ISEMPH2019: INTERNATIONAL SOCIETY FOR EVOLUTION, MEDICINE, AND PUBLIC HEALTH 2019

FULL PROGRAM WITH ABSTRACTS

PROGRAM FOR TUESDAY, AUGUST 13TH

Days:next dayall days

View: session overviewtalk overview

09:00-12:00 Session 1: Pre-conference workshop on Oxytocin

Begins Aug 12 afternoon. To register contact Adrian Jaeggi – adrian.jaeggi@iem.uzh.ch. For details see https://isemph.org/Program-2019

CHAIR: Adrian Jäggi

LOCATION: 220

12:00-13:00 Session 2: Publication committee meeting

CHAIR: Charles Nunn

LOCATION: 203

13:15-14:45 Session 3: Education committee meeting

For members of the Education Committee. Please contact Jay Labov if you would like to help with the work of this committee

CHAIR: Jay Labov

LOCATION: 203

15:00-16:30 Session 4: Developing the field meeting

All who are running or considering developing an evolutionary medicine program are welcome to attend and share notes and ideas

CHAIR: Randolph Nesse

LOCATION: 203

17:30-19:30 Welcome Reception

LOCATION: Terrace

19:30-21:45 Session 5: Council meeting

At Restaurant Mère Catherine, Nägelihof 3, 8001 Zürich

CHAIR: Randolph Nesse

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PROGRAMAUTHORSKEYWORDS

PROGRAM FOR WEDNESDAY, AUGUST 14TH

Days:previous daynext dayall days

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09:00-09:30 Session 6: Opening notes

With welcoming words by the President of the University of Zurich Prof. Michael Hengartner.

CHAIR: Frank Rühli

LOCATION: Aula

09:30-10:30 Session 7: Keynote Kayla King

CHAIR: John Baines

LOCATION: Aula

09:30

Kayla King

Protectors and killers: microbial drivers of pathogen evolution

ABSTRACT. Most hosts are colonised by a diversity of microbes. Some can be beneficial to the host and provide protection against pathogen infection. Pathogens can readily adapt to challenges from hosts and treatments, but the extent to which conflict from microbes accelerates pathogen evolution is unclear. By experimentally evolving microbial systems, my group has shown that host-protective microbes can have big consequences for the evolution of pathogen virulence and resistance. I will show that some pathogens can adapt to microbial protection at the cost of host exploitation, while others can rapidly evolve generalist defence strategies. This work suggests that host-associated microbes warrant consideration as a driver of infection outcomes and pathogen transmission over time.

10:30-11:00Coffee Break

11:00-12:20 Session 8A: Antibiotic resistance

CHAIR: Joseph Graves

LOCATION: Aula

11:00

Hinrich Schulenburg and Roderich Roemhild

Evolutionary ecology meets the antibiotic crisis: Can we control pathogen adaptation?

ABSTRACT. Evolutionary processes are responsible for the current antibiotic crisis. Surprisingly, they are usually ignored during design of novel therapy, which mainly focuses on finding new drugs. In general, bacteria show an enormous potential to adapt to constant environments, even if extreme such as those defined by many antibiotics. Adaptation may however be more difficult, if conditions change fast. Therefore, rapid fluctuations in the application of drugs may enhance pathogen extinction and minimize resistance evolution. To date, such fast fluctuations are usually not considered for antibiotic therapy. My lab uses evolution experiments in combination with genomics, functional genetics, mathematical modelling, and also analysis of clinical material to explore novel, evolution-informed ideas for antibiotic therapy. I will present some of our most recent results with the model pathogen Pseudomonas aeruginosa that highlight the particular potency of fast sequential treatments and the likely underlying evolutionary and molecular mechanisms.

11:20

Lindsay Sonnenkalb, Silvia Maass, Vanessa Mohr, Fenja Boysen, Stefan Niemann and Matthias Merker

Antibiotic resistance evolution of Mycobacterium tuberculosis complex bacteria, during sub-lethal drug exposure

ABSTRACT. Tuberculosis (TB) continues to be the deadliest human infection caused by bacterial strains of the Mycobacterium tuberculosis complex (MTBC). TB-treatment of a susceptible strain requires, at minimum, a six month regimen comprising of four antibiotics. Once the bacteria develop resistance towards the two most effective drugs isoniazid and rifampicin, the infection is classified as multidrug resistant tuberculosis (MDR-TB) and treatment is changed to more toxic medications for up to two years. In 2016, nearly half a million patients were newly infected with an MDR strain worldwide, killing 240.000. Pharmacokinetic and pharmacodynamic studies have revealed the inability of many anti-TB drugs to reach all sights of infection, e.g. granuloma, at a therapeutic level. Our work is focused on the hypothesis, that exposure to low (ineffective) drug concentrations might particularly select for highly resistant and highly competitive MTBC strain populations. In this study, we designed an in vitro model to investigate the evolutionary effects of moxifloxacin (MFX), a second-line drug which disrupts DNA transcription through binding of the DNA gyrase, and bedaquiline (BDQ), the most recently released anti TB-drug which inhibits ATP synthase. After long-term exposure of the laboratory strain H37Rv to sub-lethal concentrations we analysed mutant enrichment and resistance allele diversity using whole genome sequencing (WGS) and phenotypic assays. When H37Rv is exposed to 1-4 dilution below the minimum inhibitory concentration (MIC) we could almost exclusively recover mutations frequently seen in patient derived isolates resistant to MFX. Preliminary results further suggest that a particular concentration range selects for mutants with higher MICs. There is virtually no data available on mutations that confer resistance to BDQ in MDR-TB patients. Thus, we are confident that our in vitro model also detects clinically relevant BDQ resistance conferring mutations that will contribute to resistance mutation catalogues employed by WGS resistance predictions for personalized medicine approaches.

