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COMPARATIVE QUANTITATIVE IMMUNOPROTEOMIC STUDY OF RAW AND ROASTED PEANUT MAJOR ALLERGEN MODIFICATIONS

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Peanut allergy affects approximately up to 3 % of children and up to 2 % of the adult world population, causing reactions ranging from mild to severe. Major peanut allergens are well characterized but little is known about their post-translational modifications and even less is known about the influence of thermal treatment on their profile. Protein post-translational modification patterns may differ between raw and thermally treated peanuts, which could affect its functional properties, such as allergic potential. In this study we combined proteomic and immunological methods to characterize the modifications or proteoforms of four major peanut allergens - Ara h 1, Ara h 2, Ara h 3 and Ara h 6 in raw and roasted peanut. Bottom-up highresolution accurate mass spectrometry and a specialized proteomics software package to identify, map and compare modifications of major peanut allergens between differently treated peanut kernels. Modification-specific antibody western blot was used to confirm the presence of modifications major allergens both on extracts. Twenty different post-translational modifications in four prominent peanut allergens (Ara h 1-3, 6) were identified, while twelve were quantitatively compared between raw and roasted peanuts by high-resolution mass spectrometry and a proprietary proteomics software. post-translational modification specific antibodies confirmed the presence of these modifications in western-blots of raw and roasted peanuts. This study initiates appreciation of modifications and thermal processing affecting food quality, and development of state-of-the-art methodology in the risk assessment of allergen contamination.

Keywords: peanut allergens, post-translational modifications, quantitative profiling, proteomics, label free quantification

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