Influence of dynamic digestion by SHIME® on bioaccessibility of polyphenols from table olives extract and human microbiota modulation

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Table olives are a typical vegetable of the Mediterranean area, and their polyphenols content and composition can be influenced by several factors, such as cultivars, climate, fruits ripeness, and, mainly, the processing methods. The starter driven fermentation, using selected autochthonous LAB and yeast strains, demonstrates to be an excellent debittering method, reducing the time and preserving the polyphenols. In addition, scientific evidence permits to consider the table olives as functional foods since their polyphenols content (as hydroxytyrosol and its derivatives) is higher respect those estimated in extra-virgin olive oil for which the Nutritional Claim table EU (n. 433/2012 of 23 May 2012) was reported.
In this study, the Simulator of Human Intestinal Microbial Ecosystem (SHIME®) was used to evaluate the polyphenols fate during a daily administration of a polyphenolic extract from *Leccino* cv table olives, fermented with a selected LAB strain from CNR-ISPA microbial collection. The SHIME is a dynamic artificial digestive system that mimics all the sections of the GI tract and permit to follow the gut microbiome shift in response to various factors, including dietary supplements, pre-probiotic preparations, but also to simulate the GI digestion starting from healthy or non-healthy human microbiota inoculum.
The preliminary results showed the following polyphenols bioaccessibility: hydroxytyrosol 70%, tyrosol 103%, verbascoside 65%, caffeic derivatives 73%, cumaric derivatives 64%, quercetin glucoside 60%. In agreement with other studies, the results highlighted a high stability of olive polyphenols and, the high bioaccessibility recovered for some of them, could be probably related to a hydrolysis process of more complex molecules.
The analysis of microbiota reveals a taxonomic shift of microbial population along olive extract administration and a possible modification of gut microbial metabolism.

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