Determination of transport properties and mechanistic modeling of the coupled salt and water transport during osmotic dehydration of salmon induced by dry salting

A mechanistic forward osmosis model based on nonideal principles and the continuity equation was adapted to the dry salting of salmon. The novelty of this model is that the water loss is coupled to the salt uptake by means of the activity gradient. Consequently, besides the primarily desired predictive purposes, the model also explains why the ion uptake triggers the osmotic dehydration. The determination of the model parameters, as well as the validation of the model was carried out by comparing the results of the simulations with experimental salt and water concentration distributions. The good predictions of the model allow the establishment of a tool to have a better control of the time the salting process must last to meet both organoleptic and safety requirements. Additionally, it is transversally applicable to other food matrices, and by extension, to other engineering situations involving dehydration induced by ion uptake.

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Contributors: Martinez Lopez, B., Bertelsen, N. W., Jessen, F.
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Foam based on fish skin collagen by-product: a colloidal approach

General information
Publication status: Published
Organisations: National Food Institute, Research group for Food Production Engineering, Danish Technological Institute, Marinova A/S
Corresponding author: Casanova, F.
Contributors: Casanova, F., Mohammadifar, M. A., Kobbelgaard, S., Jakobsen, G., Jessen, F.
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Foaming and interfacial properties of gelatin from fish skin

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Organisations: National Food Institute, Research group for Food Production Engineering
Corresponding author: Casanova, F.
Contributors: Casanova, F., Mohammadifar, M. A., Jessen, F.
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Publication date: 2019
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Event: Poster session presented at 8th International Symposium on Food Rheology and Structure - ISFRS , Zürich, Switzerland.
Mechanistic modelling of the coupled salt and water transport in herring during brining and curing

Salting of fish tissue triggers a water movement to equilibrate the activity gradient. A mechanistic model that can predict the development of salt and water concentration as well as the water activity distributions, was validated by developing an experimental methodology that allows the access to the salt and water concentration distributions at any stage of the process. The model succeeded on offering reasonable predictions, with average RMSEs of 0.019 and 0.033kgkg⁻¹ for the salt and water concentration distributions, and 0.022 for the water activity; as well as a mathematical framework that is independent of the salting conditions (e.g. brining, curing), which helps to understand why the system behaves the way it does. Additionally, it allows the establishment of a tool to have a better control of the salting time in order to ensure both organoleptic and safety requirements.

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Contributors: Laub-Ekgreen, M. H., Jessen, F., Martinez Lopez, B.
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Research output: Contribution to journal – Journal article – Annual report year: 2019 › Research › peer-review

Proteomic and microscopic approaches in understanding mechanisms of shell-loosening of shrimp (Pandalus borealis) induced by high pressure and protease

Shell-loosening is of importance in facilitating shrimp peeling. In this study, enzyme and high pressure (HP) improved the shell-loosening at different degrees, which were observed as gaps by microscopy. The shell-loosening gap induced by an endoprotease with broad specificity (Endocut-03L, 53 μm) was much higher than that induced by HP at 100 MPa (HP100, 12 μm), followed by an endoprotease with high specificity (Tail21, 8 μm), and HP at 600 MPa (HP600, 5 μm). The degree of shell-loosening was found to be correlated to the extent of protein changes that were obtained by 2D gel electrophoresis. Shell-loosening due to HP100 and Endocut-03L was mainly caused by physical and enzymatic degradation of high molecular-weight proteins in shell and epidermis and subsequent loss of degradation products, disrupting the structure of muscle-shell connection. However, HP100 was less effective than Endocut-03L due to its stabilizing effect on the shell collagen, lowering its shell-loosening effect.

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Organisations: National Food Institute, Research group for Food Production Engineering, University of Copenhagen, Royal Greenland A/S
Corresponding author: Orlien, V.
Contributors: Dang, T. T., Jessen, F., Martens, H. J., Gringer, N., Olsen, K., Bøknæs, N., Orlien, V.
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Publication date: 2019
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Publication Information
Journal: Food Chemistry
Volume: 289
Enzyme-assisted peeling of cold water shrimps (Pandalus borealis)

An enzymatic method to facilitate the peeling of cold water shrimps (Pandalus borealis) was developed. The protease solutions were used to mature the shrimps to promote shell-loosening prior to peeling. The efficiency of peeling enzyme-treated shrimps was evaluated by a new quantitative measurement based on the tensile force, presented as a peelability profile. It was found that enzymatic maturation efficiently improved the peelability of shrimps. The factors affecting the peelability of the enzyme-matured shrimps were the type of enzyme, enzyme concentration and maturation duration, while changes in pH had no impact. Maturation of shrimps in solutions of the endoproteases Endocut-01L (180 NU/g) and Endocut-03L (60 U/g) and the exoprotease Exocut-A0 (100 U/g) resulted in better peelability compared to shrimps matured in endoprotease Tail21 (65 U/mL) and 2% NaCl. A combination of 0.25% Endocut-03L and 0.25% Exocut-A0 for 20 h resulted in the best peeling of shrimps (100% completely peeled shrimps, 3 mJ/g work and 89% meat yield). Reuse of the enzyme solution was possible due to a 95% retention rate of proteolytic activity after two 20-h cycles of maturation. The studied enzymatic maturation offered a better shrimp product with respect to texture and color in comparison with an industrial brine-matured reference, i.e., ~22% higher redness and ~31% higher hardness. Industrial relevance: Enzymatic maturation is an attempt made as a pre-treatment to facilitate the removal of the shell from meat of shrimp. This approach would benefit the shrimp processing industry by 1) enhancing peeling efficiency that includes least efforts to remove the shell, high rate of completely peeled shrimps and high meat yield; 2) shortening the duration of maturation but still sufficiently loosening the shell for machine peeling; 3) performing as a chemical-free peeling aid, which may increase the preference of consumers over chemical compounds; and 4) being environmentally friendly since disposal of enzyme waste is harmless to the environment.

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Corresponding author: Orlien, V.
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Publication information
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Scopus rating (2018): CiteScore 4.4 SJR 1.43 SNIP 1.388
Web of Science (2018): Impact factor 4.085
Web of Science (2018): Indexed yes
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Research output: Contribution to journal › Journal article – Annual report year: 2018 › Research › peer-review

A quantitative method to measure and evaluate the peelability of shrimps (Pandalus borealis)

A novel, standardized method has been developed in order to provide a quantitative description of shrimp peelability. The peeling process was based on the measure of the strength of the shell-muscle attachment of the shrimp using a texture analyzer, and calculated into the peeling work. The self-consistent method, insensitive of the shrimp size, was proven valid
for assessment of ice maturation of shrimps. The quantitative peeling efficiency (peeling work) and performance (degree
of shell removal) showed that the decrease in peeling work correlated with the amount of satisfactory peeled shrimps,
indicating an effective weakening of the shell-muscle attachment. The developed method provides the industry with a
quantitative analysis for measurement of peeling efficiency and peeling performance of shrimps. It may be used for
comparing different maturation conditions in relation to optimization of shrimps peeling.

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Corresponding author: Gringer, N.
Contributors: Gringer, N., Dang, T. T., Orlien, V., Olsen, K., Bøknæs, N., Jessen, F.
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Web of Science (2018): Indexed yes
Original language: English
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Research output: Contribution to journal – Annual report year: 2018 – Research – peer-review

Emerging and potential technologies for facilitating shrimp peeling: A review
Ready-to-eat shrimp processing is challenging due to the complex biological design with the shell tightly connected to the
meat. Several techniques have been developed to weaken or loosen this connection, thus facilitating the subsequent
peeling. The loosening process is typically undertaken by maturing the shrimps on ice or in brine, which requires several
days, consequently risking loss in food quality and safety. To overcome those issues, developing novel technologies that
not only assist the shell loosening but also retain the meat quality, safety and yield, is of paramount importance. This
article reviews some essential characteristics of shrimp, the current methods of maturation, the use of the emerging
technologies (high pressure, microwave, ultrasound, and enzyme) to facilitate the peeling of foods and clarify the potential
of using them in shrimp shell removal. Industrial relevance During the production of peeled products, the shrimp
processing industry has suffered from drawbacks of the traditional ice/brine maturation processes - a step facilitating the peeling.
The drawbacks include yield loss, reduction of organoleptic quality, risk of microorganisms, time consuming issue and
discontinuous process due to a long time soaking in maturing tanks. Therefore the need for seeking alternative methods to
replace the traditional long maturation stages has grown, that address the future trends in sustainable processing of ready-to-eat
shrimps. Emerging technologies e.g. high pressure, enzyme, ultrasound and microwave can potentially become the
alternatives since they have strong peeling effects on lobsters, crabs, bivalve mollusks, eggshells, human skin, fruits and
vegetables. Also these technologies offer benefits such as short process time, retained nutritional and sensorial
characteristics, energy and water efficiency which all promise higher profits for the shrimp industry.

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Journal: Innovative Food Science and Emerging Technologies
Volume: 45
ISSN (Print): 1466-8564
Facilitating shrimp (Pandalus borealis) peeling by power ultrasound and proteolytic enzyme

The potential of power ultrasound (24-kHz frequency) as an individual treatment and in combination with proteolytic enzyme to promote the shell-loosening of cold-water shrimp (Pandalus borealis) was investigated. Textural properties of shrimp were highly dependent on temperature control during the ultrasonic process (27.6-μm amplitude, 120min duration and 0.9-s pulse), while the peelability of shrimp monitored as peeling work, meat yield and proportion of completely peeled shrimp were less dependent on the temperature. Increasing amplitude (0–46μm) and time (0–45min) of ultrasound prior to enzymatic maturation (0.5% Endocut-03L, 6h, and 3°C) increased the peelability of shrimp. The parallel combination of ultrasound and enzyme (18.4-μm amplitude, 0.9-s pulse, 0.5% Endocut-3L, 3-h and 4-h duration, and T≤5°C) considerably improved the shrimp peelability without detrimental effect on the texture and color of shrimp. Ultrasound was found to inactivate proteolytic enzyme in solution and to modify the structural properties of shrimp shells. From scanning electron micrographs (SEM), we proposed a mechanism for the ultrasound-enzyme-induced shell-loosening based on ultrasonic shell surface erosion and enzyme diffusion. Cavitation bubbles generated from sound waves pitted the surface of shrimp shell, generating pathways for enzyme diffusion into the muscle-shell attachment.
salt values. A principal component analysis performed on the NIR spectra showed that the first principal component described the evolution of the spectra according to the determined salt values. A partial least-squares regression model between the selected region of the NIR spectra and the salt content of the fish gave a correlation coefficient of 0.81 and a prediction error (RMSECV) of 0.41g/100g with the prerequisite that salt concentration in fish and marinade was in equilibrium. The results indicate that NIR spectroscopy can be used as a fast and non-destructive method for assessing the salt concentration in fish during the herring marinating process in order to ensure product safety.

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Web of Science (2018): Impact factor 3.714
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Keywords: Marinated herring, Food safety, Salt, Multivariate calibration, NIR spectroscopy
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Research output: Contribution to journal › Journal article – Annual report year: 2018 › Research › peer-review

The influence of processing conditions on the weight change of single herring (Clupea herengus) fillets during marinating
One of the main issues in the manufacturing of marinated herring is the variation in yield, which in turn, is affected by the processing conditions and the variance in fat content. In the present work, we study these effects on individual herring fillets, with focus on the intermediate brining process. Brining time, brine concentration, marinade composition and storage time were varied. For brine concentrations 8%, 16% and 26%, the diffusion coefficient was $2.31 \times 10^{-9}$ m$^2$ s$^{-1}$, which was used for model development of salt change prediction in herring during brining. Conducting experiments on single fillets revealed a correlation between the fat content and the weight change after 35 days of marinating. The greatest change occurred within the first few days and only minor changes were seen during the storage period of up to one year. These results contribute to a better understanding of the herring marinating process, which can aid the optimization process in the industry.

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Organisations: National Food Institute, Research group for Food Production Engineering, Technical University of Denmark
Contributors: Laub-Eksgreen, M. H., Martinez Lopez, B., Frosch, S., Jessen, F.
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Web of Science (2018): Impact factor 3.579
Web of Science (2018): Indexed yes
Original language: English
Keywords: Brining, Herring, Marinating, Modeling, Weight change, Yield
DOIs:
Discovery, cloning and characterisation of proline specific prolyl endopeptidase, a gluten degrading thermo-stable enzyme from Sphaerobacter thermophiles

Gluten free products have emerged during the last decades, as a result of a growing public concern and technological advancements allowing gluten reduction in food products. One approach is to use gluten degrading enzymes, typically at low or ambient temperatures, whereas many food production processes occur at elevated temperature. We present in this paper, the discovery, cloning and characterisation of a novel recombinant thermostable gluten degrading enzyme, a proline specific prolyl endopeptidase (PEP) from Sphaerobacter thermophiles. The molecular mass of the prolyl endopeptidase was estimated to be 77 kDa by using SDS-PAGE. Enzyme activity assays with a synthetic dipeptide Z-Gly-Pro-p-nitroanilide as the substrate revealed that the enzyme had optimal activity at pH 6.6 and was most active from pH 5.0-8.0. The optimum temperature was 63 °C and residual activity after one hour incubation at 63 °C was higher than 75 %. The enzyme was activated and stabilized by Co2+ and inhibited by Mg2+, K+ and Ca2+ followed by Zn2+, Na+, Mn2+, Al3+, and Cu2+. The Km and kcat values of the purified enzyme for different substrates were evaluated. The ability to degrade immunogenic gluten peptides (POQLPYPOQQLPY (a-gliadin) and SQQQFPQPQPPQQP (γ-hordein)) was also confirmed by enzymatic assays and mass spectrometric analysis of cleavage fragments. Addition of the enzyme during small scale mashing of barley malt reduced the gluten content. The findings here demonstrate the potential of enzyme use during mashing to produce gluten free beer, and provide new insights into the effects of proline specific proteases on gluten degradation.
that the identification of these proteins and their significance for the measured texture will contribute to further understanding of the Atlantic salmon muscle texture.