11:40

Joseph Graves Jr and Jian Han

Surviving the Greek Gift: Experimental Evolution of Gallium Resistance in Escherichia coli.

ABSTRACT. There has been an increased usage of metallic antimicrobial materials to control pathogenic and multi-drug resistant bacteria, yet there is a corresponding need to know if this may lead to genetic adaptations that produce even more dangerous bacterial varieties. Here we utilize experimental evolution to produce strains of Escherichia coli K-12 MG1655 resistant to Gallium Nitrate (Ga3+NO3). Gallium is an analog for iron. By day 10, increased gallium resistance was evident in populations cultured in medium containing a sublethal concentration of gallium. Furthermore, these populations showed increased resistance to ionic silver and iron (III), but not iron (II). There was no increase in traditional antibiotic resistance compared to controls. Genomic analysis identified hard selective sweeps of mutations in several genes in the gallium (III)-resistant lines including; fecA (iron citrate outer membrane transporter), insl1 (IS30 tranposase), one intergenic mutations arsC → / → yhiS; (arsenate reductase/pseudogene); and in one pseudogene yedN ←; (iapH/yopM family). Two additonal significant intergenic polymorphisms were found at frequencies > 0.500 in fepD ← / → entS (iron‑enterobactin transporter subunit/enterobactin exporter, iron‑regulated) and yfgF ← / → yfgG (cyclic‑di‑GMP phosphodiesterase, anaerobic/uncharacterized protein). This study corroborates recent results observed in experiments utilizing pathogenic Pseudomonas strains that also showed that bacteria can rapidly evolve resistance to an atom that mimics an essential micronutrient and illustrates a pleiotropic consequence of this adaptation.

12:00

Nasreen Haque and Niloufar Haque

Whole genome sequencing reveals the evolutionary trajectories of antibiotic resistance in Staphylococcus pasteuri isolates from human atherosclerotic plaques

ABSTRACT. Atherosclerotic cardiovascular diseases, chronic inflammatory diseases of multifactorial etiology, are the leading cause of death worldwide. We propose that the evolutionary trajectory of persistent infection at the site of the atheroma may predict disease progression. In this study we identified the source of persistence infection in human atherosclerotic plaque and determined how antibiotic resistance and/or virulence in the pathogen mediate plaque vulnerability. Whole genome sequencing (WGS) was used to identify bacteria from pure cultures obtained from atherosclerotic tissues of living subjects diagnosed with more than 70% occlusion of the carotid artery undergoing carotid endarterectomy (CE). WGS identified the predominant species as S. pasteuri variants (SPVs) in all CE isolates grown in pure culture except in one isolate which was identified as B. licheniformis. All SPVs were found to have multiple antibiotic resistant (AR) and virulent genes which were unique for each sequenced isolate. Unsurprisingly, virulence was negatively co-related with antibiotic resistance in all isolates tested. These variations found in our isolates suggest that while SPVs may remain dormant, they have the potential to become activated under specific physiological conditions. As macrophages play a decisive role at all stages of atherosclerotic lesion progression we treated mouse macrophages (RAW 264.7) with SPVs. All tested SPVs showed their ability to survive phagocytosis and the propensity of highly virulent SPVs to direct macrophages towards an inflammatory (M1) state. In conclusion, we show that (i) persistant infection occurs in atherosclerotic plaques, (ii) diverse AR genes are found within these isolates and (ii) the degree of AR is co-related with virulence. Genetic variation in SPVs may alter host immunity and provide a causal link between infection and atherosclerosis. Thus, mapping the evolutionary trajectories of resistance to virulence and host response may help determine the fate of a vulnerable plaque and ultimately the disease process.

11:00-12:20 Session 8B: Morphology

CHAIR: Martin Häusler

LOCATION: 217

11:00

Aaron Blackwell

Quantifying the relationship between somatic maintence costs and adult body size

ABSTRACT. To date, studies relating the costs of immune function to growth outcomes have not distinguished between growth deficits as a response to short term energetic deficits, versus changes in growth trajectories as responses to cues of future energetic needs and availability. In part, these alternatives have been difficult to distinguish because the actual energetic costs of growth and other life history allocations, such as reproduction, maintenance, and activity were not available or sufficiently detailed. Here, I address this lack by combining precise data on organ size and tissue specific metabolic rates with detailed population studies providing data on body composition, immune function, activity, and reproduction across the lifespan, to generate detailed estimates of lifetime and age-specific energy allocations for both the Tsimane, a group of Bolivian forager-horticulturalists, and for a cross-section of the United States. Key insights from these estimates include the observation that except in infancy, the costs of physical growth are dwarfed by the costs of maintenance for a larger body, supporting the idea that predictive adaptive responses, rather than constraints, regulate trade-offs with growth. Moreover, given the higher costs of maintenance for Tsimane adults, Tsimane males save 132,000 kcal per year by maintaining an average fat-free-mass of 52kg vs 64kg for the average American. Thus, relative maintenance costs may be a key determinate of adult body size and degree of sexual dimorphism across populations.

