiosis in the sleeping chironomid Polypedilum vanderplanki

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Abstract

© 2018 National Academy of Sciences. All Rights Reserved. Polypedilum vanderplanki is a striking and unique example of an insect that can survive almost complete desiccation. Its genome and a set of dehydration–rehydration transcriptomes, together with the genome of Polypedilum nubifer (a congeneric desiccation-sensitive midge), were recently released. Here, using published and newly generated datasets reflecting detailed transcriptome changes during anhydrobiosis, as well as a developmental series, we show that the TCTAGAA DNA motif, which closely resembles the binding motif of the Drosophila melanogaster heat shock transcription activator (Hsf), is significantly enriched in the promoter regions of desiccation-induced genes in P. vanderplanki, such as genes encoding late embryogenesis abundant (LEA) proteins, thioredoxins, or trehalose metabolism-related genes, but not in P. nubifer. Unlike P. nubifer, P. vanderplanki has double TCTAGAA sites upstream of the Hsf gene itself, which is probably responsible for the stronger activation of Hsf in P. vanderplanki during desiccation compared with P. nubifer. To confirm the role of Hsf in desiccation-induced gene activation, we used the Pv11 cell line, derived from P. vanderplanki embryo. After preincubation with trehalose, Pv11 cells can enter anhydrobiosis and survive desiccation. We showed that Hsf knockdown suppresses trehalose-induced activation of multiple predicted Hsf targets (including P. vanderplanki-specific LEA protein genes) and reduces the desiccation survival rate of Pv11 cells fivefold. Thus, cooption of the heat shock regulatory system has been an important evolutionary mechanism for adaptation to desiccation in P. vanderplanki.

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Keywords

Anhydrobiosis, Desiccation tolerance, Heat shock, Polypedilum vanderplanki, RNA-seq

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