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Organisations: National Food Institute, Research group for Food Production Engineering, Novo Nordisk Foundation Center for Biosustainability, ChO Core, iLoop, University of Iceland
Contributors: Johansson, G. Ø., Frosch, S., Gudjónsdóttir, M., Wulff, T., Jessen, F.
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Web of Science (2017): Indexed yes
Original language: English
Keywords: Biological Materials, Biology, Chemistry, Organic Compounds, Statistical Methods, Optical Variables Measurements, PLS, prediction model, proteome, Salmo salar, tandem mass spectrometry, texture, two-dimensional electrophoresis (2DE), Electrophoresis, Forecasting, Mass spectrometry, Molecular biology, Multivariant analysis, Muscle, Spectrometry, Textures, Developing solutions, Dipeptidyl peptidase, Heat shock protein 70, Multivariate data analysis, Prediction model, Tandem mass spectrometry, Two-dimensional electrophoresis (2DE), Proteins

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**Antioxidant activity of cod (Gadus morhua) protein hydrolysates: Fractionation and characterisation of peptide fractions**
This study aimed to characterise peptide fractions (>5 kDa, 3–5 kDa and <3 kDa) with antioxidative activity obtained from a cod protein hydrolysate. The free amino acids in all fractions were dominated by Ala, Gly, Glu and Ser. The total amino acid composition had high proportions of Lys, Ala and Glu. The 3-5 kDa and <3 kDa fractions were further fractionated by size exclusion chromatography. All sub-fractions showed high Fe2+ chelating activity. The DPPH radical-scavenging activity of the 3–5 kDa fraction was exerted mainly by one sub-fraction dominated by peptides with masses below 600 Da. The DPPH radical-scavenging activity of the <3 kDa fraction was exerted by sub-fractions with low molecular weight. The highest reducing power was found in a sub-fraction containing peptides rich in Arg, Tyr and Phe. Both free amino acids and low molecular weight peptides thus seemed to contribute to the antioxidative activity of the peptide fractions, and Tyr seemed to play a major role in the antioxidant activity.

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Organisations: National Food Institute, Research group for Food Production Engineering, Research group for Bioactives – Analysis and Application, University of Copenhagen
Contributors: Farvin Habebullah, S., Andersen, L. L., Otte, J., Nielsen, H. H., Jessen, F., Jacobsen, C.
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Bioactive compounds in commercial nitrite-cured cooked pork products

General information
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Organisations: National Food Institute, Research group for Food Production Engineering, Research group for Analytical Food Chemistry
Contributors: Pedersen, S. T., Duedahl-Olesen, L., Jessen, F.
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Event: Poster session presented at First Food Chemistry Conference - Shaping the Future of Food Quality, Health and Safety, Amsterdam, Netherlands.
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Biological variation of the raw material and processing conditions affect the yield and quality of fast-marinated herring

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Contributors: Ekgreen, M. H., Jørgensen, B. M., Martinez Lopez, B., Frosch, S., Jessen, F.
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Effect of sodium bicarbonate and varying concentrations of sodium chloride in brine on the liquid retention of fish (Pollachius virens L.) muscle: High quality low salt saithe muscle

BACKGROUND Negative health effects associated with excessive sodium (Na) intake have increased the demand for tasty low-Na products (<2% NaCl) rather than traditional heavily salted fish products (~20% NaCl). This study investigates the causes of improved yield and liquid retention of fish muscle brined with a combination of salt (NaCl) and sodium bicarbonate (NaHCO3).

RESULTS Water characteristics and microstructure of saithe (Pollachius virens L.) muscle brined in solutions of NaCl and NaHCO3 or NaCl alone were compared using low-field nuclear magnetic resonance (LF-NMR) T2 relaxometry, microscopy, salt content, liquid retention and colorimetric measurements. Saithe muscle was brined for 92 h in 0, 30, 60, 120 or 240 g kg−1 NaCl or the respective solutions with added 7.5 g kg−1 NaHCO3. NaHCO3 inclusion improved the yield in solutions ranging from 0 to 120 g kg−1 NaCl, with the most pronounced effect being observed at 30 g kg−1 NaCl. The changes in yield were reflected in water mobility, with significantly shorter T2 relaxation times in all corresponding brine concentrations. Salt-dependent microstructural changes were revealed by light microscopy, where NaHCO3 supplementation resulted in greater intracellular space at 30 and 60 g kg−1 NaCl. CONCLUSION Sodium bicarbonate addition to low-salt solutions can improve yield and flesh quality of fish muscle owing to altered water mobility and wider space between the muscle cells.
Growth promotion in pigs by oxytetracycline coincides with down regulation of serum inflammatory parameters and of hibernation-associated protein HP-27

The growth promoting effect of supplementing animal feed with antibiotics like tetracycline has traditionally been attributed to their antibiotic character. However, more evidence has been accumulated on their direct anti-inflammatory effect during the last two decades. Here we used a pig model to explore the systemic molecular effect of feed supplementation with subtherapeutic levels of oxytetracycline (OTC) by analysis of serum proteome changes. Results showed that OTC promoted growth, coinciding with a significant down regulation of different serum proteins related to inflammation, oxidation and lipid metabolism, confirming the anti-inflammatory mechanism of OTC. Interestingly, apart from the classic acute phase reactants also down regulation was seen of a hibernation associated plasma protein (HP-27), which is to our knowledge the first description in pigs. Although the exact function in non-hibernators is unclear, down regulation of HP-27 could be consistent with increased appetite, which is possibly linked to the anti-inflammatory action of OTC. Given that pigs are good models for human medicine due to their genetic and physiologic resemblance, the present results might also be used for rational intervention in human diseases in which inflammation plays an important role such as obesity, type 2 diabetes and cardiovascular diseases.
Interactions between Surfactants in Solution and Electrospun Protein Fibers: Effects on Release Behavior and Fiber Properties

Intermolecular interaction phenomena occurring between endogenous compounds, such as proteins and bile salts, and electrospun compounds are so far unreported, despite the exposure of fibers to such biorelevant compounds when applied for biomedical purposes, e.g., tissue engineering, wound healing, and drug delivery. In the present study, we present a systematic investigation of how surfactants and proteins, as physiologically relevant components, interact with insulin-loaded fish sarcoplasmic protein (FSP) electrospun fibers (FSP-Ins fibers) in solution and thereby affect fiber properties such as accessible surface hydrophilicity, physical stability, and release characteristics of an encapsulated drug. Interactions between insulin-loaded protein fibers and five anionic surfactants (sodium taurocholate, sodium taurodeoxycholate, sodium glycocholate, sodium glycodeoxycholate, and sodium dodecyl sulfate), a cationic surfactant (benzalkonium chloride), and a neutral surfactant (Triton X-100) were studied. The anionic surfactants increased the insulin release in a concentration-dependent manner, whereas the neutral surfactant had no significant effect on the release. Interestingly, only minute amounts of insulin were released from the fibers when benzalkonium chloride was present. The FSP-Ins fibers appeared dense after incubation with this cationic surfactant, whereas high fiber porosity was observed after incubation with anionic or neutral surfactants. Contact angle measurements and staining with the hydrophobic dye 8-anilino-1-naphthalenesulfonic acid indicated that the FSP-Ins fibers were hydrophobic, and showed that the fiber surface properties were affected differently by the surfactants. Bovine serum albumin also affected insulin release in vitro, indicating that also proteins may affect the fiber performance in an in vivo setting.

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Organisations: National Food Institute, Research group for Nano-Bio Science, Research group for Food Production Engineering, University of Copenhagen
Contributors: Boutrup Stephansen, K., García-Díaz, M., Jessen, F., Chronakis, I. S., Nielsen, H. M.
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Web of Science (2016): Impact factor 4.44
Web of Science (2016): Indexed yes
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Research output: Contribution to journal › Journal article – Annual report year: 2016 › Research › peer-review

Non-invasive volume estimation of fish fillets/cutlets using structured light

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Organisations: National Food Institute, Research group for Food Production Engineering
Contributors: Skytte, J. L., Ekgreen, M. H., Jessen, F.
Number of pages: 1
Bioactive protein-based nanofibers interact with intestinal biological components resulting in transepithelial permeation of a therapeutic protein

Proteins originating from natural sources may constitute a novel type of material for use in drug delivery. However, thorough understanding of the behavior and effects of such a material when processed into a matrix together with a drug is crucial prior to further development into a drug product. In the present study the potential of using bioactive electrospun fish sarcoplasmic proteins (FSP) as a carrier matrix for small therapeutic proteins was demonstrated in relation to the interactions with biological components of the intestinal tract. The inherent structural and chemical properties of FSP as a biomaterial facilitated interactions with cells and enzymes found in the gastrointestinal tract and displayed excellent biocompatibility. More specifically, insulin was efficiently encapsulated into FSP fibers maintaining its conformation, and subsequent controlled release was obtained in simulated intestinal fluid. The encapsulation of insulin into FSP fibers provided protection against chymotrypsin degradation, and resulted in an increase in insulin transport to around 12% without compromising the cellular viability. This increased transport was driven by interactions upon contact between the nanofibers and the Caco-2 cell monolayer leading to the opening of the tight junction proteins. Overall, electrospun FSP may constitute a novel material for oral delivery of biopharmaceuticals.

General information
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Design and characterization of self-assembled fish sarcoplasmic protein-alginate nanocomplexes

Macrostructures based on natural polymers are subject to large attention, as the application range is wide within the food and pharmaceutical industries. In this study we present nanocomplexes (NCXs) made from electrostatic self-assembly between negatively charged alginate and positively charged fish sarcoplasmic proteins (FSP), prepared by bulk mixing. A concentration screening revealed that there was a range of alginate and FSP concentrations where stable NCXs with similar properties were formed, rather than two exact concentrations. The size of the NCXs was 293 +/- 3 nm, and the zeta potential was -42 +/- 0.3 mV. The NCXs were stable in water, gastric buffer, intestinal buffer and HEPES buffered glucose, and at all pH values from 2 to 9 except pH 3, where they aggregated. When proteolytic enzymes were present in the buffer, the NCXs were degraded. Only at high concentrations the NCXs caused a decreased viability in HeLa and U2OS cell lines. The simple processing procedure and the high stability of the NCXs, makes them excellent candidates for use in the food and pharmaceutical industry. (C) 2015 Elsevier B.V. All rights reserved.

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Organisations: National Food Institute, Research group for Nano-Bio Science, Research group for Food Production Engineering, Technical University of Denmark, University of Copenhagen, University of Münster
Contributors: Boutrup Stephansen, K., Mattebjerg, M. A., Wattjes, J., Milisavljevic, A., Jessen, F., Qvortrup, K., Goycoolea, F. M., Chronakis, I. S.
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Growth hormone transgenesis influences muscle proteome of Coho salmon (Oncorhynchus kisutch)

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Organisations: National Food Institute, Research group for Food Production Engineering, University of Aberdeen, Fisheries and Oceans Canada
Contributors: Jessen, F., Causey, D. R., Macqueen, D. J., Devlin, R. H.
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Publication date: 2015
Peer-reviewed: Yes
Event: Poster session presented at 5th Trans-Atlantic Fisheries Technology conference (45th WEFTA meeting), Nantes, France.
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Interactions between electrospun fibers and the surrounding biological environment; cells and small molecules

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Organisations: National Food Institute, Research group for Nano-Bio Science, Research group for Food Production Engineering, University of Copenhagen
Contributors: Stephansen, K., García-Díaz, M., Jessen, F., Nielsen, H. M., Chronakis, I. S.
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Poster presentation
Research output: Contribution to conference

Proteomanalyse: To-dimensjonal gelelektroforese av Nordsjøsild i forhold til modningstid

General information
Publication status: Published
Organisations: National Food Institute, Research group for Food Production Engineering, Nofima
Contributors: Jessen, F., Skåra, T.
Number of pages: 11
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Publication information
Place of publication: Tromsø
Publisher: Nofima
The effects of eating marine- or vegetable-fed farmed trout on the human plasma proteome profiles of healthy men

Most human intervention studies have examined the effects on a subset of risk factors, some of which may require long-term exposure. The plasma proteome may reflect the underlying changes in protein expression and activation, and this could be used to identify early risk markers. The aim of the present study was to evaluate the impact of regular fish intake on the plasma proteome. We recruited thirty healthy men aged 40 to 70 years, who were randomly allocated to a daily meal of chicken or trout raised on vegetable or marine feeds. Blood samples were collected before and after 8 weeks of intervention, and after the removal of the twelve most abundant proteins, plasma proteins were separated by two-dimensional gel electrophoresis. Protein spots <66 kDa with a pI >4.3 visualised by silver staining were matched by two-dimensional imaging software. Within-subject changes in spots were compared between the treatment groups. Differentially affected spots were identified by matrix-assisted laser desorption ionisation-time of flight/time of flight MS and the human Swiss-Prot database. We found 23/681 abundant plasma protein spots, which were up- or down-regulated by the dietary treatment (P<0.05, q<0.30), and eighteen of these were identified. In each trout group, ten spots differed from those in subjects given the chicken meal, but only three of these were common, and only one spot differed between the two trout groups. In both groups, the affected plasma proteins were involved in biological processes such as regulation of vitamin A and haem transport, blood fibrinolysis and oxidative defence. Thus, regular fish intake affects the plasma proteome, and the changes may indicate novel mechanisms of effect.

