Validation of a novel one-step reverse transcription polymerase chain reaction method for detecting viral haemorrhagic septicaemia virus

Viral haemorrhagic septicaemia (VHS) is one of the most serious viral diseases in salmonid and olive flounder farms. Various diagnostic methods for detecting VHS virus (VHSV) are described in the VHS chapter of the World Organization for Animal Health (OIE) Aquatic Diagnostic Manual. A conventional reverse transcription-PCR (cRT-PCR) targeting the viral nucleocapsid gene is recommended for the detection of VHSV and, to some extent, for genotypic classification. However, the recommended assay exhibits low sensitivity for the detection of VHSV genotype IVa isolates and often shows non-specific amplicons when the RNA template is extracted from non-infected fish cell lines. For these reasons, it is necessary to develop a new RT-PCR method for the foolproof detection of all VHSV genotypes and elimination of non-specific results. In this study, we selected five candidate primer sets that target the VHSV nucleoprotein (N) gene, and selected the most sensitive among them (3F/2R). We then established the optimal reaction conditions for these primers, and ensured that no non-specific amplification had occurred in the fish tissues, fish cell lines, or heterologous viruses. The analytical sensitivity of the novel cRT-PCR was compared to that of cell culture assays, real-time RT-PCR, and other cRT-PCR methods and was found to be as sensitive as or superior to the other methods for detecting all VHSV genotypes. Our newly developed cRT-PCR assay was tested with 80 isolates, representing a collection of all known VHSV genotypes worldwide. Clear and unique amplicons were amplified from all 80 VHSV isolates. The reproducibility, and partly the robustness, of the assay were confirmed by an inter-laboratory proficiency tests including nine laboratories. A high diagnostic sensitivity and specificity was confirmed on tissue material from affected fish. In conclusion a highly robust, sensitive and specific cRT-PCR for detection of VHSV was developed and validated.
Evolution of complex asexual reproductive strategies in jellyfish

Many living organisms in terrestrial and aquatic ecosystems rely on multiple reproductive strategies to reduce the risk of extinction in variable environments. Examples are provided by the polyp stage of several bloom-forming jellyfish species, which can reproduce asexually using different budding strategies. These strategies broadly fall into three categories: (1) fast localized reproduction, (2) dormant cysts, or (3) motile and dispersing buds. Similar functional strategies are also present in other groups of species. However, mechanisms leading to the evolution of this rich reproductive diversity are yet to be clarified. Here we model how risk of local population extinction and differential fitness of alternative modes of asexual reproduction could drive the evolution of multiple reproductive modes as seen in jellyfish polyps. Depending on environmental parameters, we find that evolution leads to a unique evolutionarily stable strategy, wherein multiple reproductive strategies generally coexist. As the extinction risk increases, this strategy shifts from a pure budding mode to a dual strategy and finally to one characterized by allocation into all three modes. We identify relative fitness-dependent thresholds in extinction risk where these transitions can occur and discuss our predictions in light of observations on polyp reproduction in laboratory and natural systems.

General information

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Organisations: National Institute of Aquatic Resources, Section for Oceans and Arctic, Technical University of Denmark, Okinawa Institute of Science and Technology (OIST)
Authors: Schnedler-Meyer, N. A. (Intern), Pigolotti, S. (Ekstern), Mariani, P. (Intern)
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Main Research Area: Technical/natural sciences
Population genetic structure after 125 years of stocking in sea trout (Salmo trutta L.)

Stocking can be an effective management and conservation tool, but it also carries the danger of eroding natural population structure, introducing non-native strains and reducing genetic diversity. Sea trout, the anadromous form of the brown trout (Salmo trutta), is a highly targeted species that is often managed by stocking. Here, we assess the present-day population genetic structure of sea trout in a backdrop of 125 years of stocking in Northern Germany. The study area...
is characterized by short distances between the Baltic and North Sea river watersheds, historic use of fish from both watersheds for stocking, and the creation of a potential migration corridor between the Baltic and North Sea with the opening of the Kiel Canal 120 years ago. A survey of 24 river systems with 180 SNPs indicates that moderate but highly significant population genetic structure has persisted both within and between the Baltic and North Sea. This genetic structure is characterized by (i) heterogeneous patterns of admixture between the Baltic and North Sea that do not correlate with distance from the Kiel Canal and are therefore likely due to historic stocking practises, (ii) genetic isolation by distance in the Baltic Sea at a spatial scale of < 200 km that is consistent with the homing behaviour of sea trout, and (iii) at least one genetically distinct Baltic Sea river system. In light of these results, we recommend keeping fish of North Sea and Baltic Sea origin separate for stocking, and restricting Baltic Sea translocations to neighbouring river systems.

