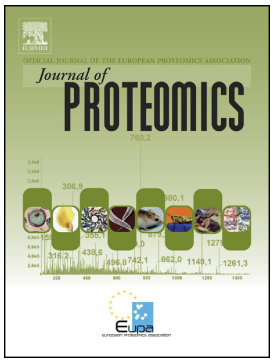

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Identification of chickpea seed proteins resistant to simulated *in vitro* human digestion

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Proteins and peptides able to resist gastrointestinal digestion and reach the intestinal mucosa have the potential to influence human health. Chickpea (*Cicer arietinum* L.) seed proteins are able to resist cooking (86.9% total protein) and/or *in vitro* simulated human digestion (15.9% total protein resists soaking, cooking and digestion with pepsin and pancreatin). To identify and characterize proteins resisting digestion we made use of different MS methodologies. The efficiency of several proteases (trypsin, AspN, chymotrypsin and LysC) was tested, and two technologies were employed (MALDI-TOF-TOF and LC-nESI-MS/MS). Digestion with trypsin and AspN were most successful for the identification of seed proteins. When analyzed by MALDI-TOF-TOF, trypsin allowed the identification of at least one protein in 60% of the polypeptide bands, while AspN allows the identification in 48%. The use of LC-ESI-MS/MS, allowed the identification of much more proteins/polypeptides from digested seeds (232 vs 17 using trypsin). The majority of the proteins found to be able to resist simulated digestion were members of the 7S vicilin and 11S legumin seed storage protein classes, which are reported to contain bio-active functions. In addition, we have found proteins that had not yet been described as potentially able to cause an impact on human health.

Significance:

This is the first proteomic study to analyze the effect of processing and simulated human gastrointestinal digestion on the proteome of chickpea seed. Chickpea is reported to have anti-nutritional effects as well as nutraceutical properties, so the identification and characterization of the proteins able to resist digestion is crucial to understand the targets underlying such properties.