Triton X-114 cloud point extraction to subfractionate blood plasma proteins for two-dimensional gel electrophoresis

A simple and reproducible procedure for enrichment of a plasma protein subfraction suitable for two-dimensional polyacrylamide gel electrophoresis (2DE) was developed, using a Triton X-114-based cloud point extraction (CPE). Appropriate conditions for such a CPE procedure were found by SDS-PAGE to be a plasma protein concentration of about 10mg/ml in 3% (w/v) Triton X-114. 2DE of proteins obtained by CPE of 400μl of human plasma revealed about 200 spots constituting a spot pattern very different from the pattern of total plasma. The CPE procedure only had a limited contribution to the technical variation. Identification of about 60 spots, representing only 22 proteins, revealed that several
proteins in the obtained subfraction were present in more isoforms or modifications. Among these were apolipoproteins (A-1, D, E, L1, and M), haptoglobin-related protein, phosphatidylcholine-sterol acyltransferase, serum amyloid A, and serum paraoxonase/arylesterase 1, which are proteins of a hydrophobic nature, as in plasma they relate to lipoprotein particles. Thus, Triton X-114-based CPE is a simple plasma prefractionation tool, attractive for detailed 2DE studies of hydrophobic plasma proteins and their isoforms or modifications.

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Contributors: Jessen, F., Wulff, T.
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Research output: Contribution to journal › Journal article – Annual report year: 2015 › Research › peer-review

**Antioxidant activity of Cod (Gadus morhua) protein hydrolysates: In vitro assays and evaluation in 5% fish oil-in-water emulsion**
Cod protein hydrolysates were fractionated according to the molecular mass into three fractions of >5kDa, 3–5kDa and

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Organisations: National Food Institute, Division of Industrial Food Research, Marinova A/S
Contributors: Farvin, S., Andersen, L. L., Nielsen, H. H., Jacobsen, C., Jakobsen, G., Johansson, I., Jessen, F.
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Web of Science (2014): Impact factor 3.391
Web of Science (2014): Indexed yes
Original language: English
Keywords: Cod protein hydrolysates, Antioxidant, Fish oil, Emulsion
DOIs:
10.1016/j.foodchem.2013.03.075
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Source-ID: n::oai:DTIC-ART:elsevier/426429245::34772
Research output: Contribution to journal › Journal article – Annual report year: 2014 › Research › peer-review
Bioactive electrospun fish sarcoplasmic proteins as a drug delivery system
Nano-microfibers were made from cod (Gadus morhua) sarcoplasmic proteins (FSP) (M_w< 200 kDa) using the electrospinning technique. The FSP fibers were studied by scanning electron microscopy, and the fiber morphology was found to be strongly dependent on FSP concentration. Interestingly, the FSP fibers were insoluble in water. However, when exposed to proteolytic enzymes, the fibers were degraded. The degradation products of the FSP fibers proved to be inhibitors of the diabetes-related enzyme DPP-IV. The FSP fibers may have biomedical applications, among others as a delivery system. To demonstrate this, a dipeptide (Ala-Trp) was encapsulated into the FSP fibers, and the release properties were investigated in gastric buffer and in intestinal buffer. The release profile showed an initial burst release, where 30% of the compound was released within the first minute, after which an additional 40% was released (still exponential) within the next 30 min (gastric buffer) or 15 min (intestinal buffer). The remaining 30% was not released in the timespan of the experiment. © 2014 Elsevier B.V. All rights reserved.

Characterization of process induced changes in matjes herring, using 2D gel electrophoresis

Chilling and freezing of fish
Effect of Gastrointestinal Protease Digestion on Bioactivity of Marine Peptides

Focus in nutritional science has turned towards components in, or added to, foods that may possess health beneficial activities beyond the classical nutritional value, namely functional food. Bioactive peptides are examples of such components. In vitro studies on bioactivities have mainly been executed without concerning subsequent digestion after intake and the aim of this work was hence to investigate how the in vitro antioxidative, antihypertensive and caspase activating activities of peptides are affected by digestion with gastrointestinal (GI) proteases. Five different fish protein hydrolysates were chosen to study the effect of in vitro digestion on bioactivity. The protein concentration decreased in all samples during digestion and the molecular weight distribution of the peptides shifted towards lower values. Thus, in vitro digestion with GI proteases resulted in a further degradation of the peptides obtained by hydrolysis. The antihypertensive effect increased in all samples after digestion with GI proteases whereas the antioxidative capacity decreased. The effect on the caspase activity depended on the proteases used in the preparation of hydrolysates. In conclusion, the caspase activity and antihypertensive activity are maintained during digestion with GI proteases, while the antioxidative capacity seems to be reduced.

Electrospun fish protein fibers as a biopolymer-based carrier – implications for oral protein delivery

Purpose: Protein-based electrospun fibers have emerged as novel nanostructured materials for tissue engineering and drug delivery due to their unique structural characteristics, biocompatibility and biodegradability. The aim of this study was to explore the use of electrospun fibers based on fish sarcoplasmic proteins as an oral delivery platform for biopharmaceuticals, using insulin as a model protein. Methods: Fish sarcoplasmic proteins (FSP) were isolated from fresh cod and electrospun into nanomicrofibers using insulin as a model payload. The morphology of FSP fibers was characterized using scanning electron microscopy (SEM), and the conformational stability of insulin was confirmed by circular dichroism (CD). The in vitro release and enzymatic degradation of encapsulated insulin was measured in different buffers and quantified using RP-HPLC. The permeability of released insulin across differentiated Caco-2 cell monolayers was followed by RP-HPLC and ELISA, and the transepithelial electrical resistance (TEER) was measured before and after the experiment. Cell viability was assessed by the MTS/PMS assay. Results: Insulin was encapsulated in the electrospun FSP fibers with high efficiency, high loading and without any effect on fiber morphology. Release of insulin in vitro was 75% after 3 h in simulated intestinal fluid. The secondary structure of insulin was preserved after release, and insulin functionality was confirmed by ELISA. Insulin permeability across Caco-2 cell monolayers was significantly enhanced when administered encapsulated in FSP fibers. The TEER was decreased after 4 h incubation, and no negative effect on cell viability was observed at any time. Conclusion: In this work we present electrospun FSP fibers as a novel oral drug delivery system for biopharmaceuticals. The electrospinning process did not affect the functionality of the encapsulated insulin and it provided controlled release kinetics. The epithelial permeability enhancing effect and biocompatibility of the FSP fibers provide evidence for further investigating protein-based electrospun nanofibers for delivery of proteins and peptides.
Species determination of pine nuts in commercial samples causing pine nut syndrome
Consumption of pine nuts from the species of Pinus armandii has been reported to cause dysgeusia, commonly known as pine mouth, or pine nut syndrome (PNS). However, the number of reports on pine nut consumptions of the different species and PNS is limited. This leaves open the possibility that other pine species than P. armandii could be involved in PNS as well. This study investigated 18 samples involved in PNS and received at the Danish Veterinary and Food Administration in 2011 through 2012. Samples were subjected to gas chromatographic analysis of fatty acids. The content of 11 individual fatty acids was used together with the diagnostic index and the sum of Δ5-fatty acids as diagnostic parameters. Diagnostic parameters from samples were then compared to reference material and literature data to determine the species. In a limited number of samples, the diagnostic parameters matched neither our reference materials nor literature data. However, the morphology, the fatty acid analysis, and externally obtained DNA sequencing data suggest a P. armandii subspecies or a variety. With these possible P. armandii subspecies, P. armandii was identified in all analyzed samples. The application of principal component analysis (PCA) to the data set showed a satisfactory separation of the majority of the 13 pine species included in the study.

Protein markers for the salting and ripening process in Herring production

Species determination of pine nuts in commercial samples causing pine nut syndrome
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Organisations: National Food Institute, Division of Industrial Food Research, Nofima
Contributors: Jessen, F., Skåra, T., Nielsen, H. H.
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Source-ID: 103565000
Research output: Contribution to conference › Poster – Annual report year: 2014 › Research › peer-review

Species determination of pine nuts in commercial samples causing pine nut syndrome
Consumption of pine nuts from the species of Pinus armandii has been reported to cause dysgeusia, commonly known as pine mouth, or pine nut syndrome (PNS). However, the number of reports on pine nut consumptions of the different species and PNS is limited. This leaves open the possibility that other pine species than P. armandii could be involved in PNS as well. This study investigated 18 samples involved in PNS and received at the Danish Veterinary and Food Administration in 2011 through 2012. Samples were subjected to gas chromatographic analysis of fatty acids. The content of 11 individual fatty acids was used together with the diagnostic index and the sum of Δ5-fatty acids as diagnostic parameters. Diagnostic parameters from samples were then compared to reference material and literature data to determine the species. In a limited number of samples, the diagnostic parameters matched neither our reference materials nor literature data. However, the morphology, the fatty acid analysis, and externally obtained DNA sequencing data suggest a P. armandii subspecies or a variety. With these possible P. armandii subspecies, P. armandii was identified in all analyzed samples. The application of principal component analysis (PCA) to the data set showed a satisfactory separation of the majority of the 13 pine species included in the study.

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Contributors: Mikkelsen, A. Æ., Jessen, F., Ballin, N. Z.
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Web of Science (2014): Impact factor 2.806
Web of Science (2014): Indexed yes
Original language: English
Keywords: DI - diagnostic index, FA - fatty acid(s), GC - gas chromatography, NMR - nuclear magnetic resonance, PCA - principal component analysis, PNS - pine nut syndrome, RM - reference material, S - sample
DOIs:
The impact of students’ knowledge levels on the performances in a Design-Build project

Today an important part of teaching at the university level is group work relying on the Learning pyramid (NTL), where teaching one another is much more beneficial for students than lecturing. In group work students are either put in groups of their own choice (mostly relying on social behavior) or put into predesigned groups. In this paper we have reflected on the consequences of the composition of the predesigned group and tried to evaluate the outcome based on marks given for assignments delivered as reports and oral exams. Preliminary findings indicate that the composition of the group could have an influence on the intended learning outcome (ILO -here tested by marks and knowledge of student performance); and if group composition is highly diverse (by including both students with reflective learning and superficial learning), preliminary findings presented here indicate that the ILO can be lower compared with the best individual student in the group. This finding in some ways contradicts the common perception that both reflective and superficial students will benefit from working together, however, further observations on a larger number of students are needed to verify these initial findings.

Authentication of Fish Products by Large-Scale Comparison of Tandem Mass Spectra

Authentication of food is a major concern worldwide to ensure that food products are correctly labeled in terms of which animals are actually processed for consumption. Normally authentication is based on species recognition by comparison of selected sequences of DNA or protein. We here present a new robust, proteome-wide tandem mass spectrometry method for species recognition and food product authentication. The method does not use or require any genome sequences or selection of tandem mass spectra but uses all acquired data. The experimental steps were performed in a simple, standardized workflow including protein extraction, digestion, and data analysis. First, a set of reference spectral libraries was generated using unprocessed muscle tissue from 22 different fish species. Query tandem mass spectrometry data sets from “unknown” fresh muscle tissue samples were then searched against the reference libraries. The number of matching spectra could unambiguously identify the origin of all fresh samples. A number of processed samples were also analyzed to further test the robustness and applicability of the method. The results clearly show that the method is also able to correctly identify heavily processed samples.
Tandem mass spectrometry for species recognition and phenotyping in fish

General information
Publication status: Published
Organisations: National Food Institute, Division of Industrial Food Research, Division of Toxicology and Risk Assessment, Leiden University
Contributors: Wulff, T., Jessen, F., Palmblad, M., Nielsen, M. E.
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Comparative analysis of inflamed and non-inflamed colon biopsies reveals strong proteomic inflammation profile in patients with ulcerative colitis

General information
Publication status: Published
Organisations: National Food Institute, Division of Industrial Food Research, Aarhus University, Viborg Regional Hospital
Contributors: Poulsen, N. A., Andersen, V., Moller, J. C., Møller, H. S., Jessen, F., Purup, S., Larsen, L. B.
Number of pages: 11
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Peer-reviewed: Yes

Journal: B M C Gastroenterology
Volume: 12
Dietary Tools To Modulate Glycogen Storage in Gilthead Seabream Muscle: Glycerol Supplementation

The quality and shelf life of fish meat products depend on the skeletal muscle's energetic state at slaughter, as meat decomposition processes can be exacerbated by energy depletion. In this study, we tested dietary glycerol as a way of replenishing muscle glycogen reserves of farmed gilthead seabream. Two diets were tested in duplicate (n = 42/tank). Results show 5% inclusion of crude glycerol in gilthead seabream diets induces increased muscle glycogen, ATP levels and firmness, with no deleterious effects in terms of growth, proximate composition, fatty acid profile, oxidative state, and organoleptic properties (aroma and color). Proteomic analysis showed a low impact of glycerol-supplementation on muscle metabolism, with most changes probably reflecting increased stress coping capacity in glycerol-fed fish. This suggests inclusion of crude glycerol in gilthead seabream diets (particularly in the finishing phase) seems like a viable strategy to increase glycogen deposition in muscle without negatively impacting fish welfare and quality.

