Parasites in Myodes glareolus and their association with diet assessed by stable isotope analysis

Vertebrates are hosts to numerous parasites, belonging to many different taxa. These parasites differ in transmission, being through either direct contact, a faecal-oral route, ingestion of particular food items, vertical or sexual transmission, or by a vector. Assessing the impact of diet on parasitism can be difficult because analysis of faecal and stomach content are uncertain and labourious: and as with molecular methods, do not provide diet information over a longer period of time. We here explored whether the analysis of stable isotopes in hair provides insight into the impact of diet and the presence of parasites in the rodent Myodes glareolus. Twenty-one animals were examined for parasites and their hair analysed for stable isotopes (C and N). A positive correlation between δ15N and one species of intestinal parasite was observed in females. Furthermore, several ectoparasites were negatively correlated with δ15N, indicating that infections are further associated with foraging habits (size and layout of the home range, length and timing of foraging, interaction with other rodents, etc.) that set the rodents in direct contact with infected hosts. Although a limited number of animals were included, it seemed that the isotope values allowed for identification of the association between diet and parasite occurrence in this rodent. We therefore propose that this method is useful in providing further insight into host biology, feeding preferences and potential exposure to parasites species, contributing to the understanding of the complex relationship between hosts and parasites.
road towards transition to a mechanistically-based human-focused hazard and risk assessment of chemicals requires an open mind towards stepping away from the animal study as the gold standard and defining human biologically based regulatory requirements for human hazard and risk assessment.

**General information**

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Organisations: Copenhagen Center for Health Technology, National Food Institute, Research Group for Molecular and Reproductive Toxicology, National Institute of Public Health and the Environment, Utrecht University, Federal Institute for Risk Assessment, European Chemicals Agency, Cosmetics Europe, BASF, European Commission Joint Research Centre Institute, Vrije Universiteit Brussel, SeCAM


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BFI (2014): BFI-level 1
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BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.846 SNIP 1.03 CiteScore 2.8
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.836 SNIP 1.018
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.791 SNIP 0.93
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.796 SNIP 0.906
Scopus rating (2007): SJR 0.723 SNIP 0.956
Scopus rating (2006): SJR 0.696 SNIP 1.02
Scopus rating (2005): SJR 0.644 SNIP 0.976
Scopus rating (2004): SJR 0.63 SNIP 1.038
Scopus rating (2003): SJR 0.532 SNIP 0.785
Scopus rating (2002): SJR 0.331 SNIP 0.714
Vitamin D-biofortified beef: A comparison of cholecalciferol with synthetic versus UVB-mushroom-derived ergosterol as feed source

This study investigates dietary fortification of heifer feeds with cholecalciferol and ergocalciferol sources and effects on beef total vitamin D activity, vitamer, respective 25-hydroxy metabolite contents, and meat quality. Thirty heifers were allocated to one of three dietary treatments [(1) basal diet + 4000 IU of vitamin D₃ (Vit D₃); (2) basal diet + 4000 IU of vitamin D₂ (Vit D₂); and (3) basal diet + 4000 IU of vitamin D₂-enriched mushrooms (Mushroom D₂)] for a 30 day pre-slaughter period. Supplementation of heifer diets with Vit D₃ yielded higher (p < 0.001) Longissimus thoracis (LT) total vitamin D activity (by 38–56%; p < 0.05) and serum 25-OH-D concentration (by 20–36%; p < 0.05), compared to that from Vit D₂ and Mushroom D₂ supplemented animals. Irrespective of vitamin D source, carcass characteristics, sensory and meat quality parameter were unaffected (p > 0.05) by the dietary treatments. In conclusion, vitamin D₃ biofortification of cattle diets is the most efficacious way to enhance total beef vitamin D activity.

