SCIENTIFIC REPORT - SHORT TERM SCIENTIFIC MISSION (STSM)

(COST Action FA1403, POSITIVe)

STSM topic: Extraction of nutrigenomics data from published papers for identification of cellular and molecular targets of plant food bioactives underlying their cardiometabolic health

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Background and objectives of the STSM

The aim of this STSM was to progress the extraction of the data on cellular and molecular targets of plant food bioactives from the papers that have been identified by different partners in the COST POSITIVe Action. One of the objectives of Working group 2 (WG2) of COST POSITIVe Action is to identify cellular and molecular targets of plant food bioactives underlying their cardiometabolic health properties. To reach this goal, extensive literature screenings of *in vitro*, animal or clinical studies have been performed in PubMed and WoS databases with defined key works for different bioactives. Subgroup "Animal studies" within WG2 reviewed animal studies investigating nutrigenomic effects of plant food bioactives in a cardiometabolic context. Following the screening of 666 papers, 186 met the defined criteria. Inclusion criteria were as follows: animal studies; bioactives: catechin, epicatehcin, ECGC, proanthocyanindin and phytosterols or a mix of these molecules from apple, tea or cocoa; studies had to include a control group receiving a placebo or a group who was not exposed to the bioactives, compounds had to be administrated to animals by diet, drinking water or gavage, studies had to include data on gene expression (miRNA, mRNA or protein) or epigenetic assessed in the target tissues (heart, aorta, vascular, adipose, liver tissues, muscles, circulating cells), studies had to report at least one outcome related to cardiometabolic health.

The purpose of this STSM was to help with the extraction of nutrigenomic data from the identified papers and therefore to contribute to WG2 objectives.

Description of the work carried out during the STSM and results obtained

For this STSM 51 paper of the identified animal studies investigating nutrigenomic effects of plant food bioactives were given for the data extraction. The extraction was done using the previously prepared template for the data extraction.

From these papers the following data was extracted and entered in the template:

- Data on animal model characterization (age, sex/gender, number of animal per groups, diet used to induce a disease model)
- Data on diet supplementation (major compound, source, composition in case of an extract, dose administrated to animals, the way of administration (drinking water, diet, gavage), duration of the supplementation, time period between the end of the supplementation and the sacrifice/tissue sampling
- Data on control group used to compare the effects of the supplementation
- Data on target (target tissue, target molecule (mRNA, miRNA, proteins), method of assessment)
- Data on gene expression: (examined gene/protein, modulation of the expression compared to the control group, exact values of fold changes (when data were graphically presented, authors were contacted or the ruler was used to obtain the values), unit used to represent the standard error and its value, p-value, FC and standard error values for the control, N (effective) used for the gene expression assay.

In addition to data extraction, during this STSM grantee was able to follow the experiments of the investigations of kinase activity (expertise of the host group). This involved the investigations of the effect of Echinacea extract on the Serine/Threonine Kinase activity in THP1 cells using PamChip arrays (flow-through microarray assay) and the PamStation12 (PamGene International, Netherlands). This methodology allows to determine phosphorylation activity using peptides immobilized on the PamChip and the mixture of primary antibodies and a fluorescently labelled secondary antibody. Following the experiment, grantee was able to see how the obtained data are then analyzed.

During this STSM grantee also gave a short seminar on her research topic and results that encouraged further discussion with the members of PPES team and initiated plans for further collaborations.

Follow up work

Following this data collection, bioinformatics analyses will be initiated. They will include identification of cellular pathways in which the collected genes are involved, identification of potential transcription factors mediating the nutrigenomic effect of bioactives and the analysis of kinases involved (expertise of the host group).

Future collaboration with the host institution and foreseen publications/articles resulting from the STSM

This STSM progressed the data extraction and analysis for the planed systematic review. In addition, this STSM also encouraged the future collaboration between Host and Home Institutions on kinase activity that will allow forthcoming publications.