General information
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Organisations: Department of Systems Biology, National Food Institute, Division of Industrial Food Research, University of Algarve, University of Porto, Unity of Innovation of Fish and Aquaculture Products
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Source: dtu
Source-ID: n:oai:DTIC-ART:acs/369924393::20079
Research output: Contribution to journal › Journal article – Annual report year: 2012 › Research › peer-review

Effects of Preslaughter Stress Levels on the Post-mortem Sarcoplasmic Proteomic Profile of Gilthead Seabream Muscle

Fish welfare is an important concern in aquaculture, not only due to the ethical implications but also for productivity and quality-related reasons. The purpose of this study was to track soluble proteome expression in post-mortem gilthead
seabream muscle and to observe how preslaughter stress affects these post-mortem processes. For the experiment, two
groups of gilthead seabream (n = 5) were subjected to distinct levels of preslaughter stress, with three muscle samples
being taken from each fish. Proteins were extracted from the muscle samples, fractionated, and separated by 2DE.
Protein identification was performed by MALDI-TOF-TOF MS. Analysis of the results indicates changes on several cellular
pathways, with some of these changes being attributable to oxidative and proteolytic activity on sarcoplasmic proteins,
together with leaking of myofibrillar proteins. These processes appear to have been hastened by preslaughter stress,
confirming that it induces clear post-mortem changes in the muscle proteome of gilthead seabream.

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Industrial Food Research, University of Algarve
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Volume: 60
Issue number: 37
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Web of Science (2012): Impact factor 2.906
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
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Keywords: gilthead seabream, preslaughter stress, proteomics, post-mortem muscle, sarcoplasmic proteins
DOIs:
10.1021/jf301766e
Source: dtu
Source-ID: n::oai:DTIC-ART:acs/368066328::19037
Research output: Contribution to journal › Journal article – Annual report year: 2012 › Research › peer-review

Proteome Analysis of Pyloric Ceca: A Methodology for Fish Feed Development?
Changing the protein source of fish feed from fish meal to alternative sources of protein will affect traits such as fish
growth, quality, and feed utilization. The present investigation was initiated to introduce a two-dimensional gel
electrophoresis based proteomic workflow as a tool to investigate feed effects on fish by analyzing protein changes in the
fish gut. The workflow was used to study the effect of substituting fish meal in fish feed by alternative sources of protein.
Rainbow trout divided into five groups were fed for 72 days with feeds varying in protein composition. By two-dimensional
gel electrophoresis proteins extracted from the pyloric ceca were separated, making it possible to measure the abundance
of more than 440 protein spots. The expression of 41 protein spots was found to change due to differences in feed
composition. By mass spectrometry 31 of these proteins were identified, including proteins involved in digestion
(trypsinogen, carboxylic ester hydrolase, and aminopeptidase). The many expression changes indicated that the trout,
when adapting to differences in feed formulation, alter the protein composition of the gut.

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Publication status: Published
Organisations: Department of Systems Biology, Enzyme and Protein Chemistry, National Food Institute, Division of
Industrial Food Research, University of Southern Denmark, Aller Aqua A/S
Contributors: Wulff, T., Petersen, J., Nørrelykke, M. R., Jessen, F., Nielsen, H. H.
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Volume: 60
Issue number: 34
ISSN (Print): 0021-8561
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BFI (2012): BFI-level 2
PROTEOMICS in aquaculture: Applications and trends

Over the last forty years global aquaculture presented a growth rate of 6.9% per annum with an amazing production of 52.5 million tonnes in 2008, and a contribution of 43% of aquatic animal food for human consumption. In order to meet the world's health requirements of fish protein, a continuous growth in production is still expected for decades to come. Aquaculture is, though, a very competitive market, and a global awareness regarding the use of scientific knowledge and emerging technologies to obtain a better farmed organism through a sustainable production has enhanced the importance of proteomics in seafood biology research. Proteomics, as a powerful comparative tool, has therefore been increasingly used over the last decade to address different questions in aquaculture, regarding welfare, nutrition, health, quality, and safety. In this paper we will give an overview of these biological questions and the role of proteomics in their investigation, outlining the advantages, disadvantages and future challenges. A brief description of the proteomics technical approaches will be presented. Special focus will be on the latest trends related to the aquaculture production of fish with defined nutritional, health or quality properties for functional foods and the integration of proteomics techniques in addressing this challenging issue. This article is part of a Special Issue entitled: Farm animal proteomics.
Quality of frozen fish

General information
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Contributors: Goncalves, A. A., Nielsen, J., Jessen, F.
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Quality of frozen seafood Goncalves Jette Flemming.pdf

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Source: dtu
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Research output: Contribution to journal › Journal article – Annual report year: 2012 › Research › peer-review

Standardized and simple sub-fractionation of human plasma reveals enrichment of many low abundant hydrophobic proteins

General information
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Organisations: National Food Institute, Division of Industrial Food Research, Department of Systems Biology
Contributors: Jessen, F., Wulff, T.
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Publication date: 2012
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Event: Poster session presented at 9th Siena Meeting From Genome to Proteome, Siena, Italy.
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Source-ID: u::5861
Research output: Contribution to conference › Poster – Annual report year: 2012 › Research › peer-review

Time-dependent changes in protein expression in rainbow trout muscle following hypoxia
Adaptation to hypoxia is a complex process, and individual proteins will be up- or down-regulated in order to address the main challenges at any given time. To investigate the dynamics of the adaptation, rainbow trout (Oncorhynchus mykiss) was exposed to 30% of normal oxygen tension for 1, 2, 5 and 24h respectively, after which muscle samples were taken. The successful investigation of numerous proteins in a single study was achieved by selectively separating the sarcoplasmic proteins using 2-DE. In total 46 protein spots were identified as changing in abundance in response to
hypoxia using one-way ANOVA and multivariate data analysis. Proteins of interest were subsequently identified by MS/MS following tryptic digestion. The observed regulation following hypoxia in skeletal muscle was determined to be time specific, as only a limited number of proteins were regulated in response to more than one time point. The cellular response to hypoxia included regulation of proteins involved in maintaining iron homeostasis, energy levels and muscle structure. In conclusion, this proteome-based study presents a comprehensive investigation of the expression profiles of numerous proteins at four different time points. This increases our understanding of timed changes in protein expression in rainbow trout muscle following hypoxia.

### General information

**Publication status:** Published  
**Organisations:** Section for Aquatic Protein Biochemistry, National Food Institute, Division of Industrial Food Research, National Institute of Aquatic Resources, Section for Aquaculture, Technical University of Denmark  
**Contributors:** Wulff, T., Jokumsen, A., Højrup, P., Jessen, F.  
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**Publication date:** 2012  
**Peer-reviewed:** Yes

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**BFI (2012):** BFI-level 1  
**Scopus rating (2012):** CiteScore 4.29 SJR 1.231 SNIP 1.163  
**Web of Science (2012):** Impact factor 4.088  
**ISI indexed (2012):** ISI indexed yes  
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**Source:** dtu  
**Source-ID:** n::oai:DTIC-ART:elsevier/363540355::15481  
**Research output:** Contribution to journal  

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Vegetable based fish feed changes protein expression in muscle of rainbow trout (Oncorhynchus mykiss)

### General information

**Publication status:** Published  
**Organisations:** National Food Institute, Division of Industrial Food Research, Department of Systems Biology, Enzyme and Protein Chemistry, Technical University of Denmark  
**Contributors:** Jessen, F., Wulff, T., Bach Mikkelsen, J., Hyldig, G., Nielsen, H. H.  
**Pages:** 134-137  
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**Publisher:** Wageningen Academic Publishers  
**Editors:** Rodrigues, P., Eckersall, D., de Almeida, A.  
**ISBN (Print):** 978-90-8686-195-8  
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**Research output:** Chapter in Book/Report/Conference proceeding  

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Report from workshop on Bioactive peptides from aquatic raw materials: Copenhagen, 2 March 2010

### General information

**Publication status:** Published  
**Organisations:** National Food Institute, Division of Industrial Food Research  
**Contributors:** Andersen, L. L., Nielsen, H. H., Jessen, F.  
**Number of pages:** 133
Antioxidant Activity of Fish Protein Hydrolysates in in vitro Assays and in Oil-in-Water Emulsions.
The aim of this study was to screen different protein hydrolysates with respect to their antioxidative properties in order to select the most promising extracts for further evaluation in oil-in-water emulsions. Three fractions of protein hydrolysates (Crude, >5kDa and 5kDa, 3-5kDa and

Dietary Tools To Modulate Glycogen Storage In Fish Muscle: A Proteomic Assessment
Post-mortem flesh deterioration is dependent on the energy reserves present at the time of death. Early depletion of muscle glycogen leads to the buildup of lactate and to the early onset of rigor mortis, resulting in the activation of endogenous proteases and the degradation of myofibrillar proteins, and consequent muscle softening. The purpose of this study was to modulate the energy status of the muscle at the time of death through the use of dietary muscle buffering compounds, namely glycerol and maslinic acid. Four fish groups of gilthead seabream (in duplicate) were fed for three months with four different diets. The four diets were obtained by starting from a commercial diet formulation and applying a 2×2 factorial design, with two levels of glycerol supplementation (0 and 5%) and two levels of maslinic acid supplementation (0 and 0,025%). The diets were formulated to be isonitrogenous and isolipidic. Fish were slaughtered by immersion in ice-salt water slurry and muscle samples were immediately obtained from three fish of each tank, for a total of six muscle samples per treatment. Sarcoplasmic proteins were extracted from each muscle sample, separated/quantified by 2D-DIGE and identified by peptide fragment fingerprinting using MALDI-TOF MS. Preliminary analysis of the results shows an effect of the diets on muscle parameters such as measured pH and onset of rigor mortis. At the proteome level, the addition of glycerol and maslinic acid to the diets seemed to have affected the abundance of proteins related to oxidative stress (HSC70, HSC71, peroxiredoxin, transferrin), aldehyde toxification (ALDH1A2, ALDH6A1, ALDH7A1), energy homeostasis (adenylate kinase, nucleoside-diphosphate kinase), cytoskeleton (cofilin-2) and signalling (phosphohistidine phosphatase).
Differences in fish feed composition influence protein expression in the pyloric caeca in rainbow trout

Effect of a dietary supplementation of glycerol and maslinic acid on the muscle proteome of gilthead seabream

Feed based on vegetable materials changes the muscle proteome of the carnivore rainbow trout
**Effect of Protein Hydrolysates on Pancreatic Cancer Cells**

Effect of Fish Protein Hydrolysates on Pancreatic Cancer Cells Carlo G. Ossum1, Lisa Lystbæk Andersen2, Henrik Hauch Nielsen2, Else K. Hoffmann1, and Flemming Jessen2 1University of Copenhagen, Department of Biology, Denmark, 2Technical University of Denmark (DTU), National Food Institute, Denmark Corresponding author: Carlo G. Ossum (cgossum@gmail.com) A large number of bioactive peptides have been identified in and isolated from various food sources. Milk seems to be a particularly rich source but also different fish species have been found to yield bioactive peptides. Bioactive peptides, usually consisting of 3 to 20 amino acids, can be released from proteins upon degradation by proteolytic enzymes, e.g. in the intestinal tract. The numerous described bioactivities include antihypertensive, anticancerous, antimicrobial, and immunomodulating effects. Here, we investigate the effect of fish protein hydrolysates obtained by enzymatic hydrolysis on cancer cell proliferation. Skin and belly flap muscle from trout were hydrolysed with the unspecific proteases Alcalase, Neutrase, or UE1 (all from Novozymes, Bagsværd, Denmark) to a hydrolysis degree of 1-15%. The hydrolysates were tested for biological activities affecting cell proliferation and ability to modulate caspase activity in pancreatic cancer cells COLO357 and BxPC-3 in vitro. A number of the hydrolysates showed caspase promoting activity; in particular products containing muscle tissue, i.e. belly flap, were able to stimulate caspase activity. Selected hydrolysis products were further fractionated by ultrafiltration into molecular sizes above and below 5 kDa and their activity and dose-dependence was tested.