General information
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Organisations: National Food Institute, Research Group for Bioactives – Analysis and Application, University College Dublin, University College Cork
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Scopus rating (2017): CiteScore 5.19 SJR 1.793 SNIP 2.109
Web of Science (2017): Indexed yes
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Scopus rating (2016): CiteScore 4.85 SJR 1.731 SNIP 2.095
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.582 SNIP 1.946 CiteScore 4.31
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.557 SNIP 2.01 CiteScore 3.92
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
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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 1.762 SNIP 2.342 CiteScore 3.98
Combination of sodium caseinate and succinylated alginate improved stability of high fat fish oil-in-water emulsions

Sodium caseinate (CAS) and commercial sodium alginate (CA), long chain modified alginate (LCMA) or short chain modified alginate (SCMA) were used in combination for emulsifying and stabilizing high fat (50–70%) fish oil-in-water emulsions. Physical (creaming, droplet size, viscosity and protein determination) and oxidative (primary and secondary oxidation products) stabilities of the emulsions were studied during 12 days of storage. Creaming stability was higher for emulsions produced with alginates and CAS compared to emulsions prepared with only CAS. Combined use of CAS + LCMA performed better in terms of physical stability compared to emulsions produced with only CAS. However, the oxidative stability of this emulsion was inferior probably due to the presence of an unsaturated carbon chain in LCMA structure. CAS + SCMA emulsions not only showed better physical stability such as smaller droplet size, lower creaming and higher viscosity, but also had an improved oxidative stability than emulsions produced with only CAS.

General information
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Organisations: National Food Institute, Research Group for Bioactives – Analysis and Application, Aarhus University, Division of Food Technology
Authors: Yesiltas, B. (Intern), Sørensen, A. M. (Intern), García Moreno, P. J. (Intern), Anankanbil, S. (Ekstern), Guo, Z. (Ekstern), Jacobsen, C. (Intern)
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  Web of Science (2016): Indexed yes
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  Web of Science (2015): Indexed yes
  BFI (2014): BFI-level 2
  Scopus rating (2014): SJR 1.557 SNIP 2.01 CiteScore 3.92
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  Scopus rating (2013): SJR 1.554 SNIP 2.056 CiteScore 3.87
  ISI indexed (2013): ISI indexed yes
  Web of Science (2013): Indexed yes
  BFI (2012): BFI-level 2
  Scopus rating (2012): SJR 1.762 SNIP 2.342 CiteScore 3.98
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  BFI (2010): BFI-level 2
  Scopus rating (2010): SJR 1.981 SNIP 2.253
  Web of Science (2010): Indexed yes
  BFI (2009): BFI-level 2
  Scopus rating (2009): SJR 1.789 SNIP 2.023
  Web of Science (2009): Indexed yes
  BFI (2008): BFI-level 2
  Scopus rating (2008): SJR 1.47 SNIP 1.706
  Web of Science (2008): Indexed yes
  Scopus rating (2007): SJR 1.475 SNIP 2.087
  Web of Science (2007): Indexed yes
  Web of Science (2006): Indexed yes
  Scopus rating (2005): SJR 1.028 SNIP 1.526
  Web of Science (2005): Indexed yes
  Scopus rating (2004): SJR 1.077 SNIP 1.438
  Scopus rating (2003): SJR 0.876 SNIP 1.248
  Web of Science (2003): Indexed yes
  Scopus rating (2002): SJR 0.966 SNIP 1.235
  Web of Science (2002): Indexed yes
  Scopus rating (2001): SJR 0.785 SNIP 0.975
Genome-wide association and HLA fine-mapping studies identify risk loci and genetic pathways underlying allergic rhinitis

Allergic rhinitis is the most common clinical presentation of allergy, affecting 400 million people worldwide, with increasing incidence in westernized countries. To elucidate the genetic architecture and understand the underlying disease mechanisms, we carried out a meta-analysis of allergic rhinitis in 59,762 cases and 152,358 controls of European ancestry and identified a total of 41 risk loci for allergic rhinitis, including 20 loci not previously associated with allergic rhinitis, which were confirmed in a replication phase of 60,720 cases and 618,527 controls. Functional annotation implicated genes involved in various immune pathways, and fine mapping of the HLA region suggested amino acid variants important for antigen binding. We further performed genome-wide association study (GWAS) analyses of allergic sensitization against inhalant allergens and nonallergic rhinitis, which suggested shared genetic mechanisms across rhinitis-related traits. Future studies of the identified loci and genes might identify novel targets for treatment and prevention of allergic rhinitis.

