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Genetics and Epigenetics of Aging

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Message from the Guest Editors

Dear Colleagues,

Aging is an independent risk for many common diseases, such as cardiovascular diseases, cancers, and dementia. It is known that genetic, epigenetic, and environmental factors affect the aging process profoundly. Over the past decades, candidate approach, particularly in multiple omics tools, such as genome-wide association, methylation, chromatin conformation, RNA sequencing, and all types of proteomics, have been used in the search of genes and epigenetic changes, including their interactions with environmental factors associated with aging and age-related diseases at the genome level. This provides a comprehensive view on the aging process, both temporally and spatially. Integration of these omics data with functional assessments has provided a unique tool to define and interpret the effects of genetic variance and epigenetic alteration on the aging process. For instance, a number of genetic and epigenetic markers and signaling pathways, including those in mitochondrion, were found to estimate or explain the mechanisms on aging and longevity. These provocative findings help to gain new insights into the aging process, i.e., the old myth.



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Special Issue



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Message from the Editor-in-Chief

Genes are central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fastmoving field. There is a need for good quality, open access journals in this area, and the *Genes* team aims to provide expert manuscript handling, serious peer review, and rapid publication across the whole discipline of genetics. Starting in 2010, the journal is now well established and recognised.

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