11:20

Beverly Strassmann, Zachary Dolo, Claudius Vincenz and Kerby Shedden

Test of two evolutionary hypotheses using longitudinal data on body size and blood pressure

ABSTRACT. Due to the paucity of longitudinal studies in low income countries, the effect of under-nutrition on blood pressure is less well understood than is the role of over-nutrition. Under the First Thousand Days of Life hypothesis, undernutrition to age two years is more important for adult blood pressure than is undernutrition later in childhood. Under the Predicted Adaptive Response Hypothesis, the greatest risk occurs when the adult nutritional environment is different from the childhood environment. We tested these hypotheses using a prospective cohort study of 1698 individuals in Mali, West Africa. The participants were followed for twenty years (1998 to 2018) and a total of 8500 blood pressure measurements were taken throughout adolescence and young adulthood. We predicted the adult blood pressure for children whose internal BMI z-scores from age 0 to 10 followed one of 5 trajectories: constant at z=-1, 0, or +1, transitioning from z=0 to z=-1, and transitioning from z=-1 to z=0. We found that in the first ten years of life there was no critical window in which undernutrition was more strongly associated with later blood pressure; instead its effects were cumulative. Moreover, at each level of adult BMI, the highest blood pressure was found in persons who had a childhood z-score trajectory of -1 to -1 and the lowest blood pressure was observed in persons who had a childhood z-score trajectory of +1 to +1. The catch-up (-1 to 0) and catch-down (0 to -1) trajectories were intermediate and similar to each other. In sum, it was good to be big in childhood and small in adulthood. These results are significant because they disentangle the effects of childhood and adult nutrition on blood pressure. Further they go against two prominent hypotheses in the evolution and public health field.

11:40

Viktoria A. Krenn, Nicole M. Webb, Robert D. Martin and Martin Haeusler

Why is human childbirth so complex? The obstetrical dilemma hypothesis revisited

ABSTRACT. Obstructed labour is a leading cause of maternal and neonatal morbidity and mortality. Most cases result from discordance of dimensions between the foetal head and the mother’s pelvis. Traditionally, this has been attributed to the Obstetrical Dilemma (OD). The associated hypothesis posits that a narrow pelvis is selected for efficiency during bipedal locomotion, while the birth of large-headed newborns contrastingly favours a broader pelvic configuration in females. The consequent evolutionary trade-off can potentially explain the unique challenges during childbirth, sexual dimorphism in human pelvic shape, and the unusual degree of nervous system immaturity in our neonates. Recently, several aspects of the original OD hypothesis have been challenged, raising doubts about its validity and reigniting academic debate. Specifically, it has been proposed that a mother’s energy availability, rather than spatial constraints of her pelvis, might limit gestation length. Experimental data also reportedly indicate that the wider pelvis of women compared to men does not entail increased energetic costs for bipedal locomotion. Moreover, thermoregulatory pressures or abdomino-pelvic stability needs, instead of locomotor costs, may conflict with obstetrical advantages of a broader pelvis. Finally, cephalo-pelvic disproportion might have been exacerbated relatively recently following the emergence of agriculture, with maternal stature and pelvic dimensions decreasing as a result of less secure food availability. Here, we review available evidence with the aim of identifying and emphasizing aspects of the obstetrical dilemma that remain pertinent for both evolutionary studies and clinical contexts. Although the alternative hypotheses currently envisaged are not mutually exclusive, we show that each fails to explain all aspects of the obstetrical dilemma. Specifically, the evolution of our complex birth process, neurologically immature neonates, and marked sexual dimorphism in human pelvic shape remain problematic. We conclude that there is still no valid alternative to the obstetrical dilemma hypothesis.

12:00

Kaspar Staub, Nicole Webb, Viktoria Krenn, Cinzia Fornai, Joël Floris, Nicole Bender, Nikola Koepke and Martin Haeusler

Does the ecological model challenge the obstetrical dilemma? Evidence from historical Swiss data

ABSTRACT. Cephalo-pelvic disproportion results mainly from a misfit between the maternal pelvis and fetal head size. It remains the dominant cause for obstructed labour, and an important indication for Caesarean section. Traditionally, the obstetrical dilemma hypothesis explained this as a trade-off between the antagonistic selection for large-brained neonates and biomechanically efficient, or narrower pelvis equipped for bipedal locomotion. Recently the obstetrical dilemma hypothesis has been challenged by a series of alternative explanations, including “the ecological model”, which posits that cephalo-pelvic disproportions only exacerbated relatively recently, when maternal stature and pelvic dimensions decreased due to unsteady food availability.

To further evaluate the ecological model, we analyse a large data set of birth records between 1896 and 1945 from the archives of the maternal hospital Basel, Switzerland, to better understand the multifaceted and interrelated aspects of maternal and offspring body size. Analysed data included head circumference, length and weight of the neonate, type of head presentation and position, birth complications, parity, as well as maternal stature and external pelvic dimensions. This dataset permits the assessment of both fetal and maternal development; specifically, growth and stature relationships including changes in pelvic dimensions across different generations during times of fluctuating socioeconomic stress These factors generate complex interactions that potentially intensify the obstetrical dilemma.

Moreover, we explore the relationship between external and internal pelvic dimensions in a worldwide skeletal sample to better understand the causes of obstructed labour, namely cephalo-pelvic disproportion. We demonstrate that several external pelvic dimensions are useful predictors of birth canal size, while stature itself is only weakly related to pelvic measures. This is at odds with previous studies highlighting the importance of maternal stature for cephalo-pelvic disproportion. Our findings suggest that the ecological model is no valid alternative to the obstetrical dilemma hypothesis.

11:00-12:20 Session 8C: Symposium Translational aspects

CHAIR: Nicole Bender

LOCATION: 204

11:00

Joe Alcock

Applications of evolutionary medicine to emergency medicine and critical care

ABSTRACT. Interest in evolutionary medicine is fueled by the observation that many evolutionary principles have direct applications to clinical practice. Although the scope of evolutionary medicine is broad, this discipline may be particularly well suited to emergency medicine and critical care, in which clinical decisions frequently have life and death consequences. I will provide examples – starting with a review of fever and its treatment - of how evolutionary biology can be applied to emergent conditions. Opportunities to improve emergency and critical care with evolutionary medicine fall into two broad categories: I. understanding adaptation in human physiology and pathophysiology. II. recognizing evolutionary tradeoffs in disease phenotypes and in the response to medical treatments. This talk will review several of the most promising applications of evolutionary medicine in these categories and will offer a road map for leveraging evolutionary medicine in emergency and critical care.