General information

State: Accepted/in press
Organisations: Department of Biotechnology and Biomedicine, Disease Systems Immunology, Department of Bio and Health Informatics, Immunoinformatics and Machine Learning, University of Copenhagen, Helmholtz Zentrum Muenchen German Research Center for Environmental Health, University of Manchester, 23andMe Inc., University of Chicago, Hospital Universitario Nuestra Senora de Candelaria, Vrije Universiteit Amsterdam, Imperial College London, Instituto de Salud Global de Barcelona, University Medicine Greifswald, University of Kiel, University of Arizona, Universitat Politecnica de Catalunya, Icahn School of Medicine at Mount Sinai (ISMMS), University of California at San Francisco, University of Southern California, University of Basel, Erasmus University Rotterdam, University of Melbourne, University of Liege, University of Bristol, Henry Ford Health System, Telethon Kids Institute, University of Oulu, deCODE Genetics, University Children’s Hospital Regensburg (KUNO), University of Helsinki, National Institute for Health and Welfare, Karolinska Institutet, MAX DELBRUCK CENTER FOR MOLECULAR MEDICINE, University of Southern Denmark, University of Newcastle, Stockholm County Council, University of Western Australia, Institut d’Investigacio Sanitaria Illes Balears (IdISBa), Queensland Institute of Medical Research, University of London, Ludwig-Maximilians-University Munchen, Swiss Tropical Institute, Universidad de La Laguna, University of Iceland, Harvard University


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Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 20.87 SNIP 5.222
Web of Science (2008): Indexed yes
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Web of Science (2007): Indexed yes
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 14.345 SNIP 5.272
Web of Science (2005): Indexed yes
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Scopus rating (2003): SJR 13.523 SNIP 5.059
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 13.631 SNIP 5.2
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 15.204 SNIP 5.584
Web of Science (2001): Indexed yes
Web of Science (2000): Indexed yes
Stability of vitamin D₃ and vitamin D₂ in oil, fish and mushrooms after household cooking

Information on the retention of vitamin D in food following household cooking is scarce. So far the retention of its metabolites vitamin D₃, vitamin D₂, and 25-hydroxyvitamin D₃ has shown that the type of food and the cooking method are the essential determinants, and there is no significant difference between the metabolites. We investigated the retention of vitamin D₃ and vitamin D₂ in sunflower oil, vitamin D₃ in rainbow trout, and vitamin D₂ in button mushrooms. The investigated cooking methods were boiling at different pH, steamed cooking, microwave cooking, pan-frying, and oven baking. There was no difference between the retention of vitamin D₃ and vitamin D₂ added to sunflower oil, which ranged from 70 to 99%. In rainbow trout, the retention of vitamin D₃ at 85–114% was not significantly different from 100%, except for panfrying at 85%. However, the retention of vitamin D₂ in mushrooms at 62–88% was significantly different from 100% (p ≤ 0.05).

General information
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Organisations: National Food Institute, Research Group for Bioactives – Analysis and Application
Authors: Ložnjak, P. (Intern), Jakobsen, J. (Intern)
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Scopus rating (2016): CiteScore 4.85 SJR 1.731 SNIP 2.095
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ISI indexed (2013): ISI indexed yes
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Scopus rating (2012): SJR 1.762 SNIP 2.342 CiteScore 3.98
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.911 SNIP 2.383 CiteScore 4.17
ISI indexed (2011): ISI indexed yes
The mismatch between the in-country determinants of technology transfer, and the scope of technology transfer initiatives under the United Nations Framework Convention on Climate Change

Despite decades of international political emphasis, little is known about the in-country determinants of technology transfer for climate change mitigation. We draw upon the conclusions of a series of standardised, official governmental statements of technology priorities, coupled with questionnaire-based data collection, to shed light on the nature of those determinants. We find that there is a disconnect between what developing country governments perceive as the key enablers of, and barriers to, technology transfer, and what bilateral and multilateral technology transfer programmes can offer, given budgetary constraints and the logic of development aid spending. We show that the well-established notion of making climate change mitigation actions an integral part of sound development plans is especially relevant for technology transfer. We offer pointers as to how this might be done in practice, in the context of the ‘technology action plans’ developed as part of the United Nations-sponsored technology needs assessment process.

