Determining the spatial chromatin organization upon desiccation process in the insect cells using Hi-C technology.

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For investigating biological processes, a number chromosome conformation capture methods are developed for determining the spatial organization of chromatin and the character of interactions between genomic loci in model organisms. However, little is known about pattern of changes in chromatin under the influence of environmental stresses. Herewith, the stress-resistant organisms, or extremophiles, facing extreme environmental stresses, is an attractive model.

Among abiotic factors, desiccation is one of the most severe stresses for living cells. Anhydrobiosis is an adaptation to water loss, in which an organism can withstand almost complete desiccation. The most complex and largest anhydrobiotic animal known today – larvae of *Polypedilum vanderplanki* that inhabit some semiarid areas of West and Central Africa. Dehydrated state is a natural phase in the lifecycle of the larvae, and under favorable conditions, they quickly come back to life. Such extreme structural changes in the body along with compact genome size can mean possible specific features of chromatin architecture. Pv11, a cell line derived from the embryos of *P. vanderplanki,* is also able to endure water loss as larvae. Previous studies showed a similar effect of desiccation on larvae and incubation with trehalose on Pv11, making the cells an ideal model object for anhydrobiosis studies.

For understanding the character of chromatin interactions during anhydrobiosis, we applied Hi-C method on intact Pv11 cells and cells in transition to anhydrobiotic state by trehalose pretreatment for 48 hours. In our study, we focused on several key questions. First, one of the advantages of getting information of spatial proximity of genome fragments, derived by Hi-C, is improving of current genome assembly. We applied this method to the genome contigs of the *P. vanderplanki*. By now, the number of genome scaffolds decreased from several hundreds to tenths, including four chromosome-length scaffolds. Thus we demonstrated that remarkable improvement of the assembly

can be achieved not only in well characterized model insect species, but also in non-model ones, with only partial known genomic data.

Second, the key purpose is determining peculiarities of spatial chromatin organization in chironomids and possible alteration of chromatin packaging driven by desiccation. In addition, of a special interest is the spatial configuration of *P. vanderplanki* specific regions of closely located anhydrobiosis-related genes (ARIDs) and their interactions. These genes encode the main protectants of biomolecules and cell membranes during desiccation process, such as: antioxidants, late embryogenesis abundant proteins (LEA), protein L-isoaspartyl methyltransferases (PIMT) and heat-shock proteins. The most part of these anhydrobiosis-related genes dramatically increase their expression while entering an anhydrobiotic state.

The study of the spatial chromatin organization and its course of action in response to influence of adverse factors in stress-resistant organisms will be the next step to understanding the anhydrobiosis -survival machinery.

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