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Organisations: Technical University of Denmark, National Institute of Aquatic Resources, Section for Marine Living Resources, GEOMAR - Helmholtz Centre for Ocean Research Kiel, NLWKN – Lower Saxony Water Management, Mecklenburg-Vorpommern State Research Center for Agriculture and Fisheries, Fish Hatchery Altmühlendorf, University of Kiel
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Scopus rating (2016): SJR 0.768 SNIP 0.788 CiteScore 1.62
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Scopus rating (2012): SJR 0.881 SNIP 0.962 CiteScore 1.7
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Scopus rating (2011): SJR 0.829 SNIP 0.92 CiteScore 1.61
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Scopus rating (2010): SJR 0.735 SNIP 0.812
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Scopus rating (2009): SJR 1.065 SNIP 1.032
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Scopus rating (2008): SJR 1.104 SNIP 1.168
Scopus rating (2007): SJR 1.216 SNIP 1.043
Scopus rating (2006): SJR 0.876 SNIP 0.86
Scopus rating (2005): SJR 1.141 SNIP 1.059
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.9 SNIP 0.91
Differences in Carbohydrates Utilization and Antibiotic Resistance Between Streptococcus macedonicus and Streptococcus thermophilus Strains Isolated from Dairy Products in Italy

Streptococcus thermophilus and S. macedonicus are the only two species of the genus related to food production so far known. In the present study, eight S. thermophilus and seven S. macedonicus strains isolated from dairy environments in Italy were compared in order to evidence possible species-specific technological characteristics. Their capability to use lactose, galactose, fructose, and glucose, sugars commonly present in foods and two carbohydrates considered as prebiotics, xylose and inulin, along with the respective growth kinetics were studied. Results showed a luxuriant growth on lactose and different behaviors on galactose, glucose, and fructose. No growth on inulin and xylose was recorded, which is a positive feature for strains intended to be used as starter cultures. Growth parameters, namely, $\lambda$, $\mu_{max}$, and $N_{max}$, were estimated by using the Gompertz model. Antibiotic resistance to 14 drugs revealed an overall similar behavior between the two species with only a marked difference regarding gentamycin. Antimicrobial activity was also tested against six deleterious bacterial strains, but none of the strains evidenced inhibitory capabilities. The results presented here could be helpful to compare technological potentialities of the two species and to choose strains of the most suitable species for selected microbiological food transformations.
Probabilistic structural assessment of conical grouted joint using numerical modelling

Conical grouted joints have been proposed as a solution for the relative settlement observed between the sleeve and the pile on monopiles for wind turbines. In this paper, the influence of the design parameters such as steel wall thicknesses and conical angle on the failure modes associated to continual loadings are assessed based on finite element analysis. It is found that both the sleeve's and pile's wall thicknesses have a significant impact on the grouted joint health. Namely, the larger are the wall thicknesses, the more vulnerable the grout is with respect to fatigue and material degradation but the more limited the progressive settlement is, and inversely. This implies that the appropriate wall thicknesses should be chosen by designers having in mind that neither extreme is conservative. Based on statistical modeling, the grout length is found to be the most influential parameter of the settlement caused by extreme loadings: longer grout significantly contributes to the reduction of extreme settlement. To ensure that the inevitable settlement does not jeopardize the joint's structural integrity, a probability-based method has been developed to estimate the minimal gap between the pile top and the brackets required to achieve a targeted annual reliability index (of 3.3).

