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POSITIVe|COST|Action

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gene-polyphenol interactions, and benefits of aronia juice consumption. Further research is warranted.

P13 Metabolic fingerprinting associated with legume consumption: discovery of food intake biomarkers by untargeted LCMS metabolomics

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Consumption of legumes has been associated with beneficial effects on human health. To go in depth to the protective effects of these foods, biomarkers of intake are needed. However, only a few number of studies dealing with this topic have been already published and therefore there are not still reliable biomarkers to monitor legumes intake, particularly for pulses. The aim of this study was to identify dietary biomarkers related to an acute nutritional intervention with lentils, chickpeas and white beans, as well as to monitor their kinetics following 48h after the intake of these foods. We conducted a randomised, placebo-controlled, crossover study. Participants were healthy volunteers who ingested a single dose of the test meals (lentils, chickpeas and white beans) or control meal (pasta). Firstly, two pools of the collected urinary samples were produced: one pool with the samples of each subject after eating each food during the first 6 hours, and another pool covering the first 24 hours after each intervention. These samples were analysed by LCMS untargeted metabolomics. The excretion patters of the identified metabolites were further evaluated through the first 48h after the intake of the corresponding foods. Results showed a high number of metabolites which urinary excretions allowed the discrimination between the different treatments, which could be potential biomarkers of legume intake. Trigonelline, several dipeptides and polyphenol-derived metabolites demonstrated to be the most discriminating urinary compounds following the consumption of the different types of legumes, being some of them common for all the three types of legumes, and other ones particular of one of them. The

excretion of most dipeptides were higher after the intake of chickpeas when compared with the other two types of legumes. Epicatechin metabolites and their microbial derivatives were identified exclusively after intake of lentils, whereas ascorbic acid only after consumption of chickpeas.

P14 Transcriptome-based Identification of New Anti-inflammatory Properties of the Olive Oil Hydroxytyrosol in Vascular Endothelial Cell under Basal and Proinflammatory Conditions

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The olive oil polyphenol hydroxytyrosol(HT) is regarded as responsible for the beneficial effects associated with olive oil consumption. However, the underlying molecular basis remains incompletely defined. Using a microarray technology, we investigated the variation in gene expression profile of human endothelium conditioned by HT under basal and pro-inflammatory conditions.
Methods: Human umbilical vein endothelial cells(HUVECs) were treated with 10μmol/L HT for 1 hour and then stimulated with 5ng/mL IL-1β for 3 hours. Total RNA was extracted and gene expression profile performed with an Agilent Microarray covering 41000 genes and transcripts. Raw data were processed with the GeneSpring®10 software and differentially expressed RNA identified using Benjamini and Hochberg False Discovery Rate. Functional and network analyses were identified by the Ingenuity Pathways Analysis.
Results: Fixing a significance threshold at 1.5 fold of change, HT, per se, changed the expression of 707 genes, down-regulating 269 and up-regulating 438. IL-1 stimulation changed the expression of 2389 genes, down-regulating 1120 and up-regulating 1269. Treatment with HT before IL-1 stimulation significantly affected the expression of 599 IL-1-deregulated genes. The application of the Ingenuity pathway analysis software allowed us to pinpoint immunological-, inflammatory- and metabolic-related pathways as the most affected. Under basal conditions HT down-regulated the expression of several chemokines and related receptor including those for the chemokine (C-C motif) ligand 2 and 20 and tumor necrosis factor receptor associated factor (TRAF)-1. Under pro-inflammatory stimulation, HT pre-treatment again counter-regulated gene expressions involved in inflammatory and proliferative pathways.