General information
State: Accepted/In press
Organisations: Technical University of Denmark, Department of Management Engineering, UNEP DTU Partnership
Authors: Puig, D. (Intern), Haselip, J. A. (Intern), Bakhtiari, F. (Intern)
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Main Research Area: Technical/natural sciences

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Journal: International Environmental Agreements: Politics, Law and Economics
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BFI (2018): BFI-level 1
The prehistoric peopling of Southeast Asia

The human occupation history of Southeast Asia (SEA) remains heavily debated. Current evidence suggests that SEA was occupied by Hòabìnhian hunter-gatherers until ~4000 years ago, when farming economies developed and expanded, restricting foraging groups to remote habitats. Some argue that agricultural development was indigenous; others favor the “two-layer” hypothesis that posits a southward expansion of farmers giving rise to present-day Southeast Asian genetic diversity. By sequencing 26 ancient human genomes (25 from SEA, 1 Japanese Jōmon), we show that neither interpretation fits the complexity of Southeast Asian history: Both Hòabìnhian hunter-gatherers and East Asian farmers contributed to current Southeast Asian diversity, with further migrations affecting island SEA and Vietnam. Our results help resolve one of the long-standing controversies in Southeast Asian prehistory.

General information

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Organisations: Department of Bio and Health Informatics, Metagenomics, University of Copenhagen, Museum National d'Histoire Naturelle, Kanazawa University, Kitasato University, University of Bern, University of New England NSW, Universite Toulouse III - Paul Sabatier, Griffith University Queensland, Silpakorn University, Ministry of Information and
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.

General information
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Organisations: National Veterinary Institute, Public Sector Consultancy, Fish Diseases, National Fishery Products Quality Management Services
Authors: Kim, H. J. (Ekstern), Cuenca, A. (Intern), Olesen, N. J. (Intern)
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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.
Composition Engineering in Two-Dimensional Pb-Sn-Alloyed Perovskites for Efficient and Stable Solar Cells

Environmentally friendly tin (Sn)-based metallic halide perovskites suffer from oxidation and morphological issues. Here, we demonstrate the composition engineering of Pb-Sn-alloyed two-dimensional (2D) Ruddlesden-Popper perovskites, \((\text{BA})_2(\text{MA})_3\text{Pb}_{3-x}\text{Sn}_x\text{I}_{13}\), for efficient and stable solar cell applications. Smooth thin films with high surface coverage are readily formed without using any additive owing to the self-assembly characteristic of 2D perovskites. It is found that Sn plays a significant role in improving the crystallization and crystal orientation while narrowing the bandgap of Pb-Sn 2D perovskites. Photophysical studies further reveal that the optimal Sn ratio (25 mol %) based sample exhibits both minimized trap density and weakened quantum confinement for efficient charge separation. Consequently, the optimized \((\text{BA})_2(\text{MA})_3\text{Pb}_3\text{Sn}_{13}\)-based solar cells yield the best power conversion efficiency close to 6% with suppressed hysteresis.
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 practices, (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, GEMAR - 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
Authors: Petereit, C. (Ekstern), Bekkevold, D. (Intern), Nickel, S. (Ekstern), Dierking, J. (Ekstern), Hantke, H. (Ekstern), Hahn, A. (Ekstern), Reusch, T. (Ekstern), Puebla, O. (Ekstern)
Publication date: 20 Jun 2018
Main Research Area: Technical/natural sciences
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 productions 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, \( \lambda \), \( \mu_{\text{max}} \), and \( N_{\text{max}} \) 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.

**General information**

State: Accepted/In press
Organisations: Department of Environmental Engineering, Residual Resource Engineering, University of Padova, Universidade Federal de Vicosa
Authors: Tarrah, A. (Ekstern), Treu, L. (Intern), Giaretta, S. (Ekstern), Duarte, V. (Ekstern), Corich, V. (Ekstern), Giacomini, A. (Ekstern)
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BFI (2016): BFI-level 1
Scopus rating (2016): SJR 0.627 SNIP 0.652 CiteScore 1.54
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.618 SNIP 0.626 CiteScore 1.37
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.66 SNIP 0.862 CiteScore 1.64
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.632 SNIP 0.842 CiteScore 1.62
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
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ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.711 SNIP 0.958 CiteScore 1.82
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.647 SNIP 0.715
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.648 SNIP 0.765
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.674 SNIP 0.813
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 0.598 SNIP 0.67
Scopus rating (2006): SJR 0.581 SNIP 0.611
Scopus rating (2005): SJR 0.597 SNIP 0.627
Scopus rating (2004): SJR 0.653 SNIP 0.708
Scopus rating (2003): SJR 0.658 SNIP 0.754
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 0.664 SNIP 0.719
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).