11:20

Katharina Quack Lötscher

Obstetrics in translational medicine

ABSTRACT. The influence of the mother’s behavior on the development of the fetus has been of interest for many years. The Barker hypothesis is based on the connections between the maternal food intake and birth weight as well as many NCDs later in the life of the baby. As one of the most successful interventions in terms of energy intake in pregnancy the screening for gestational diabetes has influenced pregnancies since more than ten years now. With the control of glucose in the maternal blood the baby’s exposure to glucose can be well monitored and the sometimes dramatic consequences of macrosomia, hyperinsulinism and hypoglycemia in the fetus can be avoided. Therefore, the behavior of the mother during pregnancy, and now growing evidence that the pre-pregnancy phase is as important, should be of concern and mothers should be instructed carefully about the options. New research investigates the changes of the microbiome during pregnancy. As studies show not only the classical sites like mouth, intestine and vaginal microbiome change in the course of pregnancy, there is also a placental microbiome that might influence pregnancy outcomes.

11:40

Nicole Bender

Mindful eating and common diet programs lower weight similarly: Meta-Analysis

ABSTRACT. Introduction: Common strategies for reducing body weight rely on limiting energy intake and restricting food choices. However, these strategies have often been proven ineffective in achieving long-term and sustainable weight reduction. More recently, mindful eating as an alternative weight management strategy has gained increasing attention, yet systematic reviews on intuitive or mindful eating published so far present contradictory results. Methods: We performed a systematic review and meta-analysis on randomized controlled trials on weight loss programs based on mindful or intuitive eating. We analysed results using meta-regressions. Results: We included a total of ten studies and found a significant weight loss effect of mindful eating strategies compared to non-intervention controls (-0.348 kg, 95% CI: -0.591 to -0.105, p=0.005). However, there was no difference compared to conventional diet programs (p=0.99). Reduction of BMI (-0.137 kg/m2, 95% CI: -0.365 to 0.091, p=0.240) or waist circumference (-0.358 cm, 95% CI: -0.916 to 0.200, p=0.209) were not statistically significant. Discussion: Mindful eating could be a practical approach to weight control. Limitations of this study include the unbalanced sex, origin, and place of residence of the participants and the short duration of interventions. Future research should aim at investigating long-term effects and include a more heterogeneous study population, and how to translate these results into public health practice.

12:00

Milo Puhan

Balancing population health benefits and harms of interventions and policies

ABSTRACT. Medical and public health interventions can have a large beneficial impact at low cost for entire populations even if the relative effects itself are small. However, this equally applies to harms of public health intervention, which may have substantial negative impact even if the relative increase in risk is small. Thus on a population level these benefits and harms counterbalance one another and it is of great importance to have quantitative estimates of that benefit harm balance of medical and public health interventions and policies. Evolutionary Medicine may inform such benefit-harm assessment by informing (at least) two key steps. Firstly, the question and decision making context needs to be carefully designed and must include “all” determinants and consequences of a medical or public health intervention on population health. It is well possible that current benefit harm assessments fail to consider more long-term benefits and harms across the lifetime of a population. Although rarely done so far, Evolutionary Medicine could inform the decision making context by identifying determinants, from the genotype to the phenotype, along the life history of a specific population at issue. Secondly, modelling different scenarios of how a medical or public health intervention impacts on population health, again from the genotype to the phenotype depends on certain assumptions. Evolutionary Medicine may help to design such analyses. This talk will discuss how insights from Evolutionary Medicine may inform benefit harm assessments of medical and public health interventions and the impact this may have on the development of policies and recommendations.

12:20-13:20Lunch Break

13:20-13:50 Session 9: Poster session I

All posters are exhibited during the whole congress, not just the ones listed in the specific session list.

LOCATION: Patio

13:20

Noel Boaz

Retrodictive Disproof of the Onto-Phylogenetic “Just-So Story” and the Role of Narrative in Evolutionary Medicine

ABSTRACT. Whereas much of biomedical science relies on the laboratory experiment as its gold-standard methodology to disprove hypotheses, investigations of historical fact in the evolutionary sciences require a time-controlled multidisciplinary approach akin to forensic science that is equally rigorous in disproving its hypotheses. When detractors, scientific and otherwise, disparage paleobiological hypotheses as “untestable” they may use the term “just-so story” pejoratively to dismiss them as fanciful fiction, drawing a comparison with the popular Just-So Stories published by Anglo-Indian author Rudyard Kipling in the early twentieth century. The experimental method tests hypothetical predictions in a uniformitarian empirical framework that is ahistorical and mechanism-focused, while the forensic method tests retrodictions in a uniformitarian empirical framework that is historical and narrative in focus. Both methods are fully compatible with each another, and non-falsified hypotheses must conform with empirical results obtained through either method. A thoroughly tested onto-phylogenetic (“evo-devo”) narrative is an essential component of Evolutionary Medicine, driving research, educational, and clinical advances. Clinical experience amply demonstrates that therapies which ignore evolutionary history and rest solely on ahistorical and mechanistic assumptions lead to less-than-optimal patient outcomes. To operationalize the retrodictive approach an anthropogenic (“human-origins”) matrix is constructed using an array of 9 paradigmatic tools, including rigorous temporal calibration, applied across 7 categories of narrative elements, including environmental context and adaptations, in order to assess hypotheses. Drawing an analogy to Kipling’s unfalsifiable “How the Rhinoceros Got His Skin” (1902) the anthropogenic matrix is used to construct a falsifiable narrative of evolutionary and developmental anatomy of the human integument, with clinical implications.

