Poster

METABARCODING-BASED AUTHENTICATION OF ETHNIC FOODS IN THE CONTEXT OF OFFICIAL CONTROL ACTIVITIES IN ITALY

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Ethnic foods are increasingly available on the European market, but their complex composition and frequently incomplete or inaccurate labelling may hinder traceability and pose risks to consumers. This study evaluated the potential of DNA metabarcoding (based on next-generation sequencing) as a screening tool for the authentication of imported ethnic foods collected in Italy within official control activities. Sixty-two pre-packed products collected in Tuscany and Latium, previously analysed by the Competent Authority using a validated and accredited DNA microarray method, were selected and re-analysed by metabarcoding. According to label information, 37 products contained ingredients of animal origin, while 25 were plant-based products in which animal DNA had previously been detected by microarray. Two primer pairs targeting the same hypervariable region of the mitochondrial 16S rRNA gene were selected to broaden taxonomic coverage across meat, poultry, fish and seafood species. Libraries were sequenced on an Illumina MiSeq platform; reads were processed using DADA2, and taxonomic assignment was performed by BLAST against GenBank, applying minimum identity and query coverage thresholds of 97% and 95%, respectively, and a 1% abundance cut-off. Mislabelling was assessed qualitatively by comparing detected animal taxa with declared ingredients.

Sequencing libraries were successfully obtained from all products. Among animal-based products, only 8/37 (21.6%) were consistent with label information, whereas 29/37 (78.4%) showed undeclared animal species, failure to detect one or more declared species, or both. Animal DNA was also confirmed in all 25 selected plant-based products. Undeclared fish was identified in 18/62 products (29.0%), while undeclared molluscs, mainly squid or scallop, were found in 10/62 (16.1%), highlighting potential allergen-related concerns. Metabarcoding frequently revealed complex and unexpected species profiles, including taxa not covered, or only broadly resolved, by targeted microarray analysis.

Although these research findings cannot be considered official control results and the approach remains qualitative because read abundance does not reliably reflect ingredient proportions, they demonstrate the value of metabarcoding for broad, simultaneous species screening in highly processed multi-ingredient foods. Following further optimisation and validation, including the definition of robust filtering criteria and integration with quantitative confirmatory methods, metabarcoding could strengthen risk-based surveillance, support fraud detection and improve consumer protection in the ethnic food sector.