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Proteomics of fruits and beverages

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The present review offers an overview about proteome investigation of fruits, alcoholic and non-alcoholic beverages via combinatorial peptide ligand libraries (CPLLs). The CPLLs methodology is able to capture the entire proteome, formed by abundant, low-abundance and trace proteins. CPLLs, coupled with mass spectrometry analysis, could represent a reliable analytical tool to obtain a specific proteomic fingerprint useful to attest food genuineness or adulteration during industrial processes before commercialization. The review reports the proteomic analysis performed on lemon, mango and Goji berries as regards fruits, on almond milk, orgeat syrup, cola drink and ginger ale, considering non-alcoholic drinks, and on beer, amaro Braulio, Cynar liqueur, French champagne and Branzi for alcoholic aperitifs.

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Introduction

In the past few years, the quality control of starting materials and final products has become very important in food technology and biotechnology [1] in order to asses food safety for consumers, to identify the presence of food allergens or toxins and to evaluate the influence of physiological activity and biological properties of food proteins and peptides [2••]. In order to defend consumers' health and to prevent food adulteration, due to fraudulent or deceptive practices in food processing, the European Union (UE) has issued rules on food safety and traceability by regulation of agricultural production, by control of production processes, by enforcing food labels concerning composition and origin [3]. For this reason the Food and Agriculture Organization of the United Nations (FAO) and the World Health Organization (WHO) carry out a wide range of activities including, but not limited to, the training on evaluation and safety assessment of pesticide residues [4], quality control of pesticide products [5] and principles of good agricultural practice. As recommended by Foodomics [6,7,2••], in order to asses food quality and consequently to maintain human health, an intensive collaboration among experts on different fields of food science and scientists of biomedical research is required to apply advanced analytical technologies of proteomics, genomics, peptidomics and metabolomics as suitable tools to control the declared geographical origin [8], the correct agricultural practices [9,10] and food components, preventing any adulteration [11] or alteration during production and storage [12,13••,14].

The interest in reliable and reproducible analytical methodologies to control food safety is increasing in relation with human health [15]: food is a rich source not only of proteins [16,17], lipids, sugars, carbohydrates, but also of micronutrients (minerals, vitamins, folic acid) and phytochemicals such as flavonoids [18–20], carotenoids [21], polyphenols [22,23] and antioxidants, fundamental for the comprehensive wellness of human beings [24,25••,26].

As concerns proteomics in nutrition [27••], quantitative proteomics has emerged as a new approach, providing an attractive opportunity to screen many metabolic pathways together with nucleic acid sequencing technologies [28••,29]. Research on fruit proteomics [30•], such as, for instance, strawberries, pears and grapes, has shown that a proteomic approach can potentially illustrate the species involved in fruit ripening and in the development of physiological disorders or allergies [31–34,12,35].

In this review, an overview of proteomics studies on fruits and on related beverages is reported to evaluate if proteomic profiles could be useful for investigation of food genuineness, of correctness of production protocols and storage conditions. In all cases reported, proteins were identified by mass spectrometry (MS) analysis after the treatment with combinatorial peptide ligand libraries (CPLLs), a suitable method to bring proteomes within the detection limits of the MS instrumentation. Briefly, CPLL is a collection of millions of hexapeptide ligands, each of them grafted covalently on beads, characterized by a great binding capacity for the capturing of proteins from the sample by enriching trace proteins and concomitantly reducing the concentration of abundant species [36–38]. The CPLLs technique was firstly applied to biological samples such as cerebral spinal fluid, human blood and serum, secondly to plant, foodstuffs and drinks: the present review describes the investigations on the last category.

The main objective is to gain a global understanding about the correlation of protein profiles with fruits or