13:20

Robert Chevalier

Bioenergetic evolution links kidney development, CKD progression and aging

ABSTRACT. There is a global epidemic of chronic kidney disease (CKD), and current therapies do not halt progression. Three key factors contribute to progression of CKD: 1) > 10-fold variation in nephron number (NN) at birth; 2) nephron hypertrophy resulting from low NN; 3) 50% decrease in NN with normal aging. These responses are products of evolution, constrained by energy availability. The rapid evolution of humans was a product of brain growth: adults devote 20% of resting metabolism to the brain. The kidney consumes more oxygen (per gram) than the brain and tubular sodium reabsorption is driven mainly by oxidative phosphorylation (OXPHOS) by mitochondria (MT). The aim of the present analysis of published reports was to apply principles of evolutionary bioenergetics to elucidate risk factors for CKD. Plasticity of nephrogenesis results from determination of progenitor cell fate in response to the maternal nutritional environment by switching between glycolytic and OXPHOS metabolism. If maternal nutrition is restricted, sensors of hypoxia (HIF) and energy availability (AMPK) respond by diverting fetal energy from nephrogenesis to brain development, resulting in lower NN. This tradeoff permits survival through reproductive years, but increases the risk of CKD in adulthood by activation of cell death pathways by MT-generated reactive oxygen species (ROS) increasing risk for progressive CKD. Idoxyl sulfate, a uremic toxin that accumulates in patients with CKD, stimulates renal hypertrophy and production of ROS. Tubular hypertrophy resulting from reduced NN is stimulated by upregulation of mTOR, a nutrient sensor that promotes hypermetabolism. Enlarging tubular cells reach a critical volume for oxygen diffusion below which MT respiration is impaired (“critical pO2”), increasing ROS accumulation. By stimulating AMPK and suppressing mTOR, calorie restriction can slow progression of CKD and normal aging. Kidney structure and function are the product of evolutionary adaptation constrained by bioenergetics with tradeoffs leading to CKD.

13:20

Hans Biesalski and Tabea Hornung

Glucose Transporter 1 (GLUT1) its impact on selection of a phenotype without vitamin C synthesis and on vitamin C requirement in diabetic patients.

ABSTRACT. A couple of different species including men, monkeys, fruit bats and few others lost the ability for endogenous vitamin C synthesis due to a mutation of the gene encoding the encyme L-gulono-lactone-oxidase (GLO) The most accepted hypothesis for this selection was the availability of food sources rich in vitamin C. However, this would not explain a selective pressure on different species at different time points during evolution. In contrast to the synthesizing species all non-synthesizing express a specific glucose transporter (GLUT1) on their red blood cells (RBC). GLUT1 transports Glucose but preferentially Vitamin C if a membrane bound protein, stomatin, couples to GLUt1. To evaluate whether GLUt1 creates a real benefit we measured Vitamin C uptake in human RBC and in pigs with functional GLO. Indeed, Vitamin C was only transported into human RBC but not in pig RBC. The ability of RBCs to accumulate an intracellular electron pool decreases the daily required amount of vitamin c during seasonal changes of the availability from food and seemed to be the key for the survival of individuals without vitamin C biosynthesis. Further this recycling was energetic more efficient than the de novo synthesis of ascorbate from glucose which explains the survival of this GLO-lacking but GLUT1 positive phenotype. Diabetic patients have lower blood Vitamin C-levels. We propose that in diabetic patients an altered Glut-1 and Stomatin interaction in RBC result in decreased DHA uptake and subsequently lower vitamin C concentrations. Indeed we could show that despite equal vitamin C plasma levels, intra-RBC vitamin C concentrations in the diabetic group were significantly decreased. Decreased intra-erythrocyte vitamin C level could lead to decreased vitamin C recycling and increased renal elimination of the vitamin (diketo-gulono-acid). In this case, the required daily intake (RDI) of vitamin C for diabetic patients should be reconsidered

13:20

Chiara Rezzoagli, Martina Arianna Archetti, Michael Baumgartner and Rolf Kümmerli

Treating pathogenic bacteria with combinations of antibiotics and anti-virulence compounds can revert selection for antibiotic resistance

ABSTRACT. Antibiotics are rapidly losing efficacy due to the evolution and spreading of resistant bacteria. Approaches that reduce selection for resistance are therefore desperately needed. One such approach is the development of treatments targeting bacterial virulence factors. The reasoning is that anti-virulence drugs aim at reducing pathogen virulence instead of viability, and should therefore exert weaker selection for resistance than conventional antibiotics. Another possibility is to manage infections using combinations of multiple compounds, exploiting specific interactions between drugs that can select against resistant mutants. We have previously shown that combination therapy between antibiotics and anti-virulence compounds is effective against the opportunistic pathogen Pseudomonas aeruginosa. Here we tested whether the addition of an antivirulence compound (gallium, a siderophore-quencher, or furanone C-30, a quorum-sensing-inhibitor) to antibiotic treatments (ciprofloxacin, colistin, meropenem or tobramycin) can revert selection for antibiotic resistance. We evolved antibiotic-resistant bacteria and competed them against susceptible clones under antibiotic treatment alone or under combination treatments. We found that, for five out of eight drug combinations, the antibiotic-resistant clones maintained a relative fitness advantage in presence of the antivirulence compounds. Conversely, in three out of eight drug combinations we observed that the addition of the anti-virulence could indeed reverse selection for antibiotic resistance. Mechanistic analysis revealed that the reversion of selection is unlinked to whether drug combinations were antagonistic or synergistic, but suggest that the certain mechanisms of antibiotic resistance make bacteria more susceptible to the anti-virulence drugs. Such cross-sensitivity was especially apparent for tobramycin resistant mutants treated with both gallium and furanone, making these drug combinations a promising new way to limit or even reverse the spread of antibiotic resistance.

