Inger Vibeke Holst Kjærsgård - DTU Orbit (31/12/2017)

Inger Vibeke Holst Kjærsgård

Organisations

Department of Systems Biology
04/07/2003 → 03/09/2013 Former
ivk@dfu.min.dk
VIP

Senior Research Scientist, National Institute of Aquatic Resources
25/01/2007 → 03/09/2013 Former
ivk@aqua.dtu.dk
VIP

Others
25/01/2007 → 03/09/2013 Former
ivk@aqua.dtu.dk
VIP

Department of Systems Biology
18/02/2004 → 31/10/2013 Former
ivk@dfu.min.dk
VIP

Publications:

Protein and lipid oxidation in frozen rainbow trout

General information
State: Published
Organisations: Section for Aquatic Lipids and Oxidation, National Institute of Aquatic Resources, Section for Aquatic Protein Biochemistry
Authors: Baron, C. (Intern), Kjærsgård, I. V. H. (Intern), Jessen, F. (Intern), Jacobsen, C. (Intern)
Publication date: 2008
Event: Poster session presented at 99th AOCS Annual Meeting & Expo, Seattle, WA, United States.
Main Research Area: Technical/natural sciences

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

Protein and lipid oxidation during frozen storage of rainbow trout (Oncorhynchus mykiss)

General information
State: Published
Organisations: Section for Aquatic Lipids and Oxidation, National Institute of Aquatic Resources, Department of Systems Biology, Section for Aquatic Protein Biochemistry
Authors: Baron, C. (Intern), Kjærsgård, I. V. H. (Intern), Jessen, F. (Intern), Jacobsen, C. (Intern)
Pages: 8118-8125
Publication date: 2007
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Agricultural and Food Chemistry
Volume: 55
Issue number: 20
ISSN (Print): 0021-8561
Ratings:
BFI (2018): BFI-level 2
BFI (2017): BFI-level 2
Protein and lipid oxidation in frozen rainbow trout

General information
State: Published
Organisations: Section for Aquatic Lipids and Oxidation, National Institute of Aquatic Resources, Section for Aquatic Protein Biochemistry
Authors: Baron, C. (Intern), Kjærsgård, I. V. H. (Intern), Jessen, F. (Intern), Jacobsen, C. (Intern)
Publication date: 2007

Host publication information
Title of host publication: European Congress of Chemical Engineering (ECCE-6), Copenhagen, 16-20 September 2007
Main Research Area: Technical/natural sciences
Conference: European Congress of Chemical Engineering - 6, Copenhagen, Denmark, 16/09/2007 - 16/09/2007

Bibliographical note
Abstract and Poster
Source: orbit
Source-ID: 224859
Publication: Research › Conference abstract in proceedings – Annual report year: 2007

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 6months frozen storage with 12months 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 ?-actin fragments, and a nuclease 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
State: Published
Organisations: National Institute of Aquatic Resources, Section for Aquatic Protein Biochemistry
Authors: Kjærsgård, I. V. H. (Intern), Nørrelykke, M. (Ekstern), Jessen, F. (Intern)
Pages: 1606-1618
Publication date: 2006
Main Research Area: Technical/natural sciences

Publication information
Journal: Proteomics
Volume: 6
Issue number: 5
ISSN (Print): 1615-9853
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.85 SJR 1.492 SNIP 0.89
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.464 SNIP 0.978 CiteScore 3.7
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.436 SNIP 0.981 CiteScore 3.73
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.48 SNIP 0.985 CiteScore 3.88
ISI indexed (2013): ISI indexed yes
Changes in fish muscle proteins during frozen storage revealed by proteomics combined with multivariate data analysis

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Aquatic Protein Biochemistry
Authors: Kjærsgård, I. V. H. (Intern), Nørrelykke, M. (Ekstern), Jessen, F. (Intern)
Publication date: 2006
Event: Poster session presented at Dansk konference om Molekylær Biologi og Bioteknologi, Vejle, Danmark, juni, .
Main Research Area: Technical/natural sciences

Bibliographical note
Poster
Source: orbit
Source-ID: 226235
Publication: Research › Poster – Annual report year: 2006

Hvad sker der, når vi fryser torsken?

General information
State: Published
Identification of oxidised proteins from rainbow trout by mass spectrometry

General information
State: Published
Organisations: National Institute of Aquatic Resources
Authors: Nørrelykke, M. (Ekstern), Kjærsgård, I. V. H. (Intern), Petersen, J. (Ekstern), Beck, H. (Ekstern)
Publication date: 2006
Event: Poster session presented at 17th International Mass Spectrometry Conference, Aug 27 - Sep 1, 2006, Prague, Czech Republic.
Main Research Area: Technical/natural sciences

Bibliographical note
Poster
Source: orbit
Source-ID: 226237
Publication: Research - peer-review › Journal article – Annual report year: 2006

Kvalitetsforskelle i opdrætsørred - kan de forudsiges?
Protein and lipid oxidation during frozen storage of rainbow trout

Proteomics combined with multivariate data analysis

Proteomic detection of protein oxidation in fish during frozen storage and tainting
Two-dimensional gel electrophoresis detection of protein oxidation in fresh and tainted rainbow trout muscle

