

Decoding the draft genome sequence of desiccation tolerant African midge

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We completed the draft genome sequence of an African midge, *Polypedilum vanderplanki*, which has a capability to survive under extreme desiccation tolerance, or the so-called anhydrobiosis. The draft sequence shows that *P. vanderplanki*-specific gene clusters and desiccation-inducible gene expression systems contribute to anhydrobiosis.

Keywords: anhydrobiosis, genome, horizontal gene transfer, adaptive evolution, gene duplications

Background

Our collaborative research with scientists from Japan, Russia and the USA successfully deciphered the draft genome sequence of an African midge, *Polypedilum vanderplanki*, possessing the capability to survive extreme desiccation. The draft sequence reveals that *P. vanderplanki*-specific gene clusters and desiccation-inducible gene expression systems contribute to anhydrobiosis. The genes connected with anhydrobiosis will be applied to develop new technologies such as long-term storage of cells, embryos and blood in a dry state at room temperature.

Results and Discussion

1. NIAS organized the international collaborative research team comprising of Kazan Federal University (Russia), Okinawa Institute of Science and Technology Graduate University (Japan), National Institute for Basic Biology (Japan), Kanazawa University (Japan), Lomonosov Moscow State University (Russia), Scientific Research Institute of Physico-Chemical Medicine (Russia), Russian Academy of Science and Vanderbilt University (USA). The team deciphered the draft genome sequence of the anhydrobiotic midge, *P. vanderplanki* and identified approximately 17,000 protein-coding loci.
2. Comparative genome analysis of *P. vanderplanki* and a congeneric desiccation-sensitive midge *P. nubifer* (Fig. 1) led to the identification of *P. vanderplanki*-specific genomic regions where these gene sets are located as 'anhydrobiosis-related gene island' (ARId). Moreover, this analysis provides evidence on the existence of desiccation-specific gene expression system in *P. vanderplanki* (Fig. 2).
3. ARIDs consist mainly of multicopy genes for protective proteins, such as antioxidants, enzymes for repair of damaged proteins, and LEA proteins acting as molecular shields.
4. The *LEA* genes were horizontally acquired from soil bacteria in the habitat of *P. vanderplanki*.
5. We revealed the evolutionary process that led to the ability to acquire anhydrobiosis in *P. vanderplanki* diverged from an ancestral species about 25 million years ago (Fig. 3).

Future prospects

1. The key sets of genes connected with anhydrobiosis will be applied to develop new technologies for long-term storage of cells, embryos and blood in a dry state at room temperature.
2. Elucidation of the molecular mechanisms underlying dehydration-specific gene expression system will be useful in designing a methodology for induction of resistance to desiccation in different animal tissues and cells.



Fig. 1. Comparative genome analysis unveils the essential gene sets involved in anhydrobiosis.

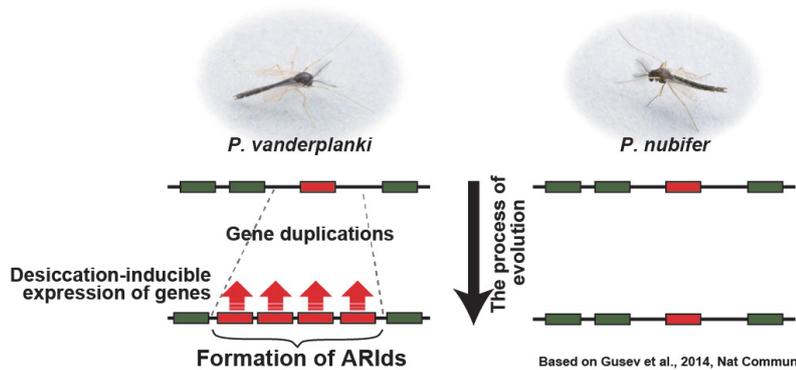


Fig. 2. The unique gene variation between *P. vanderplanki* and *P. nubifer* representing earlier species of midge. The large red blocks indicate gene clusters associated with tolerance to extreme conditions known as ARIDs.

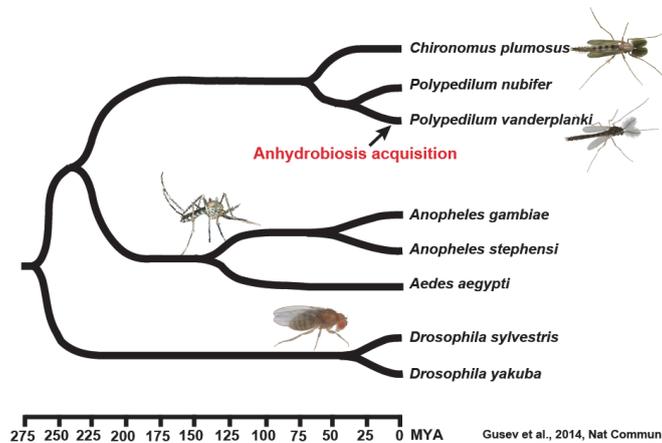


Fig. 3. The genes responsible for making *Polypedilum vanderplanki* resilient are unique genetic mutations that have been found only in this particular species. indicate gene clusters associated with tolerance to extreme conditions known as ARIDs.

Reference

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