

INTERNATIONAL SOCIETY OF ANTIOXIDANTS

21st ISANH International Conference on

**Oxidative Stress Reduction,
Redox Homeostasis & Antioxidants**

ABSTRACTS BOOK



June 20-21, 2019 | Université Pierre et Marie Curie, Paris, France



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MODULATION OF DNA METHYLATION PROFILE OF SRXN1 GENE PROMOTER IN HT29 CELLS EXPOSED TO CATECHINS OF DIFFERENT REDOX ACTIVITY

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Introduction: Our previous research indicated that treatment of HT29 cells with different catechins affected the expression of redox-related genes in a dose dependent manner with only one gene (SRXN1) being down-regulated [1]. Since catechins were reported to affect DNA methylation levels[2], the objective of current research was to find out whether the observed down-regulation of SRXN1 expression was caused by epigenetic changes.

Materials & Methods: Human colon adenocarcinoma HT29 cells were treated with 5 catechins at 4 concentrations for 24 hours and subsequently genomic DNA was isolated. To perform methylation analysis, DNA isolates were bisulfite converted using EZ DNA Methylation kit from Zymo Research (USA). DNA methylation profiles within the chosen fragment of promoter area of SRXN1 gene were examined using Methylation-Specific PCR and Methylation-Sensitive High Resolution Melting.

Results: According to Baranowska et al.[1], the treatment of HT29 cell line with 10 μM (-)-epigallocatechin caused down-regulation of SRXN1 gene. So, we hypothesized that the methylation level within the promoter CpG island of this gene will be increased by this compound and our presumptions were confirmed. Besides, significant increase of DNA methylation was observed also for high doses of (-)-epicatechin gallate.

Conclusion: Catechins may influence DNA methylation pattern of redox responsive genes.

This work was supported by the National Science Centre in the framework of programme "Maestro 6" (application no: 2014/14/A/ST4/00640). Part of this work was supported by the COST Action CA16112 "NutRedOx: Personalized Nutrition in aging society: redox control of major age-related diseases".

References:

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2. Yiannakopoulou, E. C. (2015) 'Targeting DNA methylation with green tea catechins', *Pharmacology*, 95: 111-116.