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Aquatic Protein Biochemistry
Authors: Kjærsgård, I. V. H. (Intern), Jessen, F. (Intern)
Pages: 7101-7107
Publication date: 2004
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Agricultural and Food Chemistry
Volume: 52
Issue number: 23
ISSN (Print): 0021-8561
Ratings:
BFI (2018): BFI-level 2
BFI (2017): BFI-level 2
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 3.45 SJR 1.291 SNIP 1.344
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.236 SNIP 1.253 CiteScore 3.23
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.278 SNIP 1.421 CiteScore 3.25
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.423 SNIP 1.479 CiteScore 3.44
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.43 SNIP 1.471 CiteScore 3.2
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.384 SNIP 1.446 CiteScore 3.1
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.408 SNIP 1.392
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.317 SNIP 1.303
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.361 SNIP 1.324
Web of Science (2008): Indexed yes
Proteome analysis elucidating post mortem changes in cod (Gadus morhua) muscle proteins

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Aquatic Protein Biochemistry
Authors: Kjærsgård, I. V. H. (Intern), Jessen, F. (Intern)
Pages: 3985-3991
Publication date: 2003
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Agricultural and Food Chemistry
Volume: 51
Issue number: 14
ISSN (Print): 0021-8561
Ratings:
BFI (2018): BFI-level 2
BFI (2017): BFI-level 2
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 3.45 SJR 1.291 SNIP 1.344
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.236 SNIP 1.253 CiteScore 3.23
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.278 SNIP 1.421 CiteScore 3.25
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.423 SNIP 1.479 CiteScore 3.44
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.43 SNIP 1.471 CiteScore 3.2
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.

General information
State: Published
Organisations: Section for Aquatic Protein Biochemistry, National Institute of Aquatic Resources, Section for Aquatic Process and Product Technology
Authors: Jessen, F. (Intern), Lametsch, R. (Ekstern), Bendixen, E. (Ekstern), Kjærsgård, I. V. H. (Intern), Jørgensen, B. (Intern)
Pages: 32-35
Publication date: 2002
Main Research Area: Technical/natural sciences
Projects:

**Prediction of technological and sensory quality of trout**
Manufacturing food of high and uniform quality requires good knowledge of the characteristics of the raw material, and knowledge of how these characteristics vary between different raw materials. It is also necessary to know how suitable a given raw material is for different types of product, and how the interaction between raw materials and production technology affects the sensory quality of the final product.

The most important differences between fish raw materials will be reflected in the pheno type of the fish, irrespective of whether the cause of this is genetic or environmental. Characterization of pheno type will thus we appropriate to identifying the characteristics of the raw material (protein markers) that will be included in a model to predict the technological and sensory quality of the final product.

The project will produce a number of frozen and smoked products from different raw materials. Characterisation of pheno types will take place through proteom analyses, where image analysis of 2DE gels will reveal protein markers that can potentially relate the quality of the final product to the characteristics of the original raw material. These proteins will be identified using mass spectroscopy and antibodies against them will be raised. The antibodies will be used to develop rapid immune chemical methods. The quality of both the different varieties of raw materials and the

National Food Institute
Division of Industrial Food Research
Department of Systems Biology
Enzyme and Protein Chemistry
Period: 01/08/2003 → 30/04/2009
Number of participants: 6
Project participant:
Kjærsgård, Inger Vibeke Holst (Intern)
Godiksen, Helene (Intern)
Hyløjig, Grethe (Intern)
Barkholt, Vibeke (Intern)
Frøkiær, Hanne (Intern)
Project Manager, academic:
Jessen, Flemming (Intern)

**Proteome analysis of muscle tissues: Two dimensional protein mapping of pig and cod muscle.**
Certain aspects of muscle biology such as metabolism, growth and development of muscle cells influence the quality of muscle based foods. In addition, the proteolytic processes that start immediately after slaughter or catch (post mortem metabolism) have major impact on taste and texture of meat from fish and mammals. In order to secure optimal quality, it is important to understand the basic mechanisms of muscle biology as well as to understand the post mortem processes that turn muscle into meat. Hence it is important to characterize the involved proteins and genes, and how they interact with each other and with environmental factors to influence meat quality. Proteome analysis is a new and powerful tool for characterization of cellular protein expression. This method is based on 2 dimensional (2D) electrophoretic separation of the cellular proteins so that each protein can be identified by its specific coordinates in a 2D protein map from which it can be extracted and identified by micro sequencing and mass spectrometry. Our aim is to establish and optimize such 2D protein maps of muscle tissues from cod and pork. Existing methods of tissue preparation, 2D gel separation and computer assisted image analysis of the 2D maps will be optimized. The established 2D maps will be used to study proteins that are involved in post mortem changes of muscle tissue, in order to find and identify marker proteins that can be used as assays for quality labeling.

National Institute of Aquatic Resources
Danish Institute of Agricultural Sciences
Period: 01/07/1999 → 31/05/2003
Number of participants: 3
Project participant:
Kjaersgaard, Inger Vibeke Holst (Intern)
Stampe-Villadsen, Hanne Lilian (Intern)
Project Manager, organisational:
Jessen, Flemming (Intern)
Financing sources
Source: Unknown
Name of research programme: Ukendt
Amount: 5,135,000.00 Danish Kroner
Project