13:20

Martina Arianna Archetti, Chiara Rezzoagli and Rolf Kümmerli

Combinations of antibiotics and antivirulence compounds against Pseudomonas aeruginosa: efficacy, nature of drug-interactions and effect on antibiotic resistant clones

ABSTRACT. The spread of antibiotic resistance causes a rapid loss of treatment efficacy. Drug combination therapies have been proposed as one option to maintain efficacy, because simultaneous resistance against multiple drugs is less likely to evolve. Alternatively, antivirulence compounds that target virulence factors rather than cell viability are also considered to be relatively evolutionary robust as they do not directly kill bacteria. Here, we combine these two approaches using the bacterium Pseudomonas aeruginosa as a model pathogen. We combined four clinically relevant antibiotics, ciprofloxacin, colistin, meropenem, and tobramycin, with either gallium, quenching iron-scavenging siderophores, or furanone C-30, a quorum sensing inhibitor. For all drug combinations, we (a) assessed treatment efficacy, (b) quantified drug interaction patterns (ranging from synergy to antagonism), and (c) tested whether combination therapy was still effective against antibiotic-resistant clones. We exposed P. aeruginosa PAO1 to a 9x9 concentration matrix for each drug pair and found that combination therapy was effective in inhibiting both growth and virulence factor production. The nature of drug interaction was concentration dependent, resulting in a mosaic of antagonistic and synergistic interactions across the concentration matrix. Interestingly, the degrees of synergy for growth and for virulence factor inhibition were often positively correlated. Moreover, we found that many drug combinations were still effective against bacteria that were resistant against the specific antibiotic used. Our work provides a first systematic analysis of combination therapy involving an antibiotic to kill pathogens, and an antivirulence to disarm them, and reveals that such combinations could be an effective tool to manage P. aeruginosa infections, even in presence of antibiotic resistant clones.

13:20

Dhweeja Dasarathy and Barbara Natterson-Horowitz

Evolutionary Insights into Insomnia in Athletes: Using Systematic Review to Identify Natural Animal Models

ABSTRACT. Background: The syndrome of sleep disturbance has been reported in overendurance athletes [1,2]. Despite a number of proximate explanations, the functional or adaptive perspectives of this disorder are currently unexplored [3]. The identification of a natural animal model would advance the development of a non-proximate understanding of this disorder. This study was, therefore, designed to identify such a natural animal model.

Methods: To identify a natural animal model for overreaching exercise, formal methods of systematic review were used. Literature from Zoological Records, Biosis, and Pubmed between the years of 1999 and 2007 were reviewed [4,5,6,7,8,9,10,11,12]. These results were synthesized and sourced, excluding duplicates and articles that did not relate to overreaching exercise in animals or sleep disorders. Further selection criteria included identifying animals that fit specific criteria (i.e. animals that exercised excessively and suffered from insomnia and/or other sleep disorders).

Results: From an initial 6323 articles identified, 10 sources that fit our inclusion criteria were selected and analyzed to identify potential natural animal models for this phenomenon [4,5,6,7,8,9,10,11,12]. Since birds were noted to be consistently identified to exercise over prolonged periods of time during long distance flying, search terms were then refined to “birds with insomnia,” AND “birds with sleep disorders,” “migratory sleeplessness,” AND “restlessness after migration.” These studies were reviewed to identify relevant physiology and the existence of data to support the use of these species as natural models. One species in particular, the migrating white crowned sparrow, represented a possible natural model that we identified through systematic review [4]. Early EEG work suggested differential sleep patterns during periods of migration vs. non-migration with migration as a surrogate for exercise in overendurance athletes [4, 13,14].

Conclusion: The identification of a natural animal model provides the basis for developing a nonproximate adaptive hypothesis for sleep disturbance in overendurance human athletes.

13:20

Adrian Williams and Lisa Hill

Lessons from Pellagra – Human evolution in reverse gear?

ABSTRACT. Pellagra caused the “3Ds” of Dementia and Diarrhoea plus a characteristic Dermatitis (Casal’s necklace). Pellagra was an intriguing ecological model of premature ageing and of societal and transgenerational breakdown. In 18thC European epidemics it was recognised as an atavistic degeneration of evolutionary importance but this, like the broad neuropsychiatric phenotype, has been forgotten. Pellagra is caused by Nicotinamide (Vitamin B3) deficiency on a low meat and high maize diet - a reverse on the meat-rich omnivorous diet on which we evolved our cognitive strengths. Gut dysbioses were common as was TB – the latter association is curious as TB excretes nicotinamide that is an anti-TB antibiotic as are analogues, such as Isoniazid. Under some dietary circumstances this may be a nutritional symbiotic-dysbiotic relationship “farming” TB within immunologically fenced granulomas. We link the unexplained reduction of TB in the UK 1850-1950 with increased meat (and nicotinamide) intake and consequently with disease and demographic transitions toward longevity and immune intolerance with more auto-immune disease and lower fertility. This transition can reverse at times of dietary stress in wars. Correlations will be shown between increased meat intake and longevity with lowered TB and fertility rates mirrored across the contemporary world. Suppression of the need to utilise the “in house” tryptophan degradation pathway to yield nicotinamide known to affect immune tolerance (including to the foetus) could provide a biochemical mechanism - including for the “Hygiene hypothesis” as “Old Friends” such as TB disappear. (Rook G. 2019: The Immune System in the Oxford Textbook of Evolutionary Medicine by Brune M & Schiefenhovel W).

