Секция «Биоинформатика»

Search for methylation sites in the genome of Baeotendipes noctivagus chironomids based on nanopore sequencing data

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DNA methylation is one of the most significant epigenetic mechanisms for the regulation of gene expression in eukaryotes, involved in many biological processes. This process transfers a methyl group to a cytosine, mostly in positions 5' of a guanine (CpG sites).

While the most popular methods for detection of modified cytosines still are based on bisulfite sequencing data [1], a recent alternative is nanopore sequencing [2,3]. Here, nanopore sequencing data is used to investigate the existence of DNA methylation in the genome of chironomid *Baeotendipes noctivagus*. It is a non-biting midge from the Diptera order whose larva can survive in hypersaline lakes with the salinity rate of 80-240 g/l. It is the most halotolerant chironomid known [4]. It adapts to extreme conditions (hypoxia and osmotic stress) on the genomic level by extensive duplication of hemoglobin genes and responds to high salinity by high expression of the *Eglp1* gene encoding. That makes this midge an interesting model to study regulation gene expression.

The obtained results show the lack of methylation in *Baeotendipes noctivagus* genome. It can be explained by the absence of DNA methyltransferases 3 and 1 in Diptera insects, which are responsible for creating *de novo* methylation and maintaining existing.

It confirms that methylation is not a leading epigenetic mechanism in dipterans, and they may use other ways to regulate genes expression.

This study is a part of a large project, the goal of which is to understand how *Baeotendipes noctivagus* has adapted to hypersaline lakes.

References

1) Bewick A.J. et al. Evolution of DNA Methylation across Insects // Mol. Biol. Evol. 2017. Vol. 34, № 3. P. 654–665.
2) Yuen Z.W.-S. et al. Systematic benchmarking of tools for CpG methylation detection from nanopore sequencing // Nat. Commun. 2021. Vol. 12, № 1. P. 3438.
3) Liu Y. et al. DNA methylation-calling tools for Oxford Nanopore sequencing: a survey and human epigenome-wide evaluation // Genome Biol. 2021. Vol. 22, № 1. P. 295.
4) Shadrin N.V. et al. Chironomidae larvae in hypersaline waters of the Crimea: diversity, distribution, abundance and production // The European Zoological Journal. Taylor & Francis, 2017. Vol. 84, № 1. P. 61–72.