

WHAT ROLE DOES THE ENVIRONMENT PLAY IN LONGEVITY? EPIGENETIC APPROACH

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Aging increases the risk for numerous chronic diseases. Epigenetics (acquired or heritable changes in gene function or phenotypes without changes in DNA sequence), has emerged as an important factor in predicting gene expression and disease risk. We focused on epigenetic modifications involving cytosine methylation, which have been shown to be associated with age-related diseases. Cytosine methylation levels at specific sites appear to change with aging mostly through hypermethylation. We hypothesized that: epigenetic changes associated with aging could serve as markers for healthy life span, epigenetic changes (especially changes in methylation pattern with age) may represent one of the central mechanisms of gene regulation by which many aging process are buffered, and therefore facilitate healthy lifespan. We utilized state of the art technology (i.e. Infinium methylation EPIC Kit) to obtain significant information on epigenomic changes in methylation with aging, and test it in both a cross-sectional and longitudinal study. We used the Israeli multi-ethnic centenarian study (I-MECS) cohort to probe into the hallmarks of the healthy aging. This data was analyzed in a meaningful way, by assessing the occurrence of age-related diseases and its interaction with either supportive or adverse environments (i.e. epigenetic influence). This study opened the horizons for more specific and functional studies, as previously exemplified by numerous genetic studies, and led to a better understanding of the biology of the aging. Successful interpretation may lead to future crafting of treatments and interventions, which will promote aging with grace.

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