**Post-mortem sarcoplasmic proteomic profile of gilthead seabream is affected by pre-slaughter stress levels.**

**General information**
Publication status: Published
Organisations: National Institute of Aquatic Resources, Division of Seafood Research, National Food Institute
Contributors: Silva, T. S., Dias, J., Jessen, F., Cordeiro, O., Matos, E., Rodrigues, P.
Publication date: 2010
Peer-reviewed: Yes
Source: orbit
Source-ID: 271637
Research output: Contribution to conference › Poster – Annual report year: 2010 › Research › peer-review
Purification and Characterization of Bioactive Peptides from Fish Protein Hydrolysates

**General information**
Publication status: Published
Organisations: National Food Institute, Division of Industrial Food Research
Contributors: Andersen, L. L., Nielsen, H. H., Jessen, F.
Publication date: 2010
Peer-reviewed: No
Event: Poster session presented at Protein.DTU Workshop, Kgs. Lyngby, Denmark.
Source: orbit
Source-ID: 264638
Research output: Contribution to conference › Poster – Annual report year: 2010 › Research

Reproducibility of a fractionation procedure for fish muscle proteomics

**General information**
Publication status: Published
Organisations: National Institute of Aquatic Resources, Division of Seafood Research, Centro de Ciências do Mar do Algarve
Contributors: Silva, T. S., Cordeiro, O., Jessen, F., Dias, J., Rodrigues, P. M.
Pages: 8-13
Publication date: 2010
Peer-reviewed: Yes

**Publication information**
Journal: American Biotechnology Laboratory
Volume: 28
Issue number: 4
ISSN (Print): 0749-3223
Ratings:
Scopus rating (2010): SJR 0.135 SNIP 0.178
Web of Science (2010): Indexed yes
Original language: English
URLs:
Source: orbit
Source-ID: 271635
Research output: Contribution to journal › Journal article – Annual report year: 2010 › Research › peer-review

Time-dependent effect of pre-slaughter stress levels on the post-mortem sarcoplasmic proteomic profile of Sparus aurata muscle

**General information**
Publication status: Published
Organisations: National Institute of Aquatic Resources, Division of Seafood Research, National Food Institute
Publication date: 2010
Peer-reviewed: Yes
Event: Poster session presented at 6th Symposium of the Danish Proteomics Society, Odense, Denmark.
Source: orbit
Source-ID: 271643
Research output: Contribution to conference › Poster – Annual report year: 2010 › Research › peer-review

Using a cross-model loadings plot to identify protein spots causing 2-DE gels to become outliers in PCA
The multivariate method PCA is an exploratory tool often used to get an overview of multivariate data, such as the quantified spot volumes of digitized 2-DE gels. PCA can reveal hidden structures present in the data, and thus enables identification of potential outliers and clustering. Based on PCA, we here present an approach for identification of protein spots causing 2-DE gels to become outliers. The approach can potentially obviate analytical exclusion of entire 2-DE gels.

**General information**
Publication status: Published
Wound healing effect on tissue composition: facing interindividual variability

General information
Publication status: Published
Organisations: Division of Seafood Research, National Food Institute
Contributors: Wulff, T., Jessen, F., Nielsen, M. E.
Publication date: 2010
Peer-reviewed: Yes
Source: orbit
Source-ID: 271640
Research output: Contribution to conference › Poster – Annual report year: 2010 › Research › peer-review

2D gel based analysis of biological variability of the human plasma proteome

Human blood plasma is a valuable specimen for the biomarker discovery process, since it is easily accessible and contains proteins that are synthesised, secreted or lost from cells and tissue. In this way, changes in plasma proteome reflect the current state of the organism. The analysis of plasma proteome is yet challenging due to the huge dynamic range of protein abundance. When evaluating a potential biomarker, stable basal level of the protein is needed before it can be considered a functional biomarker. However, basal level differences of plasma proteins are naturally occurring between individuals and within an individual changes will also happen over time (e.g. after meal intake). Thus, the aim of the present study was to examine the inter-individual variability of plasma protein levels in humans after meal intake. Five subjects consumed three single meals in a randomised order separated by one-week interval. Blood samples were drawn before the meal intake and five times during 24 hours for proteome analysis. Plasma was fractionated by use of IgY-12 spin column depleting the 12 highly abundant proteins and further processed for two-dimensional gel electrophoresis. The plasma proteome profiling was visualized by silver staining and analysed by the software Samespots. The inter-individual variability of the plasma proteome was demonstrated by multivariate data analysis (principal component analysis and partial least squares regression) on normalised spot volumes.

General information
Publication status: Published
Organisations: Section for Aquatic Protein Biochemistry, National Institute of Aquatic Resources
Contributors: Rentsch, M. L., Jessen, F.
Publication date: 2009
Peer-reviewed: No
Source: orbit
Source-ID: 252796
Research output: Contribution to conference › Poster – Annual report year: 2009 › Research
Contribution of cathepsins B, L and D to muscle protein profiles correlated with texture in rainbow trout (Oncorhynchus mykiss)

Post-mortem softening of fish tissue often results in low yield and decreased product quality. In this study, proteolytic profiles of trout stored 5 days oil ice were obtained by SDS-PAGE. The link between protein hand intensities and firmness of trout fillets was examined through a correlation Study. In parallel, trout extracts were incubated with cathepsin B, cathepsin L and cathepsin D, alone or in combination, in order to evaluate the effect of each cathepsin on the texture-related proteins. Proteins from both myofibrillar (alpha-actinin, actin, MLC1, MLC2, and N-terminal 70 kDa MHC fragment) and sarcoplasmic (glycogen phosphorylase, creatine kinase, and TPI) fractions correlated closely with firmness. Cathepsins D, B and L affected, respectively, 10, 9 and 4 out of the 17 protein bands correlating with firmness, and most changes induced by cathepsin D were unfavourable to firmness. This implies that cathepsin D is likely to be involved in textural change of trout, due to breakdown of the muscle structure.

General information
Publication status: Published
Organisations: National Institute of Aquatic Resources, Section for Aquatic Process and Product Technology, Section for Aquatic Protein Biochemistry
Contributors: Godiksen, H., Morzel, M., Hyldig, G., Jessen, F.
Pages: 889-896
Publication date: 2009
Peer-reviewed: Yes

Publication information
Journal: Food Chemistry
Volume: 113
Issue number: 4
ISSN (Print): 0308-8146
Ratings:
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.789 SNIP 2.022
Web of Science (2009): Indexed yes
Original language: English
Keywords: Softening, Trout, Fish, Oncorhynchus mykiss, Cathepsins, SDS-PAGE, Texture
DOIs: 10.1016/j.foodchem.2008.08.012
Source: orbit
Source-ID: 229066
Research output: Contribution to journal › Journal article – Annual report year: 2009 › Research › peer-review

Multivariate data analysis of 2 DE data: Time dependent changes in protein expression in rainbow trout following hypoxia

In the last decade there has been a growing understanding of the health benefits of fish consumption. This has lead to an increased interest in studies examining which parameters will affect eating quality of fish grown in fish farms. Especially increased softening of fish muscle is a major problem since it significantly reduces the quality of the major edible part of the fish. One important stressor affecting quality is hypoxia which will occur in fish farms, when the trout is collected for transport before slaughter. In order to explore the biochemical mechanisms responsible for the changes seen in trout muscle following hypoxia, a proteome study was conducted. This will greatly aid the aquaculture industry when evaluating the type of stressors mostly affecting food quality, allowing the industry to optimise handling of the rainbow trout accordingly. In the present study a number of rainbow trout were kept in tanks where hypoxia, (30% of normal oxygen) when introduced, was the only stressor. The fish were sacrificed at different time points (1, 2, 5 and 24 hours) after the onset of hypoxia and muscle samples were taken from each individual fish. Protein expression profiles of the samples were achieved by 2-DE. Protein spots, which individually or in combination with other spots varied according to hypoxia were found by multivariate data analysis (partial least squares regression) on group scaled data (normalised spot volumes) followed by selection of significant spots by jack-knifing. Tandem mass spectrometry was used to identify protein spots of interest.

General information
Publication status: Published
Organisations: National Food Institute, Section for Aquaculture, National Institute of Aquatic Resources
Contributors: Wulff, T., Jokumsen, A., Jessen, F.
Publication date: 2009
Peer-reviewed: Yes
Source: orbit
Source-ID: 255870
On the Reproducibility of a Fractionation Procedure for Fish Muscle Proteomics

General information
Publication status: Published
Organisations: Section for Aquatic Protein Biochemistry, National Institute of Aquatic Resources
Contributors: Rodrigues, P., Silva, T. S., Jessen, F., Dias, J.
Pages: S19-S19
Publication date: 2009
Peer-reviewed: Yes

Publication information
Journal: Molecular and Cellular Proteomics
ISSN (Print): 1535-9476
Ratings:
BFI (2009): BFI-level 2
Web of Science (2009): Indexed yes
Original language: English
Source: orbit
Source-ID: 248867

PEPFISH: Utilisation of Bioactive Peptides from Fish Processing – Upgrading the Value of Secondary Products

General information
Publication status: Published
Organisations: National Food Institute, Novozymes A/S, UiT The Arctic University of Norway, Lund University, Marinova A/S, Biofac A/S, Copenhagen University Hospital, University of Copenhagen
Publication date: 2009
Peer-reviewed: No
Event: Poster session presented at 3rd Joint Trans-Atlantic Fisheries Technology Conference, Copenhagen, Denmark.
Source: orbit
Source-ID: 255920

Purification and Characterization of Peptides from Fish Protein Hydrolysates

General information
Publication status: Published
Organisations: Section for Aquatic Protein Biochemistry, National Food Institute
Contributors: Andersen, L. L., Nielsen, H. H., Jessen, F.
Publication date: 2009
Peer-reviewed: No
Event: Poster session presented at 3rd Joint Trans-Atlantic Fisheries Technology Conference, Copenhagen, Denmark.
Source: orbit
Source-ID: 255922

Two-dimensional gel electrophoresis

General information
Publication status: Published
Organisations: Section for Aquatic Protein Biochemistry, National Institute of Aquatic Resources
Contributors: Jessen, F.
Pages: 301-317
Publication date: 2009
Acute single meal effects of trout and poultry on the human plasma proteome

General information
Publication status: Published
Organisations: Section for Aquatic Protein Biochemistry, National Institute of Aquatic Resources
Contributors: Rentsch, M. L., Nielsen, H. H., Lauritzen, L., Lametsch, R., Jessen, F.
Publication date: 2008
Peer-reviewed: No
Event: Poster session presented at 8th Siena Meeting From Genome to Proteome, Siena, Italy.
Source: orbit
Source-ID: 229072
Research output: Contribution to conference › Poster – Annual report year: 2008 › Research

A molecular approach to pre-harvest impact on post-harvest quality of trout

Fish meat quality is influenced by many biological and physical factors like e.g. rearing, feeding, slaughtering, processing and storage. Observations from the commercial aquaculture industry indicate that infections in e.g. salmon caused by Moritella viscosus or Pancreas Disease (PD) results in downgrading of fish quality and subsequent a reduction in prize. Despite this, the impact of infectious diseases on the meat quality and the mechanisms behind are poorly investigated.

Wound repair is a dynamic, interactive response to tissue injury that involves a complex interaction and cross talk of various cell types, extracellular matrix molecules, soluble mediators and cytokines. In order to describe the molecular mechanisms and processes of wound repair, a panel of genes covering immunological factors and tissue regeneration were used to measure changes at the mRNA level following mechanical tissue damage in rainbow trout (Oncorhynchus mykiss). Needle disrupted muscle tissue was sampled at different time points and subject to real-time RT-PCR for measuring the expression of the genes IL-1ß, IL-8, IL-10, TGF-ß, Myostatin-1ab, MMP-2, CTGF, Collagen-1alfa, VEGF, iNOS, Arg-2 and FGF. The results showed an initial phase with up-regulation of immune-related genes followed by a regenerative phase with regulation of genes coding for muscle growth and synthesis of connective tissue.

General information
Publication status: Published
Organisations: Section for Aquatic Protein Biochemistry, National Institute of Aquatic Resources, Section for Aquatic Process and Product Technology
Contributors: Nielsen, M. E., Hyldig, G., Nielsen, H. H., Jessen, F., Ingerslev, H.
Publication date: 2008
Peer-reviewed: Yes
Event: Poster session presented at International Conference on Fish Diseases and Fish Immunology, Reykjavik, Iceland.
Source: orbit
Source-ID: 232679
Research output: Contribution to conference › Poster – Annual report year: 2008 › Research

A molecular approach to pre-harvest impact on post-harvest quality of trout

General information
Publication status: Published
Organisations: National Institute of Aquatic Resources, Section for Aquatic Protein Biochemistry, Section for Aquatic Process and Product Technology
Contributors: Nielsen, M. E., Hyldig, G., Nielsen, H. H., Jessen, F., Jacobsen, C., Ingerslev, H.
Publication date: 2008
Peer-reviewed: No
Source: orbit
Source-ID: 242449
Research output: Contribution to conference › Paper – Annual report year: 2008 › Research
Combination of statistical approaches for analysis of 2-DE data gives complementary results
Five methods for finding significant changes in proteome data have been used to analyze a two-dimensional gel electrophoresis data set. We used both univariate (ANOVA) and multivariate (Partial Least Squares with jackknife, Cross Model Validation, Power-PLS and CovProc) methods. The gels were taken from a time-series experiment exploring the changes in metabolic enzymes in bovine muscle at five time-points after slaughter. The data set consisted of 1377 protein spots, and for each analysis, the data set were preprocessed to fit the requirements of the chosen method. The generated results were one list from each analysis method of proteins found to be significantly changed according to the experimental design. Although the number of selected variables varied between the methods, we found that this was dependent on the specific aim of each method. CovProc and P-PLS focused more on getting the minimum necessary subset of proteins to explain properties of the samples. These methods ended up with less selected proteins. There was also a correlation between level of significance and frequency of selection for the selected proteins.
anoxia models and shows that great care should be taken when comparing the effects of anoxia in studies that have used different types and durations of anoxia.

