

Epigenetics and accelerated aging of Far Northern Yakutian population

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We present the results of the first epigenetic study of the Yakutian population using whole-blood DNA methylation data, supplemented with the comparison to the residents of Central Russia [1]. In particular, we aimed to improve understanding of the mechanism of accelerated aging, development of age-related diseases in extreme climate conditions, as well as adaptation of organism to the cold. Gene set enrichment analysis revealed, among others, geographic region-specific differentially methylated regions associated with adaptation to climatic conditions (water consumption, digestive system regulation), aging processes (actin filament activity, cell fate), and both of them (channel activity, regulation of steroid and corticosteroid hormone secretion). Further, it is demonstrated that the epigenetic age acceleration of the Yakutian representatives is significantly higher than that of Central Russia counterparts. For both geographic regions, we showed that epigenetically males age faster than females, whereas no significant sex differences were found between the regions.

These findings promote the fundamental understanding of the mechanisms of modulating gene activity and functional clustering of the involved gene loci associated with the age-related changes in metabolism of the residents of various regions of the Russian Federation. It also paves the way to assessing the risk of developing age-associated diseases in people living in extreme climatic conditions, and provides the basis for the development of preventive approaches and age control schemes.

References

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