Nutraceuticals in balancing redox status in ageing and age-related diseases

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Book of Abstracts

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S6. THE IMPACT OF CATECHINS ON DNA METHYLATION LEVEL WITHIN PROMOTER AREA OF SULFIREDOXIN-1 GENE IN HT29 CELL LINE

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In our previous study, treatment of HT29 cell line with catechins induced dose-dependent changes in the expression of redox-related genes. Uniquely, only one gene (SRXN1, sulfiredoxin-1) was down-regulated upon treatment with 10 μM (-)-epigallocatechin (EGC). The aim of the current study was to investigate whether the observed down-regulation of SRXN1 expression was affected by epigenetic changes. HT29 cells were treated with catechins at different concentrations for 24 h and subsequently genomic DNA was isolated and bisulfite converted. DNA methylation profiles of selected regions within SRXN1 promoter were examined using Methylation-Specific PCR (MSP) and Methylation-Sensitive High Resolution Melting (MS-HRM). MSP analysis showed no differences in DNA methylation level between any of the treatments compared to control. However, the difference was observed when the bigger area of CpG island was analyzed by MS-HRM. Significant increase in DNA methylation level was observed after cell treatment with higher doses of EGC and (-)-epicatechin gallate (ECG). DNA demethylation requires oxidative modifications of methylated cytosine. Catechins, which are strong antioxidants, may lead to inhibition of DNA demethylation by changing cellular environment to more reduced state, especially in the case of higher doses. Thus, we report that catechins can act as methylation inducers and probably this function derives from their ability to influence cellular redox homeostasis.

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