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

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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*, *Placopecten 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".

Figure 1:
A) Characteristic scallop shell and shell with adductor muscle and corail**.**
B)„Jakobsmuscheln" from retail level.

Recent investigation of scallop products of various origins by determining the species using molecular biological techniques showed that the species had been mislabeled 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 alphacyanohydroxycinnamon 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 *Placopecten 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™ Anagonstec, 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!

Results

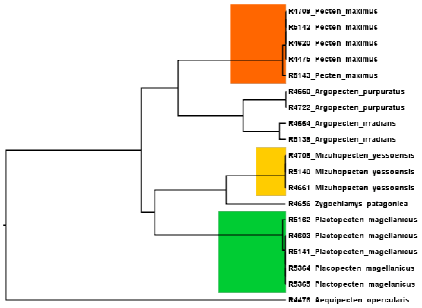

Figure 2: Mitochondrial DNA sequence based dendrogramm of the reference samples used.

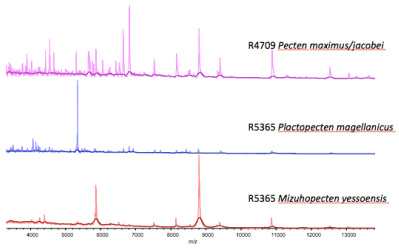

Figure 3: Species specific protein mass patterns

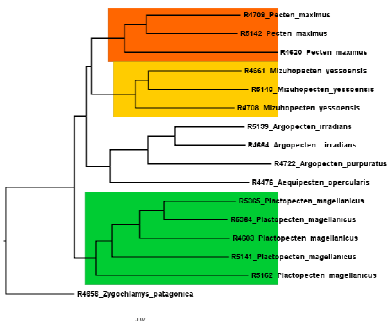

Figure 4: MALDI-TOF MS mass spectra based dendrogramm of the 16 reference samples (see Figure 2) tested.

Literature: Globefish, Highlights 2/2011; Näumann et al. (2012)Fischereiforsch. 59: 1–7.