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Organisations: Department of Wind Energy, Wind Turbine Structures and Component Design
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Microbial electrolytic disinfection process for highly efficient Escherichia coli inactivation

Water quality deterioration caused by a wide variety of recalcitrant organics and pathogenic microorganisms has become a serious concern worldwide. Bio-electro-Fenton systems have been considered as cost-effective and highly efficient water treatment platform technology. While it has been extensively studied for recalcitrant organics removal, its application
potential towards water disinfection (e.g., inactivation of pathogens) is still unknown. This study investigated the inactivation of Escherichia coli in a microbial electrolysis cell based bio-electro-Fenton system (renamed as microbial electrolytic-Fenton cell) with the aim to broaden the application of microbial electrochemistry. Results showed that a 4-log reduction of Escherichia coli (10^7 to hundreds CFU/mL) was achieved with an external applied voltage of 0.2 V, 0.3 mM Fe^{2+} and cathodic pH of 3.0. However, non-notable inactivation was observed in the control experiments without external voltage or Fe^{2+} dose. The disinfection effect was enhanced when cathode air flow rate increased from 7 to 41 mL/min and was also in proportion to the increase of Fe^{2+} concentration from 0.15 to 0.45 mmol/mL. Fatal cell membrane destruction by [rad]OH was identified as one potential mechanism for disinfection. This study successfully demonstrated the feasibility of bio-electro-Fenton process for pathogens inactivation, which offers insight for the future development of sustainable, efficient, and cost-effective biological water treatment technology.

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Organisations: Department of Environmental Engineering, Residual Resource Engineering, South China University of Technology, Technical University of Denmark
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BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 3.03
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Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
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Web of Science (2007): Indexed yes
Climate change risks for severe storms in developing countries in the context of poverty and inequality in Cambodia

Least developed countries are generally regarded as particularly sensitive to climate change due to among other vulnerable locations and low adaptation capabilities. In the present study, we address climate change hazards in least developed countries by presenting a methodological framework, which is suitable for the estimation damage costs as a function of risk aversion, equality, income distribution and climate scenario using state-of-the-art climate model projections. As a case study, the methodology is applied to study severe storms in Cambodia based on two future climate scenarios and data on historical damages from storm events, which are used as a proxy in performing a sensitivity analysis on all input parameters. For the assumptions and parameter ranges used here, the study shows a high sensitivity to the income distribution (reflected by discount rates) and risk aversion and smaller effects from equality measures and extreme wind climate scenario. We emphasize that the assumptions on risk aversion reflecting consumption smoothing possibilities of low-income households clearly depicts that climate risks can be particularly high as a consequence of poverty and therefore recommend that context-specific vulnerabilities and equity concerns in climate risk studies should be included when making assessments for least developed countries.

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Transcriptional profiles of PBMCs from pigs infected with three genetically diverse porcine reproductive and respiratory syndrome virus strains

Porcine reproductive and respiratory syndrome virus is the cause of reproductive failure in sows and respiratory disease in young pigs, which has been considered as one of the most costly diseases to the worldwide pig industry for almost 30 years. This study used microarray-based transcriptomic analysis of PBMCs from experimentally infected pigs to explore the patterns of immune dysregulation after infection with two East European PRRSV strains from subtype 2 (BOR and ILI) in comparison to a Danish subtype 1 strain (DAN). Transcriptional profiles were determined at day 7 post infection in three tested groups of pigs and analysed in comparison with the expression profile of control group. Microarray analysis revealed differential regulation (> 1.5-fold change) of 4253 and 7335 genes in groups infected with BOR and ILI strains, respectively, and of 12518 genes in pigs infected with Danish strain. Subtype 2 PRRSV strains showed greater induction of many genes, especially those involved in innate immunity, such as interferon stimulated antiviral genes and inflammatory markers. Functional analysis of the microarray data revealed a significant up-regulation of genes involved in processes such as acute phase response, granulocyte and agranulocyte adhesion and diapedesis, as well as down-regulation of genes enrolled in pathways engaged in protein synthesis, cell division, as well as B and T cell signaling. This study provided an insight into the host response to three different PRRSV strains at a molecular level and demonstrated variability between strains of different pathogenicity level.
Stress response and cognitive performance modulation in classroom versus natural environments: A quasi-experimental pilot study with children

Stress during childhood can have mental and somatic health influences that track throughout life. Previous research attributes stress-reducing effects to natural environments, but has mainly focused on adults and often following leisurely relaxation in natural environments. This pilot study explores the impact of natural environments on stress response during rest and mental load and cognitive performance in 47 children aged 10–12 years in a school context. Heart rate variability measures indexing tonic, event, and phasic vagal tone and attention scores were compared across classroom and natural environments. Tonic vagal tone was higher in the natural environment than the classrooms, but no differences were found in event or phasic vagal tone or cognitive performance measures. These findings suggest a situational aspect of the conditions under which natural environments may give rise to stress-buffering influences. Further research is warranted to understand the potential benefits in a real-life context, in particular with respect to the underpinning mechanisms and effects of accumulated exposure over time in settings where children spend large proportions of time in natural environments.
Echinococcus multilocularis in Denmark 2012–2015: high local prevalence in red foxes