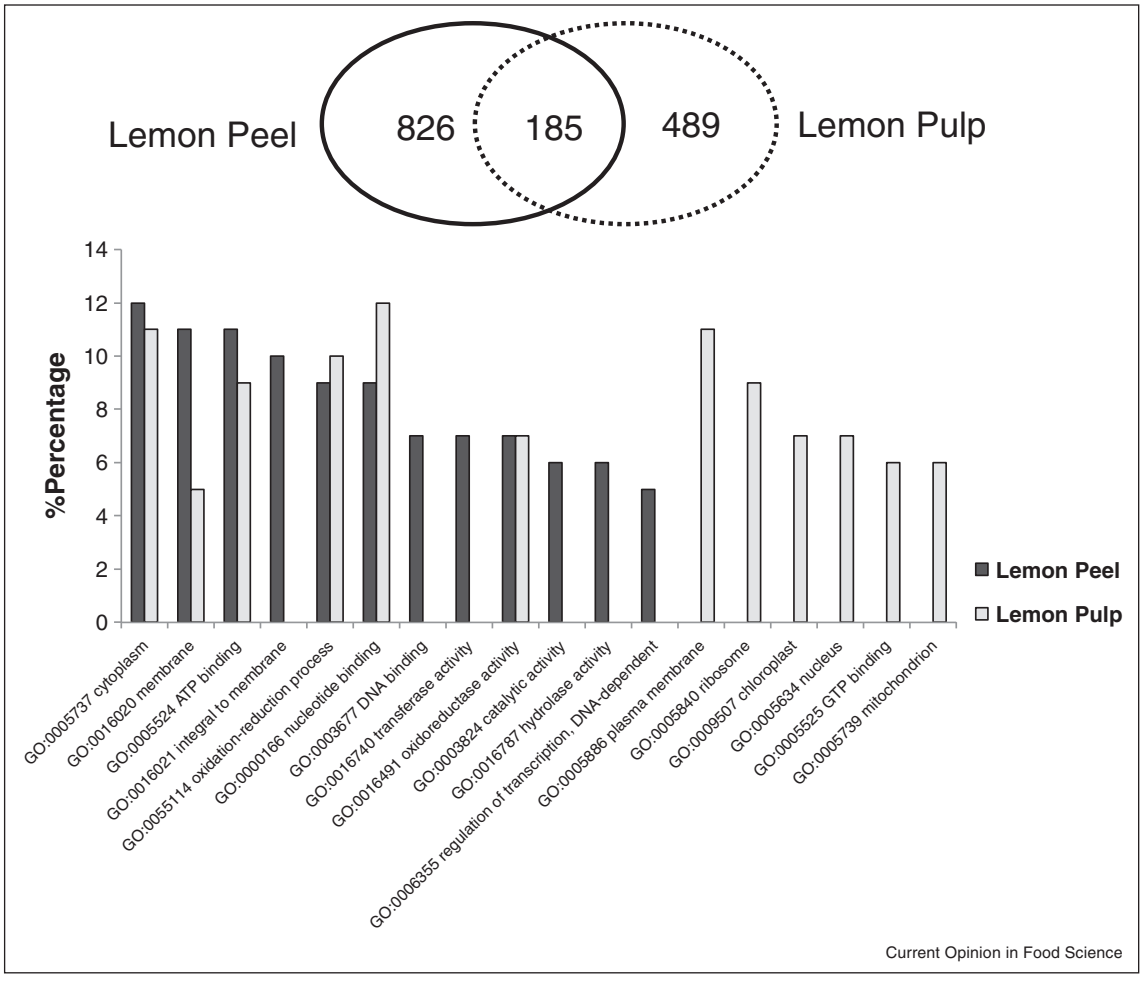
beverages quality in order to alert consumers about any possible adulteration, able to reduce nutritional values or to increase negative effects of food.

Fruit proteomics

Fruits are important sources of fiber, minerals, vitamins and other beneficial compounds such as antioxidants. Therefore modern fruit research focuses on promoting nutritional and health-related compounds [39]: large-scale application of proteomics in combination with phenotypical and physiological data is a particularly promising approach for characterizing fruit quality, thereby allowing the identification of biomarkers in breeding programs aiming at ameliorating fruit quality. New mass spectrometric techniques are being deployed as analytical platforms for the assessment of health, sensory, quality, and safety aspects of food, including fruits [40]. Although proteomic strategies were successfully established for allergen detection, identification, and characterization in fruits [41], more detailed and comprehensive characterization of specific peptides with antioxidant properties are required.

Considering the increasing importance of fruit proteomic for the correlation with nutrition properties, a first deep investigation was performed on the lemon proteome, by analysing separately peel and pulp samples [42]. Both lemon peel and pulp proteomes have been evaluated via prior capture with CPLLs at different pH values (2.2 and 7.2) and, via MS analysis, a total of 1011 unique gene products were identified in the peel extracts and 674 in the pulp (Figure 1, Venn diagram), thus substantially improving previous data reported on literature [43]. Considering that numerous allergenic proteins belong to low-abundance species, it is very important to have a reliable technology able to enrich trace components: this research has confirmed the presence of all known citrus allergens (non-specific lipid-transfer protein, profilin and germin-like protein) in lemon peel and pulp after CPLLs

Figure 1



Venn diagram comparing the total protein discovery of lemon peel and pulp. The biological functions of proteins are reported and compared in the histogram.