Rapid and reliable species identification of scallops by MALDI-TOF Mass spectrometry

Roger Stephan¹, Noémie Oesterlé², Guido Vogel³, Valentin Pflüger³

¹Institute for Food Safety and Hygiene, Vetsuisse Faculty University of Zurich, Zurich, Switzerland; ²Bell Schweiz AG, Basel, Switzerland; ³Mabritec AG, Riehen, Switzerland

Key Findings

We evaluated the application of matrix-assisted laser desorption ionization-time of flight mass spectrometry (MALDI-TOF MS) for rapid species identification of scallop species (Pecten maximus/jacobei, Argopecten purpuratus, Mizuhopecten yessoensis, Zygochlamys patagonica, Placopesten magellanicus). The selected species are important in view of possible deceptions and mislabelling.

To this end, we developed a reference MS database library for these species.

For the target species the mass spectrometry-based identification scheme yielded identical results compared to a second independent identification system. All target samples were correctly identified and no non-target sample was misidentified. Our study demonstrates that MALDI-TOF-MS is a reliable and powerful tool for the rapid species identification of scallops.

Background

In the last years scallops have reached a considerable popularity and the import of scallops into the EU has increased about 20 % over the last five years from some 50.000 t to nearly 63.000 t in the year 2010 (Globefish, Highlights 2011). According to legislation only the scallop species Pecten jacobaeus (Mittelmeer-Pilgermuschel) and Pecten maximus (Grosse Pilgermuschel) can be labelled as „Jakobsmuscheln“.

Recent investigation of scallop products of various origins by determining the species using molecular biological techniques showed that the species had been mislabelled in a considerable proportion of samples (Neumann et al., 2012).

Method development and evaluation

The samples were used refrigerated (4° C) as well as frozen (3 days at -20° C). The protein extraction was performed with two different procedures: formic acid (25%) and formic acid (25%) followed by an additional defatting step (chloroform/methanol/formic acid). The extracts were analysed in two different matrices: sinapic acid and alphacyanoxydroxycinnamonic acid.

A first set of reference samples, already identified using a PCR-based DNA-analysis of mitochondrial DNA (Näumann et al., 2012) was used: five Pecten maximus; four Argopecten purpuratus; three Mizuhopecten yessoensis; one Zygochlamys patagonica; five Placopesten magellanicus (Figure 2). By MALDI-TOF MS, the different species provided reproducible and unique mass spectra profiles covering a wide molecular mass range (3000 to 30000Da) (Figure 3). Species-specific biomarker protein mass patterns (SARAMIS SuperSpectrum™ Anagonostik, Potsdam, Germany) were determined. For the reference samples the mass spectrometry-based identification scheme yielded identical results compared to the molecular based identification system (Figure 4).

Thereafter, a second set of 11 samples collected from retail level in Switzerland (most of them labeled as “Jakobsmuscheln”) was tested by MALDI-TOF MS. Facit- a high proportion of samples was mislabeled!