In Western Europe, the Echinococcus multilocularis lifecycle is predominantly sylvatic, typically involving red foxes (Vulpes vulpes) as the main definitive hosts with Microtus spp. and Arvicola spp. as intermediate hosts. During a 4-year surveillance study (2012–2015), Danish red foxes and raccoon dogs (n = 1345) were examined for E. multilocularis. Moreover, 134 insectivores and rodents collected in South Jutland during spring and summer 2016 were examined for the presence of metacestodes. The sedimentation and counting technique and molecular typing were used to identify E. multilocularis infections in the carnivores, while the rodent livers were examined macro- and microscopically for parasite lesions. Following morphological identification of E. multilocularis adult worms, the identity was verified by sequence analysis of the 12S rRNA gene in most cases (n = 13). Echinococcus multilocularis infection was demonstrated in 19 red foxes (Vulpes vulpes) originating from only two specific areas of South Jutland, namely Højer and Grindsted, and in two raccoon dogs (Nyctereutes procyonoides), originating from Højer. In Højer, 28.5% (CI 95% 11.7–45.3) of the examined red foxes were E. multilocularis positive per year. Moreover, positive red foxes were identified each year from 2012 to 2015, while E. multilocularis positive red foxes were only identified in Grindsted in 2013 (4.0%) and 2014 (6.4%). In contrast, all collected rodents were negative for E. multilocularis. We conclude that E. multilocularis is locally endemic in South Jutland with a high local prevalence in Højer.
Transcriptome analysis of the adult human Klinefelter testis and cellularity-matched controls reveals disturbed differentiation of Sertoli- and Leydig cells article

The most common human sex chromosomal disorder is Klinefelter syndrome (KS; 47, XXY). Adult patients with KS display a diverse phenotype but are nearly always infertile, due to testicular degeneration at puberty. To identify mechanisms causing the selective destruction of the seminiferous epithelium, we performed RNA-sequencing of 24 fixed paraffin-embedded testicular tissue samples. Analysis of informative transcriptomes revealed 235 differentially expressed transcripts (DETs) in the adult KS testis showing enrichment of long non-coding RNAs, but surprisingly not of X-chromosomal transcripts. Comparison to 46,XY samples with complete spermatogenesis and Sertoli cell-only-syndrome allowed prediction of the cellular origin of 71 of the DETs. DACH2 and FAM9A were validated by immunohistochemistry and found to mark apparently undifferentiated somatic cell populations in the KS testes. Moreover, transcriptomes from fetal, pre-pubertal, and adult KS testes showed a limited overlap, indicating that different mechanisms are likely to operate at each developmental stage. Based on our data, we propose that testicular degeneration in men with KS is a consequence of germ cells loss initiated during early development in combination with disturbed maturation of Sertoli- and Leydig cells.

General information
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Organisations: Department of Bio and Health Informatics, DTU Multi Assay Core, Aarhus University, Copenhagen University Hospital, University of Copenhagen
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Kinetic Modeling of Texture and Color Changes During Thermal Treatment of Chicken Breast Meat

Heat treatment is commonly applied as a primary method for ensuring the microbial safety of poultry meat and to enhance its palatability. Although texture and color of cooked chicken breast meat are important quality parameters for the consumers that need to be controlled during thermal processing, studies assessing the temperature-time-dependent quality changes during thermal treatment are lacking. This work aims to investigate the texture and color changes of chicken breast meat during thermal processing and to develop kinetic models that describe these changes. We studied the storage modulus changes of chicken breast meat as function of temperature. The storage modulus increases from 55 °C until leveling off in an equilibrium value above 80 °C, which was attributed to microstructure changes and described with a sigmoidal function. The changes in the texture (TPA) and color (CIE L*a*b*) of chicken breast meat were measured as function of temperature and time. The texture and color parameters show a rise with heating time until reaching an equilibrium value, while the rate of change increased with temperature. Kinetic models that take the non-zero equilibrium into account were developed to describe the color (lightness) and texture (hardness, gumminess, and chewiness) changes with heating time and temperature. The kinetic models provide a deeper insight into the mechanisms of texture and color changes during thermal treatment. They can be used to predict the texture and color development of chicken breast meat during thermal processing and, thus, help to optimize the process.

