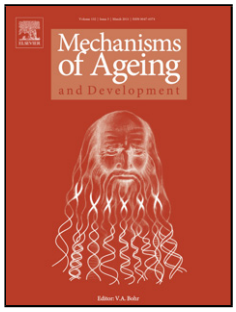

Title: Epigenetics in Ageing and Development

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PII: S0047-6374(18)30117-9
DOI: https://doi.org/10.1016/j.mad.2018.05.005
Reference: MAD 11057

To appear in: *Mechanisms of Ageing and Development*

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Please cite this article as: Gabbianelli R, Malavolta M, Epigenetics in Ageing and Development, *Mechanisms of Ageing and Development* (2018), https://doi.org/10.1016/j.mad.2018.05.005

Editorial: Epigenetics in Ageing and Development

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The idea that a universal epigenetic program, which is reset during embryogenesis and influenced by diet and other environmental factors, can drive not only development but also ageing is gaining recognition, and embodies the idea that this is a major target for the future development of therapeutic strategies to improve health and longevity.

Indeed, multiple and progressive epigenetic changes have emerged as key hallmarks of ageing. These changes include patterns of DNA methylation and histone posttranslational modifications, altered noncoding RNA expression, replacement of canonical histones with histone variants and reduced bulk levels of the core histones (Pal and Tyler 2016). While part of these changes act like an epigenetic clock and are tightly related to chronological age (Horvath 2013), others diverge (age-dependently) from chronological age likely reflecting the increasing inter-individual variation in health of old organisms (Slieker et al. 2016). Reasons for these variations, are not well understood, but they seem to occur in all tissues and cells regardless of their developmental potential.

The impact of epigenetic changes in reflected by altered gene expression, reactivation of endogenous retroelements and genomic instability that can have systemic effects on ageing from cellular to the organismal level.

In this special issue of *Mechanisms of Ageing and Development*, the hot topics around the role of epigenetic changes in ageing and development are covered by critical reviews or original research manuscripts provided by major experts in the field.

While DNA methylation is currently the most promising biomarker of ageing, the mechanisms underlying age-related DNA methylation changes remain mostly undiscovered. A focused review shows how the dynamics of chromatin structure and histone posttranslational modifications are related to variations of methylcytosine and its oxidative modifications (Ciccarone et al. 2017). How epigenetic clock signature could be used as a lifestyle management tool to monitor healthy ageing, as well as to evaluate the effects of interventions against chronic ageing disorders and to extend healthy lifespan is the focus of another manuscript of this special issue (Declerck and Vanden Berghe 2018).

CpG DNA methylation is among the epigenetic control mechanisms used by the cell to counteract the risk of genomic instability represented by endogenous retroelements. Indeed, these repetitive elements carry most of the methylated CpG sites of our genome. A dedicated manuscript (Cardelli 2018) describes how epigenetic changes and endogenous retroelements are tightly related and discuss the relevance of their interaction in ageing research.

How nutrition affects global DNA methylation and how these changes can be transmitted to successive generation (epigenetic inheritance) is a highly discussed topic in ageing research. An original research manuscript (Guarasci et al. 2018) provide here evidence that a low-calorie diet in rats affect the offspring's epigenetic status, in particular when administered during the maternal pre-gestational period. Fetal epigenetics has a key impact on telomere lengths and telomere loss dynamics, and both can control health and lifespan. A review describes how different nutrients and oxygen supplied to the fetus can impact the length and dynamicity of telomeres, highlighting the way in which early environmental factors can have long term effects on healthy and unhealthy ageing (Ravlić et al. 2017).