

Estimating telomere lengths of the local and imported to Russia cattle breeds from the whole-genome resequencing data

Yudin N.^{1*}, Romashov G.¹, Larkin D.²

¹ *Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia*

² *Royal Veterinary College, University of London, London, UK*

* yudin@bionet.nsc.ru

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Motivation and Aim: Health and survival are key elements in cattle selection. However, selection success is limited by the low heritability of these traits in addition to phenotype measurement difficulties. Telomere length (TL), measured in leukocytes, could be a good biomarker for breeding purposes since TL has been associated with health, ageing, and stress in humans and other species. However, we still do not know to what extent such associations in cattle would be determined by the genetics or/and the environmental factors. The TL is known to differ between human ethnic groups [1], inbred mouse strains [2], *C. elegans* strains [3] etc. The aim of the study was to investigate the differences of TL between the local and imported to Russia cattle breeds.

Methods and Algorithms: The average leukocyte telomere length (TL) from whole genome resequencing data of 59 animals of the Wagyu ($n = 20$), Yaroslavl ($n = 12$), Hereford ($n = 12$), Yakut ($n = 6$), Kholmogory ($n = 6$), and Kalmyk ($n = 3$) cattle breeds was estimated computationally using the TelSeq program (<https://github.com/zd1/telseq>).

Results: The TelSeq TL estimates in our study, ranging from 4.88 Kb to a maximum of 22.87 Kb with a median TL of 8.99 Kb, were similar to the TelSeq TL estimates for human [4] and *C. elegans* [3]. Measurements of TLs in younger animals were significantly higher in the whole dataset ($r = -0.30$, $p < 0.05$), and a significant difference was observed between breeds for the TLs. For example, TLs of the Wagyu bulls at the age of two years was significantly lower than in bulls of the Kholmogory ($p = 0.0005$) and Yakut ($p = 0.0007$) breeds of the same age.

Conclusion: Thus, a difference in the TLs between breeds might indicate that the genetic background affects this trait in cattle.

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