

Abstract Title: Detection of recent positive selection signatures in the cohort of the Lithuanian Chernobyl catastrophe clean-up workers

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Background/Objectives:

Ionizing radiation (IR) is one of the factors that is known to affect genomes and, therefore, challenge organisms to adapt and acquire new traits. Lithuanian Chernobyl catastrophe clean-up workers (LCCWs) are an exclusive object of research, because not only they survived extreme conditions, but also adapted to the life-lasting effects of IR. This study focuses on adaptation and the search for the recent positive selection signatures in the genomes of LCCWs.

Methods:

Whole-genome sequencing of 15 LCCWs and 15 control individuals (all males) was performed. Control group included men of Lithuanian descent, who were not involved in the clean-up work of Chernobyl catastrophe. To identify genomic regions which may be under recent positive selection analysis was performed using RAI_{SD} tool. It uses μ values as a predictor for the selective sweep signatures. Top 1% of μ values, of which were higher than a median value in a chromosome, was set for further analysis. These values and selective sweep signatures were compared between the two groups.

Results:

Eleven genomic regions under recent positive selection have been identified throughout autosomes. These regions are unique to the LCCWs compared to the control group and have the highest selective sweep values.

Conclusion:

The signatures of recent positive selection differ between LCCWs and the control group individuals. The analysis of these genomic regions might explain LCCWs adaptive abilities and why some of the LCCWs survived and age relatively healthy despite large IR doses experienced.

References:

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