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Epigenetic changes in recreational runners from a clean and an air polluted locality

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Air pollution has an unfavourable impact on the environment as well as on human health. It has been proven that exposure to polluted air, mainly in large cities or industrial zones, increases the risk of diseases such as cancer and cardiovascular disorders. Small non-coding RNA molecules (microRNAs; single-strand, approximately 22 nucleotide long RNA molecules) play a crucial role in the epigenetic regulation of gene expression. In their mature form, they complementary bind to mRNA, which causes its silencing. These molecules are affected by environmental pollutants, including airborne contaminants and have been implicated in human cancers.

Physical activity (including running) is a well-established factor positively affecting human health. Among other physiological roles, it improves respiratory and cardiovascular systems, supports immunity, as well as neurological and psychological functions and in turn, it contributes to the delayed onset of age-related diseases, thus potentially increasing lifespan. Although the area of the Czech Republic (Central Europe) is relatively small (78 781 km2), the level of air pollution highly differs across the country. In this study, RNA was isolated from collected blood, microRNA libraries were prepared and sequenced. MicroRNA expression in 393 volunteers was compared between and within two localities with different levels of air pollution or between runners and non-runners. Overall, from fourteen comparisons, most deregulated microRNAs (42) were detected when female runners were compared with non-runners in the clean locality. On the contrary, the highest deregulation rate (log2FC) of a single microRNA was observed in comparison of runners from the polluted and the clean locality. Due to deregulation of these microRNAs, various biological, including cancer-related, pathways may be altered which might lead to numerous diseases progression.

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