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To
STSM Committee
of the COST Action POSITIVE

STSM Report

It was my great pleasure and honor to be invited at INRA, Centre de Clermont-Ferrand/Theix, Unite de Nutrition Humaine, to conduct the STSM **“Bioinformatic analysis of nutrigenomics data of plant food bioactives extracted from in-vitro and in-vivo studies”**. This STSM was related to the upcoming activities of the WG2 of the COST Action POSITIVE, more specifically to the subgroup Cell and Molecular Targets.

During my stay at INRA, I conducted a pilot bioinformatics analysis of nutrigenomic data of plant food bioactives. For in-vitro studies, extracted data were grouped according to the cell type and bioactives used for treatment. For genes extracted from papers with targeted approach, some of the gene symbols were transformed to official gene symbols using the database GeneCards.

Differentially expressed genes were analyzed using the software GeneTrail2. Pathways which were significantly associated with these genes ($p < 0,05$) were identified in BioCarta and KEGG databases. Common genes and pathways for different cell types were identified with the software Venny 2.1.0. Transcription factors associated with genes in common for different cell types and bioactives were retrieved by PASTAA software.

During this STSM I tested various approaches for data analysis. In consultation with my host, Dr. Dragan Milenkovic, we were able to identify the workflow and critical points to be addressed in the upcoming analysis of extracted data from in-vitro and in-vivo studies.

During the pilot bioinformatics analysis I also obtained important information on how to improve the current templates for data extraction, which was immediately implemented.

Along with my pleasure from this fruitful and inspiring stay at INRA, I would also like to express my gratitude to my hosts, Dr. Christine Morand and Dr. Dragan Milenkovic, and of course to the COST Action POSITIVE, for making this scientific mission possible.

Sincerely,
Dr. Tatjana Ruskovska