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Organisations: National Food Institute, Research Group for Food Production Engineering
Authors: Rabeler, F. (Intern), Feyissa, A. H. (Intern)
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BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.329 SNIP 1.375 CiteScore 2.74
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Scopus rating (2013): SJR 1.234 SNIP 1.701 CiteScore 2.97
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
Scopus rating (2012): SJR 1.361 SNIP 2.346 CiteScore 3.42
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
Scopus rating (2011): SJR 1.14 SNIP 2.027 CiteScore 2.87
ISI indexed (2011): ISI indexed yes
Phone-based metric as a predictor for basic personality traits

Basic personality traits are believed to be expressed in, and predictable from, smart phone data. We investigate the extent of this predictability using data (n = 636) from the Copenhagen Network Study, which to our knowledge is the most extensive study concerning smartphone usage and personality traits. Based on phone usage patterns, earlier studies have reported surprisingly high predictability of all Big Five personality traits. We predict personality trait tertiles (low, medium, high) from a set of behavioral variables extracted from the data, and find that only extraversion can be predicted significantly better (35.6%) than by a null model. Finally, we show that the higher predictabilities in the literature are likely due to overfitting on small datasets.

General information

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Organisations: Department of Applied Mathematics and Computer Science, Cognitive Systems, University of Copenhagen
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Scopus rating (2014): CiteScore 2.46 SNIP 1.306 SJR 1.796
Scopus rating (2013): CiteScore 2.89 SNIP 1.345 SJR 1.819
Scopus rating (2012): CiteScore 2.38 SNIP 1.228 SJR 1.693
Scopus rating (2011): CiteScore 2.49 SNIP 1.26 SJR 1.693
Scopus rating (2010): SNIP 1.015 SJR 1.472
Scopus rating (2009): SNIP 1.297 SJR 1.484
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Scopus rating (2005): SNIP 1.215 SJR 1.671
Scopus rating (2004): SNIP 1.088 SJR 0.968
Scopus rating (2003): SNIP 0.894 SJR 0.926
Scopus rating (2002): SNIP 1.026 SJR 0.836
Scopus rating (2001): SNIP 0.785 SJR 0.956
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Scopus rating (1999): SNIP 0.831 SJR 1.339
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Effects of oil spill response technologies on the physiological performance of the Arctic copepod Calanus glacialis

A mesocosm study with oil in ice was performed in Van Mijenfjorden in Svalbard to compare effects of the oil spill responses (OSR) in situ burning, chemical dispersion and natural attenuation on the physiological performance of the Arctic copepod Calanus glacialis. Seawater collected from the mesocosms in winter and spring was used in laboratory incubation experiments, where effects on fecal pellet production, egg production and hatching success were investigated over a period of 14 days. Polycyclic aromatic hydrocarbon (PAH) seawater concentrations were lowest in winter. Brine channel formation in spring resulted in an 18 times increase in PAH concentration in the chemical dispersion treatment (1.67 μg L\(^{-1}\)), and a 3 fold increase in the natural attenuation (0.36 μg L\(^{-1}\)) and in situ burning (0.04 μg L\(^{-1}\)) treatments. The physiological performance of female C. glacialis was unaffected by the PAH seawater concentrations. However, a higher mortality and deformity of nauplii was observed in the chemical dispersion treatment, highlighting the importance of considering secondary effects on next generation in future environmental risk assessment of OSR. This study shows that during the ice-covered period, chemical dispersion of oil spills leads to higher PAH exposure than natural attenuation and in situ burning, with potential consequences for recruitment of Arctic copepods.

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Authors: Toxværd, K. (Intern), Pančić, M. (Intern), Eide, H. O. (Ekstern), Søreide, J. E. (Ekstern), Lacroix, C. (Ekstern), Le Floch, S. (Ekstern), Hjorth, M. (Ekstern), Nielsen, T. G. (Intern)
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Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.624 SNIP 1.179 CiteScore 3.79
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.594 SNIP 1.324 CiteScore 3.75
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.891 SNIP 1.485 CiteScore 4.06
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.89 SNIP 1.489 CiteScore 3.83
ISI indexed (2012): ISI indexed yes
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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.