**General information**
Publication status: Published
Organisations: Section for Aquatic Protein Biochemistry, National Institute of Aquatic Resources
Contributors: Wulff, T., Hoffmann, E., Roepstorff, P., Jessen, F.
Pages: 2035-2044
Publication date: 2008
Peer-reviewed: Yes

**Publication information**
Journal: Proteomics
Volume: 8
Issue number: 10
ISSN (Print): 1615-9853
Ratings:
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.61 SNIP 1.122
Web of Science (2008): Indexed yes
Original language: English
DOIs:
10.1002/pmic.200700944
Source: orbit
Source-ID: 227820
Research output: Contribution to journal > Journal article – Annual report year: 2008 > Research > peer-review

**Effects of tetracycline administration on the proteomic profile of pig muscle samples (L. dorsi)**

Effect of tetracycline (TC) administration on the proteomic profile of pig muscle was evaluated by 2D electrophoresis and MALDI-TOF mass spectrometry. The TC content at slaughter was determined in L. dorsi samples by HPLC-DAD. Mean residual concentration of TC in the muscle of treated animals, calculated as the sum of TC and epi-TC was 126.3 μg/kg, indicating a rapid elimination of TC in this tissue. Several differential spots (n = 54, p <0.05) were observed in protein profiles from control and treated animals. MALDI-TOF identification gave a positive match for 5 differential spots, that is, glycerol-3-phosphate dehydrogenase 1 (G3PD1), phosphoglycerate kinase 1, novelprotein (0610037L13Rik), leucine aminopeptidase 3 (LAP), and hypothetical protein isoform 2. Results show that proteomics could be a useful tool to reveal pharmacological treatments with TC, even if the possible uses of differential spots as biomarkers to detect illegal administration of TC require further studies. Different spot patterns as a consequence of TC treatments seem to be another interesting issue for the consequences on tissue metabolism and meat quality.

**General information**
Publication status: Published
Organisations: Section for Aquatic Protein Biochemistry, National Institute of Aquatic Resources
Contributors: Gratacos-Cubarsi, M., Castellari, M., Hortos, M., Garcia-Regueiro, J., Lametsch, R., Jessen, F.
Pages: 9312-9316
Publication date: 2008
Peer-reviewed: Yes

**Publication information**
Journal: Journal of Agricultural and Food Chemistry
Volume: 56
Issue number: 19
ISSN (Print): 0021-8561
Ratings:
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.327 SNIP 1.327
Web of Science (2008): Indexed yes
Original language: English
Keywords: glycerol 3-phosphate dehydrogenase, proteomics, residue determination, tetracycline, pig
DOIs:
10.1021/jf801390z
Source: orbit
Source-ID: 237098
Research output: Contribution to journal > Journal article – Annual report year: 2008 > Research > peer-review
Fiskerester bliver functional foods

General information
Publication status: Published
Organisations: Division of Food Production Engineering, National Food Institute, National Institute of Aquatic Resources
Contributors: Jørgensen, S. B. (ed.), Jessen, F.
Publication date: 2008
Peer-reviewed: Unknown

Publication information
Journal: FoodDTU Midt i Ugen
Original language: Danish
Source: orbit
Source-ID: 258510
Research output: Contribution to journal › Journal article – Annual report year: 2008 › Communication

Long term anoxia in rainbow trout investigated by 2-DE and MS/MS
Twenty-four hours of N-2 induced anoxia induced global perturbations on protein expression in rainbow trout hypodermal fibroblasts cell line. Anoxia was obtained by depleting the medium of O-2 by flushing with N-2, and protein changes were studied by 2-DE coupled with MS providing quantitative measurements of a large number of proteins in one single study. The anoxic insult changed the level of 33 protein spots: 22 of these were up-regulated compared to the control situation and 11 were down-regulated. Using MS/MS sequencing 19 of the 33 protein spots that changed were identified, corresponding to a success rate of more than 50%. The identified proteins included two proteins involved in energy metabolism namely phosphoglycerate mutase and isocitrate dehydrogenase. In addition we observed the up-regulation of a cluster of proteins that contribute to cytoskeleton function. These are calpain, EB1, and Rho GDP dissociation inhibitor (GDI). The up-regulation of Rho GDI was shown to develop in a time dependent manner with no significant increase for up to 8 h of anoxia. In conclusion, this study provides a thorough investigation of the effect of anoxia in a cell line from rainbow trout.

General information
Publication status: Published
Organisations: Section for Aquatic Protein Biochemistry, National Institute of Aquatic Resources
Contributors: Wulff, T., Jessen, F., Roepstorff, P., Hoffmann, E.
Pages: 1009-1018
Publication date: 2008
Peer-reviewed: Yes

Publication information
Journal: Proteomics
Volume: 8
Issue number: 5
ISSN (Print): 1615-9853
Ratings:
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.61 SNIP 1.122
Web of Science (2008): Indexed yes
Original language: English
DOIs:
10.1002/pmic.200700460
Source: orbit
Source-ID: 227822
Research output: Contribution to journal › Journal article – Annual report year: 2008 › Research › peer-review

Multivariate data analysis of two-dimensional gel electrophoresis protein patterns from few samples
One application of 2D gel electrophoresis is to reveal differences in protein pattern between two or more groups of individuals, attributable to their group membership. Multivariate data analytical methods are useful in pinpointing the spots relevant for discrimination by focusing not only on single spot differences, but on the covariance structure between proteins. However, their outcome is dependent on data scaling, and they may fail in producing valid multivariate models due to the much higher number of "irrelevant" spots present in the gels. The case where only few gels are available and where the aim is to find as many as possible of the group-dependent proteins seems particularly difficult to handle. The present paper investigates such a case regarding the effect of scaling and of prefiltering by univariate nonparametric statistics on the selection of spots. Besides, a modified ‘autoscaling’ of the full data set based on within-group standard deviations is introduced and shown to be advantageous in revealing potential group-dependent proteins additional to
those found by prefiltering.

**General information**
Publication status: Published
Organisations: National Institute of Aquatic Resources, Section for Aquatic Protein Biochemistry, Section for Aquatic Process and Product Technology
Contributors: Jensen, K. N., Jessen, F., Jørgensen, B.
Pages: 1288-1296
Publication date: 2008
Peer-reviewed: Yes

**Publication information**
Journal: Journal of Proteome Research
Volume: 7
Issue number: 3
ISSN (Print): 1535-3893
Ratings:
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 2.036 SNIP 1.106
Web of Science (2008): Indexed yes
Original language: English
DOIs: 10.1021/pr700800s
Source: orbit
Source-ID: 225989
Research output: Contribution to journal › Journal article – Annual report year: 2008 › Research › peer-review

**Protein and lipid oxidation in frozen rainbow trout**

**General information**
Publication status: Published
Organisations: Section for Aquatic Lipids and Oxidation, National Institute of Aquatic Resources, Section for Aquatic Protein Biochemistry
Contributors: Baron, C., Kjærgård, I. V. H., Jessen, F., Jacobsen, C.
Publication date: 2008
Peer-reviewed: No
Event: Poster session presented at 99th AOCS Annual Meeting & Expo, Seattle, WA, United States.

**Bibliographical note**
Abstract and poster presentation at the 99th Annual AOCS meeting Seattle, USA May 2008
Source: orbit
Source-ID: 238841
Research output: Contribution to conference › Poster – Annual report year: 2008 › Research

**Stress induced alteration in the proteome of farmed trout: investigation of the mechanism behind changes in sensory properties**

**General information**
Publication status: Published
Organisations: National Institute of Aquatic Resources, Section for Aquatic Process and Product Technology, Section for Aquatic Protein Biochemistry
Contributors: Wulff, T., Godiksen, H., Hylidg, G., Jessen, F.
Publication date: 2008
Peer-reviewed: No
Event: Poster session presented at 8th Siena Meeting From Genome to Proteome, Siena, Italy.
Source: orbit
Source-ID: 229071
Research output: Contribution to conference › Poster – Annual report year: 2008 › Research

**Acute effects of trout on cardiovascular risk markers and plasma proteome**

**General information**
Publication status: Published
A short-term intervention trial, with selenate, Se-enriched yeast and Se-enriched milk: effects on plasma proteins

General information
Publication status: Published
Organisations: Section for Aquatic Protein Biochemistry, National Institute of Aquatic Resources, Division of Toxicology and Risk Assessment, National Food Institute
Contributors: Ravn-Haren, G., Jessen, F., Krath, B., Dragsted, L., Bügel, S.
Publication date: 2007
Peer-reviewed: No
Event: Poster session presented at Nutrigenomics in Denmark, Slagelse, Denmark.

Bibliographical note
Poster
Source: orbit
Source-ID: 227209
Research output: Contribution to conference › Poster – Annual report year: 2007 › Research

Healthy, nutritious and tasty fish for the future

General information
Publication status: Published
Organisations: Section for Aquatic Protein Biochemistry, National Institute of Aquatic Resources, Section for Aquatic Process and Product Technology, Section for Aquatic Lipids and Oxidation
Publication date: 2007

Host publication information
Title of host publication: 23rd NJF-congress, Copenhagen, 27th-29 June

Bibliographical note
Abstract and Poster
Source: orbit
Source-ID: 226853
Research output: Chapter in Book/Report/Conference proceeding › Conference abstract in proceedings – Annual report year: 2007 › Research

Multivariate analysis of 2-DE protein patterns - Practical approaches

Practical approaches to the use of multivariate data analysis of 2-DE protein patterns are demonstrated by three independent strategies for the image analysis and the multivariate analysis on the same set of 2-DE data. Four wheat varieties were selected on the basis of their baking quality. Two of the varieties were of strong baking quality and hard wheat kernel and two were of weak baking quality and soft kernel. Gliadins at different stages of grain development were analyzed by the application of multivariate data analysis on images of 2-DEs. Patterns related to the wheat varieties, harvest times and quality were detected on images of 2-DE protein patterns for all the three strategies. The use of the multivariate methods was evaluated in the alignment and matching procedures of 2-DE gels. All the three strategies were able to discriminate the samples according to quality, harvest time and variety, although different subsets of protein spots were selected. The explorative approach of using multivariate data analysis and variable selection in the analyses of 2-DEs seems to be promising as a fast, reliable and convenient way of screening and transforming many gel images into spot quantities.

General information
Publication status: Published
Quality of frozen fish

General information
Publication status: Published
Organisations: Section for Aquatic Process and Product Technology, National Institute of Aquatic Resources, Section for Aquatic Protein Biochemistry
Contributors: Nielsen, J., Jessen, F.
Number of pages: 744
Pages: 577-586
Publication date: 2007

Host publication information
Title of host publication: Handbook of meat, poultry & seafood quality
Volume: VII:44
Place of publication: Oxford
Publisher: Blackwell Publishing
ISBN (Print): 08-13-82446-X
Source: orbit
Source-ID: 226868
Research output: Chapter in Book/Report/Conference proceeding – Annual report year: 2007 › Research › peer-review

Sensory characterization of different families of farmed rainbow trout

General information
Publication status: Published
Organisations: Section for Aquatic Process and Product Technology, National Institute of Aquatic Resources, Section for Aquatic Protein Biochemistry, Section for Aquaculture
Contributors: Hylldig, G., Leth, N., Jessen, F., Lund, I., Jokumsen, A.
Publication date: 2007

Host publication information
Title of host publication: 23rd NJF-congress, Copenhagen, 27th-29 June

Bibliographical note
Abstract
Source: orbit
Source-ID: 225851
Research output: Chapter in Book/Report/Conference proceeding › Conference abstract in proceedings – Annual report year: 2007 › Research

Variable selection in the analysis of proteome data. Removal of irrelevant variables prior to a Jack-knife procedure

General information
Publication status: Published
Organisations: National Institute of Aquatic Resources, Section for Aquatic Protein Biochemistry, Section for Aquatic Process and Product Technology
Contributors: Jensen, K. N., Jessen, F., Jørgensen, B.
Publication date: 2007
Peer-reviewed: No

Bibliographical note
Source: orbit
Source-ID: 225993
Research output: Contribution to conference › Poster – Annual report year: 2007 › Research
Changes in cod muscle proteins during frozen storage revealed by proteome analysis and multivariate data analysis

Multivariate data analysis has been combined with proteomics to enhance the recovery of information from 2-DE of cod muscle proteins during different storage conditions. Proteins were extracted according to 11 different storage conditions and samples were resolved by 2-DE. Data generated by 2-DE was subjected to principal component analysis (PCA) and discriminant partial least squares regression (DPLSR). Applying PCA to 2-DE data revealed the samples to form groups according to frozen storage time, whereas differences due to different storage temperatures or chilled storage in modified atmosphere packing did not lead to distinct changes in protein pattern. Applying DPLSR to the 2-DE data enabled the selection of protein spots critical for differentiation between 3 and 6 months frozen storage with 12 months frozen storage. Some of these protein spots have been identified by MS/MS, revealing myosin light chain 1, 2 and 3, triose-phosphate isomerase, glyceraldehyde-3-phosphate dehydrogenase, aldolase A and two α-actin fragments, and a nuclelease diphosphate kinase B fragment to change in concentration, during frozen storage. Application of proteomics, multivariate data analysis and MS/MS to analyse protein changes in cod muscle proteins during storage has revealed new knowledge on the issue and enables a better understanding of biochemical processes occurring.

