Untargeted mass spectrometry-based proteomics for species and tissue identification in mixed feed and food samples

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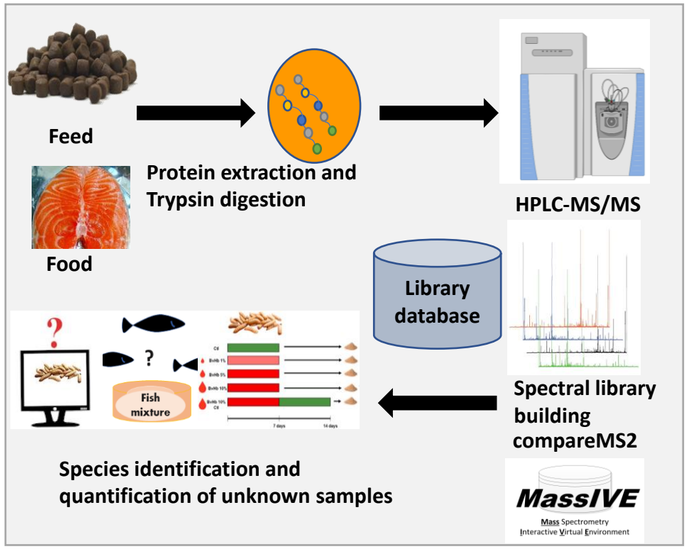
Introduction

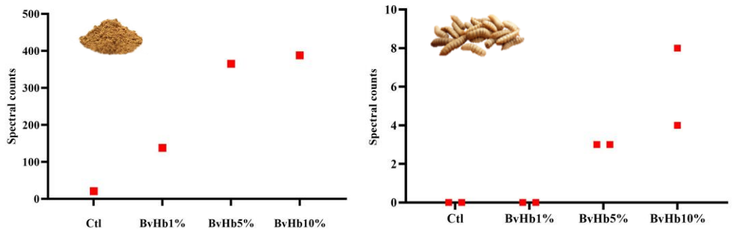
Due to globally rising demands for food and feed, novel proteinaceous ingredients are being introduced into our food systems on an increasing scale. This gives rise to novel challenges in relation to the detection of feed and food fraud and the determination of feed and food authenticity, respectively. In this context, the development and increased implementation of rapid, sensitive and robust molecular methods are key. However, progress in the application of such tools has been hampered by a general lack of well-annotated reference genomes of target species commonly used or newly introduced in feed or food preparations. Our group has been working on the development and implementation of untargeted mass spectrometry-based approaches in regulatory settings to identify, differentiate, and quantify proteic ingredients of animal and plant origin in various food and feed mixes without using any genomic information.

Methodology



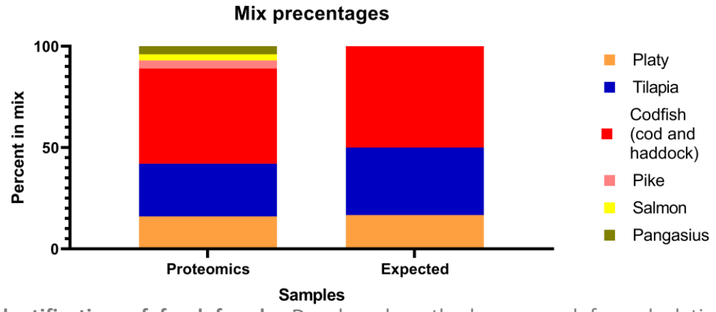
Results

Untargeted proteomics was used for food and feed authentication of processed animal proteins. Black solider fly larvae fed on prohibited substrates could be differentiated from conventionally fed insect species.



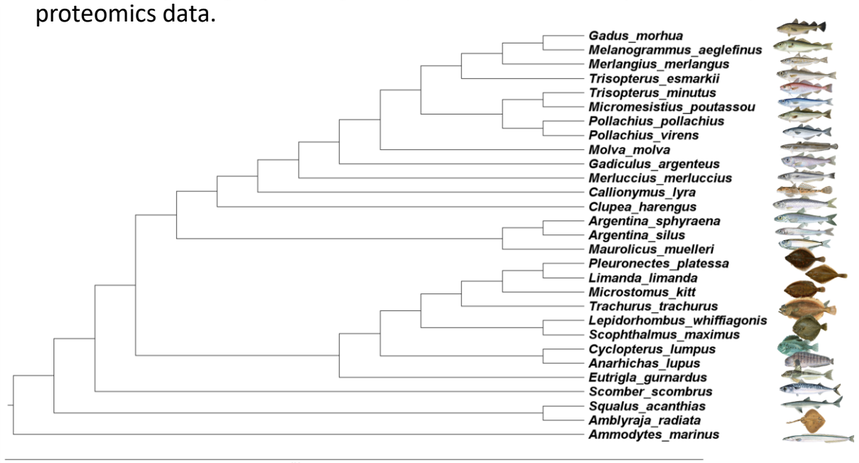
Absolute quantification of spectra matching against hemoglobin spectral library determined in the feeding media of black soldier fly larvae and the black solider fly larvae reared on the adulterated substrate at 1, 5 and 10% (w/w) (BvHb1%, BvHb5% and BvHb10%, respectively). *BvHb 10%: BvHb 10% for 7 days followed by Ctl diet for 7 additional days

Spectral library based approach successfully differentiates and authenticated 7 fish species both in pure fillet and mixed samples containing two or more fish species. Spectral libraries were created for fish species and percentages of fish in the mixture was calculated.



Identification of food frauds. Developed method was used for calculating percentages of species in fish mixture. This method can be used to authenticate processed fish products available in the market. Results indicated that for separation of cod and haddock (codfish) from gadoid family the approach is required to be modified in future studies.

29 fish species from the North sea were differentiated as per the molecular phylogeny using only tandem mass spectrometry-based proteomics data.



Fish species differentiation using compareMS2 Version 2.0.0-alpha for direct comparison of HPLC-MS/MS tandem mass spectrometric data. Molecular phylogenetic tree indicate that fish species were separated as per the taxonomic classification.

Conclusions

The untargeted proteomics spectral library based approach implemented in our laboratory was shown to be capable of both species and tissues specific identification of proteinaceous food and feed ingredients including processed animal proteins (PAP), insect proteins, plant, mammalian and fish proteins. Moreover, this approach is also suitable for allergen detection.

Literature cited and aknowledgments

MultiOmicsTools. Development of hight hroughput multiomics tools for regulatory science Nærings-ogfiskeridepartementet(NFD) funded project

- https://pubs.acs.org/doi/10.1021/acs.jafc.5b05322
- https://github.com/524D/compareMS2
- https://artsdatabanken.no/taxon
- https://fish-commercial-names.ec.europa.eu/

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