13:20

Neil Isaacs

Functional anatomy of Gluteus Maximus(GM) regarding a change of direction(cod) related to performance and injuries

ABSTRACT. Background: A strike with a sporting implement in effect is a cod from the stance or in the stride with initial rotation at the hips followed by the shoulders and upper arms. A cod in the first half of a running stride after heel strike with the position of internal rotation, adduction and flexion of the hip, with knee flexion allowing increased external rotation and abduction at the knee has been suggested as a position of risk. Programs to prevent injuries, in particular rupture of the anterior cruciate ligament, have met mixed results with interest in proximal muscles playing a role in stabilizing joints. Training in the sagittal plane has not improved change of direction performance. Aims: Analysis of the role of GM in the kinetics and kinematics of the lower limb in cod Methods: Literature review Results: GM moment arms are changed in all three planes by the greater trochanter in humans by providing a pulley effect with flexion of the hip providing torque in cod. Discussion and Conclusions: In the first half of the stride in deceleration after lateral foot placement from the line of the stride,cod may be initiated by horizontal abduction of the distal insertion portion of GM with the knee in neutral or varus position. In propulsion,the secound half of the stride,the proximal insertion portion of GM externally rotates the hip further,increasing the torque rotating the pelvis with the leg moving into the “position of risk”. This position now termed “the position of increased performance “ angles the ground reaction force by the lower leg further away from the centre of mass enabling generation of more angular momentum while limbs are closer to the vertical axis through the centre of mass.

Specificity training is suggested with the incentive of improved performance.

13:20

Neil Isaacs

Evolution of bipedalism concurrently increasing capacity for pelvic rotation in the kinetic chain.

ABSTRACT. Background Anatomy related to bipedalism

Aims Comparative and functional anatomy of pelvic rotation in man and chimpanzee.

Methods Literature review

Results The majority of moment arms of the muscles across the human hip increase their tendency towards internal rotation as flexion of the hip progresses from zero to ninety degrees.

As expected, internal rotation torque increases considerably as the hip flexes, but external rotation torque also increases unexpectedly up to five percent.

Gluteus maximus (GM)moment arms previously assessed are altered in all three planes by the greater trochanter in man providing a pulley effect with flexion of the hip as the greater trochanter slides medially to GM pushing it laterally.

Superficial GM and its tendinous insertion to the ileotibial band, shifts progressively anteriorly over the greater trochanter with increasing flexion.

This effect is enhanced by the angle of inclination of the femur..

Discussion and Conclusions: The deep posterior quarter of GM likely evolved from Ischiofemoralis in chimpanzees by moving its distal insertion proximally, improving external rotation of the hip.

The stronger biarticular connection of GM with greater moment arms stabilizes the more flexible knee in transfer of increased torque in the coronal and transverse planes from hip to tibia and in a closed chain horizontally abducts the hip to rotate the pelvis with increased flexion.

Insertion of posterior GM, via the posterior iliotibial band, stabilizes and holds external rotation of the tibia with flexion of the knee up to 90 degrees in a closed chain as it’s moment arm of insertion as it runs around and inferior to the femoral condyle becomes more ideally placed in the transverse plane.

Comparative anatomy from the big toe to the thumb involving transverse rotation evolved along with bipedalism.

Major implications are in research,sport performance and injury prevention.

13:20

Alexandru-Stefan Niculae

Anthropometric measurements in male children with ASD point to genomic imprinting imbalance

ABSTRACT. Introduction: Autism Spectrum Disorder (ASD) is a large set of neurodevelopmental disorders of complex aetiology. A mix of genetic and environmental factors are likely to cause ASD. Genetic risk for autism comes from common genetic variation. Genomic imprinting refers to genes that have different expression patterns according to the parent of origin - being silenced when imprinted. Paternally active genes increase resource extraction from the mother and reduce resource burden on the father.

Children with ASD show consistent overgrowth during their first 1-2 years of life. Recently, it has been shown that children with higher birth weight and length have an increased risk of developing ASD. This overgrowth and apparent larger birth weight and length are consistent with the notion that a paternally biased genome might underlie the risk for ASD.

Methods: The study compared height, weight, head circumference and thoracic circumference for age-matched (ages 4-8 years old) male children with ASD (n=30) with neurotypical children (n=33).

Results: No clinically significant differences were found among the two groups.

Discussion/Conclusions: After weaning, relative paternal contribution to a child's somatic development would increase, thus one would expect paternally active genes to start changing the child's behaviour, so as to make the child less demanding of resources (overall, and thus also on the father), with a counterweight represented by maternally active genes. A relative overabundance of paternally active genes would explain the data presented here, that shows children with ASD being no different from controls. Given the fact presented by other studies, that children with ASD seem to get a head start in growth, the lack of differences found in this 4-8 years old group indicates that children with ASD might actually fall behind in somatic growth, or at least stagnate by middle childhood.

13:20

Rumyana Stoyanova and Stanislava Harizanova

Burnout among nurses and correctional officers in Bulgaria: a comparative study

ABSTRACT. BACKGROUND: The work of nurses and correctional officers alike has long been pointed at as among the most stressful in the world. OBJECTIVE: The aim of the study was to evaluate the prevalence and level of occupational burnout among 214 hospital nurses and 201 correctional officers from Bulgaria. One of the focuses was to examine whether gender roles or occupational roles were more related to burnout. METHODS: The study used a descriptive cross-sectional inter-occupational comparative survey design. The sample was composed of employees working in two different occupations – nurses and correctional officers. A self-administered MBI-Bulgarian version questionnaire was used. The information was gathered at the work place of respondents between November 2014 and March 2015. The participation was voluntary, individually and anonymously without any financial compensation. The only qualification in the sample selection was that the employee had direct contact with patients and inmates respectively. Results were analyzed using descriptive statistics of the data (mean, standard deviation, number and percentage), and presented in the form of tables, using the SPSS 17.0. Other statistical analysis methods that were used include non-parametric analysis. A p-value of < 0.05 was considered as statistically significant level. RESULTS: The level of emotional exhaustion and personal accomplishment of nurses were significantly higher than that of correctional officers. Mean depersonalization score of correctional officers was significantly higher than that of nurses. Correctional officers demonstrated a higher prevalence of burnout syndrome compared with nurses. To examine whether gender is associated with burnout, Mann-Whitney U test was utilized to assess gender differences of correctional officers. Our results suggest that being male or female is not a critical determinant of burnout. CONCLUSION: Correctional officers were found to have a higher prevalence of burnout syndrome compared with nurses.