General information
Publication status: Published
Organisations: National Institute of Aquatic Resources, Section for Aquatic Protein Biochemistry
Contributors: Kjærsgård, I. V. H., Nørrelykke, M., Jessen, F.
Pages: 1606-1618
Publication date: 2006
Peer-reviewed: Yes

Publication information
Journal: Proteomics
Volume: 6
Issue number: 5
ISSN (Print): 1615-9853
Ratings:
Scopus rating (2006): SJR 1.985 SNIP 1.281
Web of Science (2006): Indexed yes
Original language: English
DOIs:
10.1002/pmic.200500252
Source: orbit
Source-ID: 226234
Research output: Contribution to journal › Journal article – Annual report year: 2006 › Research › peer-review

Changes in fish muscle proteins during frozen storage revealed by proteomics combined with multivariate data analysis

General information
Publication status: Published
Organisations: National Institute of Aquatic Resources, Section for Aquatic Protein Biochemistry
Contributors: Kjærsgård, I. V. H., Nørrelykke, M., Jessen, F.
Publication date: 2006
Peer-reviewed: No
Event: Poster session presented at Dansk konference om Molekylær Biologi og Bioteknologi, Vejle, Danmark, juni.

Bibliographical note
Poster
Source: orbit
Source-ID: 226235
Research output: Contribution to conference › Poster – Annual report year: 2006 › Research

Hvad sker der, når vi fryser torsken?

General information
Publication status: Published
Organisations: National Institute of Aquatic Resources, Section for Aquatic Protein Biochemistry
Contributors: Kjærsgård, I. V. H., Nørrelykke, M. R., Jessen, F.
Pages: 42-56
Publication date: 2006
Peer-reviewed: No
Identification of carbonylated proteins in frozen rainbow trout (Oncorhynchus mykiss) fillets and development of protein oxidation during frozen storage

General information
Publication status: Published
Organisations: National Institute of Aquatic Resources, Section for Aquatic Lipids and Oxidation, Section for Aquatic Protein Biochemistry
Contributors: Kjærsgård, I. V. H., Nørrelykke, M., Baron, C., Jessen, F.
Pages: 9437-9446
Publication date: 2006
Peer-reviewed: Yes

Investigation of two different anoxia models by 2-dimensional gel electrophoresis

General information
Publication status: Published
Organisations: Section for Aquatic Protein Biochemistry, National Institute of Aquatic Resources
Contributors: Wulff, T., Jessen, F., Hoffmann, E.
Pages: A1433-A1433
Publication date: 2006
Peer-reviewed: No

Investigation of two different anoxia models by 2-dimensional gel electrophoresis

General information
Publication status: Published
Organisations: Section for Aquatic Protein Biochemistry, National Institute of Aquatic Resources
Contributors: Wulff, T., Jessen, F., Hoffmann, E.
Pages: A1433-A1433
Publication date: 2006
Peer-reviewed: No

Bibliographical note
Abstract from conference
Source: orbit
Source-ID: 227821
Kvalitetssøkkelser i opdrætsørred - kan de forudsiges?

General information
Publication status: Published
Organisations: National Institute of Aquatic Resources, Section for Aquatic Process and Product Technology, Section for Aquatic Protein Biochemistry
Contributors: Godiksen, H., Hyldig, G., Kjærsgård, I. V. H., Jessen, F.
Publication date: 2006
Peer-reviewed: No

Bibliographical note
Poster
Source: orbit
Source-ID: 225526
Research output: Contribution to conference › Poster – Annual report year: 2006 › Research

Protein and lipid oxidation during frozen storage of rainbow trout

General information
Publication status: Published
Organisations: Section for Aquatic Lipids and Oxidation, National Institute of Aquatic Resources, Section for Aquatic Protein Biochemistry
Contributors: Baron, C., Kjærsgård, I. V. H., Jessen, F., Jacobsen, C.
Publication date: 2006
Peer-reviewed: No

Bibliographical note
Poster
Source: orbit
Source-ID: 224857
Research output: Contribution to conference › Poster – Annual report year: 2006 › Research

Proteomics combined with multivariate data analysis

General information
Publication status: Published
Organisations: National Institute of Aquatic Resources, Section for Aquatic Protein Biochemistry
Contributors: Kjærsgård, I. V. H., Nørrelykke, M., Jessen, F.
Publication date: 2006
Peer-reviewed: No
Event: Poster session presented at Systems Biology, Danish Biotechnology Forum Conference, June 1-2, Vejle, Denmark and: LMC congress, Marts 15-16, Copenhagen, Denmark.

Bibliographical note
Poster
Source: orbit
Source-ID: 226240
Research output: Contribution to conference › Poster – Annual report year: 2006 › Research

Stress induced changes in sensory properties and proteome of farmed trout

General information
Publication status: Published
Organisations: National Institute of Aquatic Resources, Section for Aquatic Process and Product Technology, Section for Aquatic Protein Biochemistry
Contributors: Godiksen, H., Hyldig, G., Jessen, F.
Publication date: 2006
Use of multivariate analysis in the transformation of 2D gel images into relevant spot quantity data

**General information**
- Publication status: Published
- Organisations: Section for Aquatic Process and Product Technology, National Institute of Aquatic Resources, Section for Aquatic Protein Biochemistry
- Contributors: Jensen, K., Søndergaard, I., Jacobsen, S., Jørgensen, B., Jessen, F.
- Publication date: 2006
- Peer-reviewed: No
- Event: Poster session presented at 7th Siena meeting from genome to proteome, September 3rd - 7th, Siena, Italy.

**Bibliographical note**
- Poster
- Source: orbit
- Source-ID: 225992
- Research output: Contribution to conference » Poster – Annual report year: 2006 » Research

Effect of age and temperature on amino acid composition and the content of different protein types of juvenile cod (Gadus morhua L.) otoliths

**General information**
- Publication status: Published
- Organisations: Section for Population- and Ecosystem Dynamics, National Institute of Aquatic Resources, Section for Aquatic Protein Biochemistry
- Contributors: Hüssy, K., Mosegaard, H., Jessen, F.
- Pages: 1012-1020
- Publication date: 2004
- Peer-reviewed: Yes

**Publication information**
- Journal: Canadian Journal of Fisheries and Aquatic Sciences
- Volume: 61
- Issue number: 6
- ISSN (Print): 0706-652X
- Scopus rating (2004): SJR 1.767 SNIP 1.532
- Web of Science (2004): Indexed yes
- Original language: English
- Source: orbit
- Source-ID: 225857
- Research output: Contribution to journal » Journal article – Annual report year: 2004 » Research » peer-review

Two-dimensional gel electrophoresis detection of protein oxidation in fresh and tainted rainbow trout muscle

**General information**
- Publication status: Published
- Organisations: National Institute of Aquatic Resources, Section for Aquatic Protein Biochemistry
- Contributors: Kjærgård, I. V. H., Jessen, F.
- Pages: 7101-7107
- Publication date: 2004
- Peer-reviewed: Yes

**Publication information**
- Journal: Journal of Agricultural and Food Chemistry
Proteome analysis elucidating post mortem changes in cod (Gadus morhua) muscle proteins

General information
Publication status: Published
Organisations: National Institute of Aquatic Resources, Section for Aquatic Protein Biochemistry
Contributors: Kjærsgård, I. V. H., Jessen, F.
Pages: 3985-3991
Publication date: 2003
Peer-reviewed: Yes

Publication information
Journal: Journal of Agricultural and Food Chemistry
Volume: 51
Issue number: 14
ISSN (Print): 0021-8561
Ratings:
Scopus rating (2003): SJR 1.152 SNIP 1.464
Web of Science (2003): Indexed yes
Original language: English
Source: orbit
Source-ID: 226238
Research output: Contribution to journal › Journal article – Annual report year: 2003 › Research › peer-review

Sarcoplasmic reticulum Ca2+-ATPase and cytochrome oxidase as indicators of frozen storage in cod (Gadus morhua)

General information
Publication status: Published
Organisations: National Institute of Aquatic Resources, Section for Aquatic Process and Product Technology, Section for Aquatic Protein Biochemistry
Contributors: Godiksen, H., Hyldig, G., Jessen, F.
Pages: 2579-2585
Publication date: 2003
Peer-reviewed: Yes

Publication information
Journal: Journal of Food Science
Volume: 68
Issue number: 8
ISSN (Print): 0022-1147
Ratings:
Scopus rating (2003): SJR 0.703 SNIP 1.013
Web of Science (2003): Indexed yes
Original language: English
Source: orbit
Source-ID: 225530
Research output: Contribution to journal › Journal article – Annual report year: 2003 › Research › peer-review

ATP, IMP, and glycogen in cod muscle at onset and during development of rigor mortis depend on the sampling location
Variation in glycogen, ATP, and IMP contents within individual cod muscles were studied in ice stored fish during the progress of rigor mortis. Rigor index was determined before muscle samples for chemical analyzes were taken at 16 different positions on the fish. During development of rigor, the contents of glycogen and ATP decreased differently in relation to rigor index depending on sampling location. Although fish were considered to be in strong rigor according to the rigor index method, parts of the muscle were not in rigor as high ATP concentrations were found in dorsal and tail muscle.
Extracting information from two-dimensional electrophoresis gels by partial least squares regression

Two-dimensional gel electrophoresis (2-DE) produces large amounts of data and extraction of relevant information from these data demands a cautious and time consuming process of spot pattern matching between gels. The classical approach of data analysis is to detect protein markers that appear or disappear depending on the experimental conditions. Such biomarkers are found by comparing the relative volumes of individual spots in the individual gels. Multivariate statistical analysis and modelling of 2-DE data for comparison and classification is an alternative approach utilising the combination of all proteins/spots in the gels. In the present study it is demonstrated how information can be extracted by multivariate data analysis. The strategy is based on partial least squares regression followed by variable selection to find proteins that individually or in combination with other proteins vary informatively in relation to the experimental conditions. Finding of such coherent protein patterns leads to identification of potential relations between the involved proteins, and will be useful for focusing further investigation of proteins that relate to the chosen experimental conditions.

God og dårlig frossen fisk - hvorfor er der en forskel?

General information
Publication status: Published
Organisations: National Institute of Aquatic Resources, Section for Aquatic Protein Biochemistry
Contributors: Jessen, F., Nielsen, J.
Pages: 16-25
Publication date: 2002
Peer-reviewed: Yes
Temperature and Ca\textsuperscript{2+}-dependence of the sarcoplasmic reticulum Ca\textsuperscript{2+}-ATPase in haddock, salmon, rainbow trout and zebra cichlid

Temperature dependence of Ca\textsuperscript{2+}-ATPase from the sarcoplasmic reticulum (SR) in rabbit muscle has been widely studied, and it is generally accepted that a break point in Arrhenius plot exist at approximately 20 degreesC. Whether the break point arises as a result of temperature dependent changes in the enzyme or its membrane lipid environment is still a matter of discussion. In this study we compared the temperature dependence and Ca\textsuperscript{2+}-dependence of SR Ca\textsuperscript{2+}-ATPase in haddock (Melanogrammus aeglefinus), salmon (Salmo, salar), rainbow trout (Oncorhynchus mykiss) and zebra cichlid (Cichlasoma nigrofasciatum). The Arrhenius plot of zebra cichlid showed a break point at 20 degreesC, and the haddock Arrhenius plot was non-linear with pronounced changes in slope in the temperature area, 6-14 degreesC. In Arrhenius plot from both salmon and rainbow trout a plateau exists with an almost constant SR Ca\textsuperscript{2+}-ATPase activity. The temperature range of the plateau was 14-21 and 18-25 degreesC in salmon and rainbow trout, respectively. Ca\textsuperscript{2+}-dependence in the four different fish species investigated was very similar with half maximal activation (K\textsubscript{0.5}) between 0.2 and 0.6 \textmu M and half maximal inhibition (I\textsubscript{0.5}) between 60 and 250 \textmu M. Results indicated that interaction between SR Ca\textsuperscript{2+}-ATPase and its lipid environment may play an important role for the different Arrhenius plot of the different types of fish species investigated. (C) 2002 Elsevier Science Inc. All rights reserved.