General information
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Organisations: Department of Wind Energy, Wind Turbine Structures and Component Design
Authors: Njomo-Wandji, W. (Intern), Natarajan, A. (Intern), Dimitrov, N. (Intern)
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Scopus rating (2017): CiteScore 2.7 SJR 1.284 SNIP 1.929
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Scopus rating (2016): CiteScore 2.46 SJR 1.258 SNIP 1.975
Web of Science (2016): Indexed yes
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Scopus rating (2015): SJR 1.235 SNIP 1.908 CiteScore 2.19
Web of Science (2015): Indexed yes
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Scopus rating (2014): SJR 1.188 SNIP 2.249 CiteScore 2.11
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.129 SNIP 2.719 CiteScore 2.2
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.14 SNIP 2.407 CiteScore 1.71
ISI indexed (2012): ISI indexed yes
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.
Gaze typing in virtual reality: Impact of keyboard design, selection method, and motion

Gaze tracking in virtual reality (VR) allows for hands-free text entry, but it has not yet been explored. We investigate how the keyboard design, selection method, and motion in the field of view may impact typing performance and user experience. We present two studies of people \( n = 32 \) typing with gaze+dwell and gaze+click inputs in VR. In study 1, the typing keyboard was flat and within-view; in study 2, it was larger-than-view but curved. Both studies included a stationary and a dynamic motion conditions in the user’s field of view. Our findings suggest that 1) gaze typing in VR is viable but constrained, 2) the users perform best (10.15 WPM) when the entire keyboard is within-view; the larger-than-view keyboard (9.15 WPM) induces physical strain due to increased head movements, 3) motion in the field of view impacts the user’s performance: Users perform better while stationary than when in motion, and 4) gaze+click is better than dwell only
Head and gaze control of a telepresence robot with an HMD

Gaze interaction with telerobots is a new opportunity for wheelchair users with severe motor disabilities. We present a video showing how head-mounted displays (HMD) with gaze tracking can be used to monitor a robot that carries a 360° video camera and a microphone. Our interface supports autonomous driving via way-points on a map, along with gaze-controlled steering and gaze typing. It is implemented with Unity, which communicates with the Robot Operating System (ROS).

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.

General information
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Organisations: Department of Management Engineering, Systems Analysis
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Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 0.798 SNIP 1.144 CiteScore 2.02
Web of Science (2016): Indexed yes
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Scopus rating (2015): SJR 0.817 SNIP 1.166 CiteScore 1.89
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Scopus rating (2014): SJR 0.835 SNIP 1.276 CiteScore 1.96
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.776 SNIP 1.352 CiteScore 1.94
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.707 SNIP 1.426 CiteScore 1.76
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.786 SNIP 1.116 CiteScore 1.6
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.697 SNIP 1.189
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Scopus rating (2009): SJR 0.667 SNIP 1.147
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Scopus rating (2007): SJR 0.742 SNIP 1.271
Scopus rating (2006): SJR 0.563 SNIP 0.961
Scopus rating (2005): SJR 0.822 SNIP 1.105
Scopus rating (2004): SJR 0.708 SNIP 1.048
Scopus rating (2003): SJR 0.477 SNIP 1.056
Scopus rating (2002): SJR 0.271 SNIP 0.352
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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.

General information
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BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.84 SJR 0.736 SNIP 0.768
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.761 SNIP 0.75 CiteScore 1.83
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.753 SNIP 0.919 CiteScore 2.04
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.715 SNIP 0.853 CiteScore 1.97
ISI indexed (2013): ISI indexed yes
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Scopus rating (2012): SJR 0.658 SNIP 1.014 CiteScore 2.23
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Scopus rating (2011): SJR 0.77 SNIP 1.13 CiteScore 2.17
ISI indexed (2011): ISI indexed yes
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.

General information
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Organisations: Department of Applied Mathematics and Computer Science, Cognitive Systems, Novo Nordisk AS, University of Copenhagen
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