«Sex-specific age-related changes in methylation of certain genes»

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For many decades, the mechanisms that underpin the differences in life expectancy for the two genders remain largely undisclosed. In this regard, understanding epigenetic regulation of gene expression, in particular, with regard to ageing has a major importance. For that all genes with age-dependent gender-specific methylation were divided into 3 groups: genes that change methylation level with age only in men (143 genes), only in women (401 genes) and in both genders ("duplicate" group) - 322 genes. KEGG analysis of the "duplicate" group revealed 6 significant changes ($p<0.05$) of metabolic cascades, including genes responsible for morphogenesis, age-dependent pathological processes and biological processes associated with functioning of the nervous system. Analysis of the biological functions of groups of genes whose age-dependent methylation is characteristic only for women revealed six important ($p<0.05$) cascades including calcium signaling pathway, synthesis of melanin, adhesive contacts. The unique changes in the female genome that is responsible for neuronal activity in the age aspect include vasopressin and oxytocin systems, synthesis of receptors for dopamine, glycine and opioid receptors. It is interesting to note that for men, changes in the methylation of genes of the serotonin system predominate, while for women, changes affect the dopaminergic system. Thus, it was found that most of the gender-dependent age-related changes in methylation belong to the genes responsible for the development and functioning of the nervous system. Importantly, the changes are found in various mechanisms, suggesting the development of features of gender-specific reactions of the body. Russian Federation mega grant DPM-AGEING (grant 2017-220-06-4741) on Digitalized and Personalized Medicine of Healthy Ageing.

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