

Book of abstracts



Nutrigenomics of Foods

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Session 2 Poster 20

Application of food metabolomics for the development of standardized food matrices

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Epidemiological evidence indicates that there is an inverse association between consumption of cruciferous vegetables (such as broccoli, Brussels sprout and cauliflower) and risk of cancer and cardiovascular disease. These vegetables contain numerous bioactive compounds (vitamins, minerals, glucosinolates and phenolic compounds) that have been considered responsible for their health-promoting properties. However, the interactions and the possible synergies between these molecules and the complexity of the food matrix make difficult to understand the real biological role of the single bioactive compound. Broccoli sprouts have a particularly high content of bioactive molecules, whose concentration in plants responds to changes of environmental growth conditions. Then, acting on growth condition, it is possible to affect the overall bioactive molecules network. In this work, we searched for the best growth conditions and inducers able to increase the content of different bioactive molecules (glucosinolates, phenolic compounds, flavonoids, anthocyanins, vitamins and β -carotene) in broccoli sprouts. Targeted food-metabolomic and multivariate analysis allowed us to identify 'light plus sucrose' as the best inducer of the bioactive network. Then, broccoli sprouts grown in the dark or in the 'light plus sucrose' were used to produce a juice. The targeted and untargeted metabolomics analysis revealed large, but reproducible, differences between the two juices. This standardized compositional diversity can be used as a tool to investigate the biological role of different bioactive molecules embedded in their food matrix, both in *in vitro* (cellular model) and in in vivo models (animal model and humans).

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