General information
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Organisations: National Food Institute, Research Group for Food Production Engineering, University of Copenhagen, Royal Greenland A/S
Authors: Dang, T. T. (Ekstern), Gringer, N. (Intern), Jessen, F. (Intern), Olsen, K. (Ekstern), Bøknæs, N. (Ekstern), Nielsen, P. L. (Ekstern), Orlien, V. (Ekstern)
Estimation and Control of Wind Turbine Tower Vibrations Based on Individual Blade-Pitch Strategies

In this brief, we present a method to estimate the tower fore-aft velocity based upon measurements from blade load sensors. In addition, a tower dampening control strategy is proposed based upon an individual blade pitch control architecture that employs this estimate. The observer design presented in this brief exploits the Coleman transformations that convert a time-varying turbine model into one that is linear and time-invariant, greatly simplifying the observability analysis and subsequent observer design. The proposed individual pitch-based tower controller is decoupled from the rotor speed regulation loop and hence does not interfere with the nominal turbine power regulation. Closed-loop results, obtained from high fidelity turbine simulations, show close agreement between the tower estimates and the actual tower velocity. Furthermore, the individual-pitch-based tower controller achieves a similar performance compared with the collective-pitch-based approach but with negligible impact upon the nominal turbine power output.

General information
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Organisations: Technical University of Denmark, Department of Wind Energy, Wind turbine loads & control, University of Sheffield
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ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.495 SNIP 3.011 CiteScore 3.7
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.585 SNIP 2.909 CiteScore 3.26
ISI indexed (2011): ISI indexed yes
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BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.098 SNIP 2.391
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.587 SNIP 2.789
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Scopus rating (2007): SJR 1.082 SNIP 2.205
Scopus rating (2006): SJR 1.021 SNIP 2.306
Corrigendum: An analysis of natural T cell responses to predicted tumor neoepitopes [Front Immunol, 8, 1566, (2017)]
An outdated version of Supplementary Table 1 was uploaded to the final version of the paper for publication. This table
has not been under peer review and does not include the information described in the paper such as the similarity
measurement column. The correct Supplementary Table 1 has now been published in the original article. The authors
apologize for this oversight. This error does not change the scientific conclusion of the article in any way. The original
article has been updated.

General information
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Organisations: Department of Bio and Health Informatics, Cancer Genomics, Immunoinformatics and Machine Learning,
Technical University of Denmark, National Veterinary Institute, T-cells & Cancer, Universidad Nacional de San Martin
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Szallasi, Z. (Intern), Eklund, A. C. (Intern)
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Scopus rating (2016): CiteScore 5.37 SJR 3.034 SNIP 1.476
Web of Science (2016): Indexed yes
Scopus rating (2015): SJR 2.827 SNIP 1.277 CiteScore 5.09
Web of Science (2015): Indexed yes
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Web of Science (2014): Indexed yes
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Understanding the impact of non-standard customisations in an engineer-to-order context: A case study

Companies operating with an engineer-to-order (ETO) manufacturing strategy produce customised solutions for their customers. While they may be able to build on a base of existing sub-solutions, e.g. standard product structures, modules or parts when engineering a customer-specific solution, they often have to create something completely new to satisfy customers’ requirements. However, it is not always clear to ETO companies what the costs associated with making customer specific solutions are, or which product or project characteristics drive costs and in what business processes. Therefore, it is not clear to companies if it is actually profitable for them to fulfil all of their customers’ requirements. Hence, making it relevant to understand how creating non-standard customisations impact project profitability. This paper presents a framework for how ETO companies can quantify the impact of the complexity associated with non-standard customisations when cost data is only available at the project level. The framework is theoretically founded; it is based on statistical regression and a definition of a complexity index for non-standard customisations. The framework is validated in the context of an ETO case company and empirical data is presented.
Direct acting antiviral treatment of chronic hepatitis C in Denmark: factors associated with and barriers to treatment initiation