ATP and glycogen content related to gaping in pre rigor cod ( Gadus morhua ) frozen in blocks at sea

ATP and glycogen content related to gaping in pre rigor cod ( Gadus morhua ) frozen in blocks at sea
Chilling and freezing of fish and fishery products

General information
Publication status: Published
Organisations: Section for Aquatic Process and Product Technology, National Institute of Aquatic Resources, Section for Aquatic Protein Biochemistry
Contributors: Nielsen, J., Larsen, E., Jessen, F.
Pages: 403-437
Publication date: 2001

Host publication information
Title of host publication: Advances in food refrigeration
Place of publication: Leatherhead
Publisher: Leatherhead Publishing
Editor: Sun, D.
ISBN (Print): 09-05-74883-2
Source: orbit
Source-ID: 226859
Research output: Chapter in Book/Report/Conference proceeding

Cytochrome oxidase as an indicator of ice storage and frozen storage
The potential of cytochrome oxidase as an indicator of ice storage and frozen storage of fish was investigated. Optimal assay conditions for cytochrome oxidase in a crude homogenate from cod muscle were studied. Maximal cytochrome oxidase activity was found at pH 6.5-7.5 and an assay temperature of 30 degreesC. Maximal activation by Triton X-100 was obtained in a range of 0.62-1.25 mM Triton X-100. The specificity of the assay was high, as cytochrome oxidase was inhibited 98% by 33 muM of the specific inhibitor sodium azide. The coefficient of variation of cytochrome oxidase activity in different cods was 21%, and the coefficient of variation of different analyses on the same homogenate was 5%. It was shown that ice storage of muscle samples before they were frozen and thawed resulted in a major freezing-induced activation of cytochrome oxidase activity. The enzyme may therefore be used as an indicator of frozen fish to determine if the fish has been stored on ice before freezing. Cytochrome oxidase activity showed also potential as an indicator of frozen storage, as it was possible to distinguish between the frozen storage temperatures -9, -20, and -40 degreesC.

General information
Publication status: Published
Organisations: National Institute of Aquatic Resources, Section for Aquatic Protein Biochemistry
Contributors: Godiksen, H., Jessen, F.
Pages: 4488-4493
Publication date: 2001
Peer-reviewed: Yes

Publication information
Journal: Journal of Agricultural and Food Chemistry
Volume: 49
Issue number: 9
ISSN (Print): 0021-8561
Ratings:
Scopus rating (2001): SJR 1.044 SNIP 1.234
Web of Science (2001): Indexed yes
Original language: English
DOIs: 10.1021/jf0015219
Source: orbit
Source-ID: 225525
Research output: Contribution to journal
Degradation of ATP and glycogen in cod (Gadus morhua) muscle during freezing
Changes in ATP, IMP, lactate and glycogen contents in the muscle of cod were followed during freezing at temperatures of -20°C and -45°C. ATP degradation was accompanied by a corresponding increase in IMP content. Simultaneous measurement of temperature showed that at both freezing rates, the greatest decrease in ATP content was observed when the temperature reached -0.8°C. Glycolysis occurred during freezing of cod as indicated by an increase in lactate content. The changes found in all measured metabolites were more pronounced when freezing was performed at a slow rate compared to a fast rate due to the thermal arrest time at about 0.8°C.

Glycolysis and ATP degradation in cod (Gadus morhua) at subzero temperatures in relation to thaw rigor
Glycolysis was shown to occur during freezing of cod of decrease in glycogen and an increase in lactate. In addition, the ATP content decreased during freezing. Synthesis of ATP was measured as degradation of glycogen. During storage at -9 and -12 degreesC it was found that degradation of ATP was faster than synthesis of ATP. This was leading to presence of glycogen even at low ATP concentrations. The ATP and glycogen degradation rates and lactate formation rate reached an optimum (both in small samples as well as in whole fish) when stored at -9 degreesC compared to -12 degreesC. Evidence of ATP synthesis at 0 degreesC during thawing was obtained in samples as well as in whole fish. Reduction or elimination of thaw rigor effects (shrinkage and drip loss) during a period of frozen storage were examined. When thawing at 5 degreesC, fillets stored at -9 degreesC showed significantly less shrinkage than fillets stored at -40 degreesC. In addition, pre-rigor fillets (-40 degreesC) showed significantly the smallest drip loss compared with fillets stored at -9 degreesC. (C) 2001 Academic Press.
Sarcoplasmic reticulum CA 2+ ATPase activity in cod (Gadus morhua) muscle measured in crude homogenates

General information
Publication status: Published
Organisations: National Institute of Aquatic Resources, Section for Aquatic Protein Biochemistry
Contributors: Godiksen, H., Jessen, F.
Pages: 343-358
Publication date: 2001
Peer-reviewed: Yes

Publication information
Journal: Journal of Food Biochemistry
Volume: 25
Issue number: 4
ISSN (Print): 0145-8884
Ratings:
Scopus rating (2001): SJR 0.681 SNIP 1.029
Web of Science (2001): Indexed yes
Original language: English
Source: orbit
Source-ID: 225529
Research output: Contribution to journal › Journal article – Annual report year: 2001 › Research › peer-review

Sarcoplasmic Reticulum Ca2+-ATPase Activity in Cod (Gadus morhua) Muscle Measured in Crude Homogenates

General information
Publication status: Published
Organisations: National Institute of Aquatic Resources
Contributors: Godiksen, H., Jessen, F.
Pages: 343-359
Publication date: 2001
Peer-reviewed: Yes

Publication information
Journal: Journal of Food Biochemistry
Volume: 25
Issue number: 4
ISSN (Print): 0145-8884
Ratings:
Scopus rating (2001): SJR 0.681 SNIP 1.029
Web of Science (2001): Indexed yes
Original language: English
Source: orbit
Source-ID: 175850
Research output: Contribution to journal › Journal article – Annual report year: 2001 › Research › peer-review

The effect of ice storage and freeze/thaw cycles on CA 2+ -ATPase and Cytochrome oxidase activity in salmon (Salmo salar)

General information
Publication status: Published
Organisations: National Institute of Aquatic Resources, Section for Aquatic Protein Biochemistry
Contributors: Godiksen, H., Jessen, F.
Pages: 151-159
Publication date: 2001
Peer-reviewed: No

Publication information
Journal: Annales Societatis Scientiarum Færoensis Supplementum
Volume: XXVIII
ISSN (Print): 0356-6772
Original language: English
Source: orbit
Source-ID: 225533
Identification of fish species after cooking by SDS-PAGE and Urea IEF: a collaborative study

General information
Publication status: Published
Organisations: Section for Aquatic Protein Biochemistry, National Institute of Aquatic Resources
Pages: 2653-2658
Publication date: 2000
Peer-reviewed: Yes

Sarcoplasmic reticulum CA 2+ -ATPASE activity changes during frozen storage depend on pre-freezing time

General information
Publication status: Published
Organisations: Section for Aquatic Protein Biochemistry, National Institute of Aquatic Resources
Pages: 412
Publication date: 2000
Peer-reviewed: No

Species identification of smoked and gravad fish products by sodium dodecylsulphate polyacrylamide gel electrophoresis, urea isoelectric focusing and native isoelectric focusing: a collaborative study

A collaborative study on the use of sodium dodecylsulphate polyacrylamide gel electrophoresis (SDS-PAGE), urea- isoelectric focusing (urea-IEF) and native isoelectric focusing for the identification of species of smoked salmonids, gravad salmonids and smoked eels was carried out by eight laboratories. With SDS-PAGE, minor changes took place in the profiles of the processed salmonid species making it impossible or very difficult to identify closely related species. With urea-IEF, there were fewer changes in the profiles due to processing and the system generally had greater species- discriminating power for the processed salmonids than SDS-PAGE. The profiles of the eel species as obtained on SDS- PAGE or urea-IEF were not affected by smoking. Urea-IEF had greater species- discriminating power than SDS-PAGE for the eel species. Native IEF was useful in providing supplementary identification on species difficult to identify by SDS- PAGE or by urea-IEF in the case of cold smoked products. (C) 2000 Elsevier Science Ltd. All rights reserved.

General information
Publication status: Published
Organisations: Section for Aquatic Protein Biochemistry, National Institute of Aquatic Resources
Pages: 1-7
Publication date: 2000
Peer-reviewed: Yes
A standardized method of identification of raw and heat-processed fish by urea isoelectric focusing: A collaborative study

General information
Publication status: Published
Organisations: Section for Aquatic Protein Biochemistry, National Institute of Aquatic Resources
Pages: 1923-1933
Publication date: 1999
Peer-reviewed: Yes

Development of a sodium dodecyl sulfate-polyacrylamide gel electrophoresis reference method for the analysis and identification of fish species in raw and heat-processed samples: A collaborative study

A collaborative study was carried out in seven European labs with the aim of achieving a sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) standard operation procedure to identify fish species in raw and cooked samples. Urea and SDS-containing solutions were evaluated as extractants. Several preelectrophoretic operations - such as treatment with RNase/DNase, ultrafiltration and desalting - and up to ten types of gels and three SDS-PAGE systems were considered. The SDS-containing solution allowed a higher protein extractability than urea. Unlike urea extraction, SDS extraction seemed not to be influenced so much by the state of the sample (raw, cooked at 60 degrees C, cooked at 85 degrees C). Desalting, ultrafiltration or treatment with RNase/DNase did not improve the discriminatory power of the protein patterns. Commercial homogeneous 15% ExcelGels, especially when they were silver stained, yielded good results and afforded higher reproducibility, thus allowing a better matching of results among the laboratories participating in this collaborative study. Under the optimized technical conditions described above, all the fish species tested, either raw and cooked, yielded reproducible and discriminant species-specific protein patterns

General information
Publication status: Published
Organisations: Section for Aquatic Protein Biochemistry, National Institute of Aquatic Resources
Pages: 1425-1432
Publication date: 1999
Peer-reviewed: Yes
Species identification of cooked fish by urea isoelectric focusing and sodium dodecylsulfate polyacrylamide gel electrophoresis: a collaborative study
The suitability and reliability of urea IEF and SDS-PAGE for the identification of cooked fish flesh was tested by a collaborative study among nine laboratories. Urea IEF was performed with CleanGels as well as with ImmobilineGels, and ExcelGels were used for SDS-PAGE, enabling all three types of gels to be run in the same flat bed electrophoresis chamber. By strictly following optimised standard operation procedures (SOPs), five unknown cooked samples had to be identified with each technique using a set of 10 raw reference samples. With urea IEF, only one out of 35 identifications was incorrect, and with SDS-PAGE a similar result was obtained. It was concluded that methods, as now developed, are suitable for checking the species declaration of fishery products. (C) 1999 Elsevier Science Ltd. All rights reserved

Synthesis and degradation of adenosine triphosphate in cod (Gadus morhua) at subzero temperatures
This study has demonstrated that the extraction step is very important when analysing ATP and its degradation products. An important factor is whether the sample is fresh, frozen or thawed when homogenised since thawing of the sample will lead to rapid loss of ATP. During frozen storage it was found that ATP in cod (Gadus morhua) was stable at -40 degrees C in small samples for at least 12 weeks. At -20 degrees C it was found that ATP content increases initially and thereafter falls. It was demonstrated that degradation of ATP in small samples occurs faster at 0 degrees C than at -2 and -5 degrees C. Furthermore, it was found that in whole cod ATP could be synthesised at a significant rate at -7 degrees C. (C) 1999 Society of Chemical Industry.
Factors affecting the quality of frozen meat and fish

General information
Publication status: Published
Organisations: Section for Aquatic Protein Biochemistry, National Institute of Aquatic Resources, Section for Aquatic Process and Product Technology
Contributors: Archer, G., Evans, J., Jessen, F., Nielsen, J., James, S.
Pages: 17-25
Publication date: 1998

Host publication information
Place of publication: Leeds
Publisher: University of Leeds
Editors: Kennedy, C., Archer, G.
Source: orbit
Source-ID: 224822

Freeze denaturation of fish proteins investigated by DSC

General information
Publication status: Published
Organisations: Section for Aquatic Protein Biochemistry, National Institute of Aquatic Resources
Contributors: Jessen, F., Geirsdottir, M.
Publication date: 1998

Host publication information
Title of host publication: Contribution at the concerted action: The preservation of frozen food quality and safety throughout the distribution chain

Bibliographical note
Portomeeting, 10-13 September 1998
Source: orbit
Source-ID: 226040

Relation between TMAOase activity and content of formaldehyde in fillet minces and bellyflap mince from gadoid fishes

General information
Publication status: Published
Organisations: National Institute of Aquatic Resources, Section for Aquatic Process and Product Technology, Section for Aquatic Protein Biochemistry
Contributors: Rehbein, H., Schubring, R., Havemeister, W., Gonzales-Sotelo, C., Nielsen, M. K., Jørgensen, B., Jessen, F.
Pages: 114-118
Publication date: 1997
Peer-reviewed: No

Publication information
Journal: Informationen für die Fischwirtschaft aus der Fischereiforschung
Volume: 44
Issue number: 3
ISSN (Print): 1437-5842
Original language: English
Source: orbit
Source-ID: 227259
Research output: Contribution to journal – Journal article – Annual report year: 1997 – Research