

SPECIAL GUEST EDITOR SECTION

Allergen Detection by Mass Spectrometry— The New Way Forward

The detection of allergens began with the use of methods such as immunoprecipitation techniques like the Ouchterlony test. Later, Western blotting was frequently used. However, these techniques are time- and cost-intensive, particularly for routine analysis in government and industry laboratories.

With the development of regulatory requirements for allergen labeling of foodstuffs in many countries worldwide, commercial ELISA kit manufacturers have produced several test kits that detect various allergens listed in the regulations. DNA-based applications like PCR or ligand-based probe-dependent amplification have also been developed for this purpose.

However, each methodology has its limitations. ELISA methods, for example, are prone to unspecific binding, giving rise to false positives, while some antibodies used in these same techniques do not recognize denatured proteins, giving rise to false negatives. In addition, only one analyte, e.g., one allergen, can be targeted with commercial ELISAs making it costly for use with composite foods in which the number of allergens potentially present can be high.

DNA techniques, such as PCR, can compensate for that. With these methods, multitarget analysis (typically up to four targets per analysis) can be achieved. However, DNA-based applications also have their own limitations. First, quantification is not easily possible. The major limitation, however, is that they detect a different substance class, i.e., DNA and not proteins. DNA can be differently distributed from proteins or can be completely absent while high quantities of allergy triggering proteins are still

present, as in the case of egg white. Other examples in which protein is in high abundance while DNA is in low abundance are milk and industrial protein concentrates. This technology can therefore give rise to false negatives, which is particularly concerning for the two major allergens, egg and milk.

As a consequence, and due to the progress made in MS analysis of proteins and peptides, several methods have been developed to overcome these limitations. MS combines several advantages: it directly detects peptides or proteins by mass/charge, and provides options for confirmatory approaches, clearly identifying amino acid sequences, e.g., by de novo sequencing. But one of the most important advantages is the capability of MS to detect multiple targets in the same analysis, thereby allowing for a multiscreening approach.

This special section of *J. AOAC Int.* describes the most recent progress of MS in the field of allergen detection. The manuscript by Haraszi et al. describes the specific problems of gluten detection and the advantages MS analysis can bring. Johnson et al. describe the best practice of allergen detection, suggesting guidelines for unique and specific identification of peptides related to allergens. The manuscripts by Monaci et al. and Lutter et al. describe the detection of milk allergens using different mass spectrometric instruments. The manuscript by Lutter et al. also demonstrates that quantification of target analytes is possible using MS, which is important to help assess exposure to undeclared allergens in the context of a health risk assessment. Finally, the manuscript of Heick et al. demonstrates the advantages of MS over ELISA in a multiple allergen detection technique,



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showing the inability to detect some allergens at higher concentrations using only ELISA methods.

These papers and the ongoing research of their authors demonstrate the growing progress of MS-based techniques in allergen detection, predicting that they will soon become standard for allergen testing, offering the allergen analytical community a broader spectrum of methods from which to choose.

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