Objectives: We describe factors associated with and barriers to initiation of Direct Acting Antiviral (DAA) treatment in patients with chronic hepatitis C, who fulfill national fibrosis treatment guidelines in Denmark. Materials and Methods: In this nationwide cohort study, we included patients with chronic hepatitis C from The Danish Database for Hepatitis B and C (DANHEP) who fulfilled fibrosis treatment criteria. Factors associated with treatment initiation and treatment failure were determined by logistic regression analyses. Medical records were reviewed from patients who fulfilled fibrosis treatment criteria, but did not initiate DAA treatment to determine the cause. Results: In 344 (49%) of 700 patients, who fulfilled treatment criteria, factors associated with DAA treatment initiation were transmission by other routes than injecting drug use odds ratio (OR) 2.13 (CI: 1.38–3.28), previous treatment failure OR 2.58 (CI: 1.84–3.61) and ALT above upper limit of normal OR 1.60 (CI: 1.18–2.17). The most frequent reasons for not starting treatment among 356 (51%) patients were non-adherence to medical appointments (n=107/30%) and ongoing substance use (n=61/17%). Treatment failure with viral relapse occurred in 19 (5.5%) patients, who were more likely to have failed previous treatment OR 4.53 (CI: 1.59–12.91). Conclusions: In this nationwide cohort study, we found non-adherence to medical appointments and active substance use to be major obstacles for DAA treatment initiation. Our findings highlight the need for interventions that can overcome these barriers and increase the number of patients who can initiate and benefit from curative DAA treatment.

General information
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Organisations: Department of Bio and Health Informatics, Disease Intelligence and Molecular Evolution, University of Copenhagen, Aalborg University, Hospital Lillebaelt, University of Southern Denmark, Aarhus University
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BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.38 SJR 1.108 SNIP 0.918
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.947 SNIP 0.764 CiteScore 2.19
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.072 SNIP 0.999 CiteScore 2.44
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Scopus rating (2013): SJR 0.122 SNIP 0.987 CiteScore 2.33
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.111 SNIP 1.023 CiteScore 2.23
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BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.107 SNIP 0.916 CiteScore 1.97
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.107 SNIP 0.824
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.171 SNIP 0.823
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.232 SNIP 0.882
Scopus rating (2007): SJR 0.304 SNIP 1.248
Scopus rating (2006): SJR 0.692 SNIP 1.429
Scopus rating (2005): SJR 0.531 SNIP 0.834
Scopus rating (2004): SJR 0.539 SNIP 0.971
Scopus rating (2003): SJR 0.552 SNIP 0.738
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 0.394 SNIP 0.521
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 0.599 SNIP 0.747
Web of Science (2001): Indexed yes
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CD103⁺ CD11b⁺ mucosal classical dendritic cells initiate long-term switched antibody responses to flagellin

Antibody responses induced at mucosal and nonmucosal sites demonstrate a significant level of autonomy. Here, we demonstrate a key role for mucosal interferon regulatory factor-4 (IRF4)-dependent CD103⁺ CD11b⁺ (DP), classical dendritic cells (cDCs) in the induction of T-dependent immunoglobulin G (IgG) and immunoglobulin A (IgA) responses in the mesenteric lymph node (MLN) following systemic immunization with soluble flagellin (sFliC). In contrast, IRF8-dependent CD103⁺ CD11b⁻ (SP) are not required for these responses. The lack of this response correlated with a complete absence of sFliC-specific plasma cells in the MLN, small intestinal lamina propria, and surprisingly also the bone marrow (BM). Many sFliC-specific plasma cells accumulating in the BM of immunized wild-type mice expressed α4β7⁺, suggesting a mucosal origin. Collectively, these results suggest that mucosal DP cDC contribute to the generation of the sFliC-specific plasma cell pool in the BM and thus serve as a bridge linking the mucosal and systemic immune system.

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Web of Science (2018): Indexed yes
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Web of Science (2016): Indexed yes
Scopus rating (2015): SJR 4.401 SNIP 1.447 CiteScore 6.53
Web of Science (2015): Indexed yes
Scopus rating (2014): SJR 4.597 SNIP 1.686 CiteScore 6.82
Scopus rating (2013): SJR 4.076 SNIP 1.623 CiteScore 6.75
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
Scopus rating (2012): SJR 3.999 SNIP 1.631 CiteScore 6.69
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
Scopus rating (2011): SJR 4.534 SNIP 1.452 CiteScore 6.66
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