Stability of vitamin D$_3$ and vitamin D$_2$ 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 D$_3$, vitamin D$_2$, and 25-hydroxyvitamin D$_3$ 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 D$_3$ and vitamin D$_2$ in sunflower oil, vitamin D$_3$ in rainbow trout, and vitamin D$_2$ in button mushrooms. The investigated cooking methods were boiling at different pH, steam cooking, microwave cooking, pan-frying, and oven baking. There was no difference between the retention of vitamin D$_3$ and vitamin D$_2$ added to sunflower oil, which ranged from 70 to 99%. In rainbow trout, the retention of vitamin D$_3$ at 85–114% was not significantly different from 100%, except for pan-frying at 85%. However, the retention of vitamin D$_2$ in mushrooms at 62–88% was significantly different from 100% ($p \leq 0.05$).

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BFI (2015): BFI-level 2
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BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.762 SNIP 2.342 CiteScore 3.98
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Web of Science (2012): Indexed yes
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ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
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
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.
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 Hōabinhian 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 Hōabinhian 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, Silpakom University, Ministry of Information and Culture, Universiti Sains Malaysia, University of Lausanne, Monash University, National Academy of Sciences of the Republic of Armenia, Mahidol University, Institute of Archaeology, Australian National University, Balai Archeology, Nara National Research Institute for Cultural Properties, University of Tokyo, University of the Ryukyus, Educational Committee of Tahara City, National Institutes for the Humanities National Museum of Japanese History, Kyushu University, National Institute of Genetics Mishima, Trinity College Dublin, University of Oxford, Universite Paris 5, Universite de Strasbourg, University of Illinois at Urbana-Champaign, Natural History Museum of La Rochelle, CNRS Centre National de la Recherche Scientifique, University of Otago, Administrative Headquarters of the Max Planck Society, École Française d'Extrême-Orient, University of Cambridge
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.
Cell culture, Conventional RT-PCR, Novel primer design, Real-time RT-PCR, Validation method, Viral haemorrhagic septicemia virus
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, (BA)$_2$(MA)$_3$Pb$_{4-x}$Sn$_x$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 (BA)$_2$(MA)$_3$Pb$_3$SnI$_{13}$-based solar cells yield the best power conversion efficiency close to 6% with suppressed hysteresis.

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Organisations: Department of Chemistry, NanoChemistry, Organic Chemistry, Fudan University, Lund University
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BFI (2015): BFI-level 1
Scopus rating (2015): SJR 2.262 SNIP 1.555 CiteScore 7.38
Web of Science (2015): Indexed yes
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, 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
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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, λ, μ_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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BFI (2015): BFI-level 1
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BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.129 SNIP 2.719 CiteScore 2.2
ISI indexed (2013): ISI indexed yes
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BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.14 SNIP 2.407 CiteScore 1.71
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.952 SNIP 2.411 CiteScore 1.85
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.05 SNIP 2.106
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 (fixed at 550 ms) interaction.

General information
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Organisations: Department of Management Engineering, Technology and Innovation Management, Transport DTU, Copenhagen Center for Health Technology, Texas A and M University
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).

General information
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Organisations: Technical University of Denmark, Department of Management Engineering, Technology and Innovation Management
Authors: Hansen, J. P. (Intern), Wang, Z. (Intern), Alapetite, A. (Intern), Minakata, K. (Intern), Thomsen, M. (Intern), Zhang, G. (Intern)
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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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Authors: Halsnæs, K. (Intern), Larsen, M. A. D. (Intern), Kaspersen, P. S. (Intern)
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BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.817 SNIP 1.166 CiteScore 1.89
Web of Science (2015): Indexed yes
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Scopus rating (2014): SJR 0.835 SNIP 1.276 CiteScore 1.96
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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
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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.

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Organisations: National Veterinary Institute, Bacteriology & Parasitology, Section for Diagnostics and Scientific Advice, Diagnostic & Development, University of Copenhagen
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 cell loss initiated during early development in combination with disturbed maturation of Sertoli- and Leydig cells.

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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**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,
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.

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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.