13:20

Megan Zhao and Barbara Natterson-Horowitz

The Animal Origins of Human Bullying: A Systematic Review of the “Oddity Effect” Literature and the Identification of Naturally Occurring Models for Appearance-Based Bullying in Humans

ABSTRACT. Adolescent depression is a major emerging public health issue (Hertz et al, 2016) with an increasing prevalence in the US (Mojtabai, 2016). Bullying during adolescence is associated with depression and suicidal idealization (Brunstein, 2007). Appearance-based bullying is most common in this age group (Jacobson, 2017). The “Oddity Effect”, a tendency for group living animals to preferentially not assort with phenotypically different individuals (Landeau, 1986), may represent a natural animal model for appearance-based bullying in humans. However, there currently are no identified model species. The goals of this study are to identify animal taxa in which the “Oddity Effect” has been reported as a first step in evaluating species with potential suitability as a model organism for appearance-based bullying. We used formal methods systematic review to identify the taxonomic range of species in which the “Oddity Effect” has been demonstrated. Twenty species including both invertebrate (plankton) and vertebral taxa (fish, birds, and mammals) were definitively determined to exhibit this collective behavior. Some emergent collective behaviors in non-human animals have been established to also occur in groups of humans (Neda et al, 2002; Milgram et al, 1969). The “Oddity Effect” is phenomenologically similar to several aspects of human appearance-based bullying. The species identified through this study may represent naturally-occurring models appearance-based bullying in humans. This study invites further investigation of the “Oddity Effect” in the identified species to provide insight in the investigation of evolutionary origins of appearance-based bullying and potentially larger xenophobic tendencies in humans.

13:20

Nantawan Soonklang

Chemoreception in the Golden Apple Snail Pomacea canaliculata: Towards the development of snail-specific control methods and novel baiting strategies.

ABSTRACT. The large freshwater snail Pomacea canaliculata is a constant and intractable pest to Thailand’s native fauna and agriculture plants. Thus, considerable research needs to be done on the molecular cellular events that take place during feeding and reproduction. We explored the neural control centre of P. canaliculata, targeting the cerebral/visceral ganglia to isolate genes responsible for driving chemoreception and reproductive behaviour. Through de novo transcriptome sequencing, we produced 60,377,982 raw reads corresponding to 4.9 Gb clean read data. From this, 179,974 contigs were assembled with Trinity and used to construct 82,029 unigenes. Distinct genes were then annotated with Blastx yielding 31,472 unigenes above the cut-off e-value set at 10-5 , with ESTscan database query analyses yielding up to 7,287 known unigene hits. Further analysis using Liquid Chromatography Mass Spectroscopy (LCMS), and our own pipeline for identification of G-protein coulpled receptors and peptides, it led to the identification of 30 gene transcripts directly involved primarily in reproduction for P. canaliculata. To target genes involved in chemoreception, we isolated the upper and lower tentacles of the snail and performed another transciptome analysis. Using CLC genomics suite (v.7.1), we performed a general assembly analysis of both tissues, with the analysis revealing ≈ 3.8 Gb and 4.15 Gb clean data respectively. From this 34 putative Gprotein coupled receptors were identified using THMM 2.0, with preliminary bioassays suggesting that anyone of these receptors could be stimulated by rice leave extract ( n = 74 ; p value = 0.003214). We expect that some of these receptors when activated, are the initial player in a signal transduction cascade which ultimately produces a nerve impulse that is transmitted to the brain stimulating chemoattracting behavior.

13:20

Magdalena Klimek, Andrzej Galbarczyk, Ilona Nenko and Grazyna Jasienska

Facial fluctuating asymmetry: is it related to higher risk of cardiometabolic diseases?

ABSTRACT. Objectives. Low degree of fluctuating asymmetry (FA) is proposed as a signal of developmental stability and good genetic quality, thus individuals with low FA should be in better biological condition and have better health. Facial FA levels are reflecting mostly the conditions of the first trimester of pregnancy, when the cardiovascular system and digestive tracts are developing. Therefore, we analyse a potential relationship between levels of facial FA and risk factors of cardiometabolic disease (i.e., hypertension and cholesterol levels). Method. The participants were 263 women aged 45-92 (mean=60.9; SD=10.94) and 81 men aged 47-87 (mean=64.9; SD=10.83) from rural population at the Mogielica Human Ecology Study Site in Southern Poland. Fasting blood sample was collected for cholesterol (total, LDL and HDL-cholesterol) levels analyses. Degree of facial FA was calculated from facial images, according to standard procedures. Age, body mass, smoking, diabetes, alcohol consumption and taking drugs lowering cholesterol were included as potential covariates in the analyses. Results. Among women lower level of facial FA was associated with lower risk of hypertension [OR=0.87; 95% CI: 0.76-0.99], lower concentration of total cholesterol (R2=0.12; p=0.04) and LDL-cholesterol (R2=0.05; p=0.02). Facial FA was not related to levels of HDL-cholesterol (p=0.19). No statistically significant results were observed for men. Conclusions. Our results suggest that among older women (but not men) higher degree of facial FA might be a visual biomarker of poorer health. This study adds to the growing body of evidence that favourable early developmental conditions are important for better later-life health and might be preferable from the evolutionary point of view.

13:20

Sandrine Motamed

Health promotion, community-campus-local authorities partnership and a new health professional profile

ABSTRACT. Meinier is a county near the city of Geneva, Switzerland. Following an initial study aiming to identify its residents' health needs, the local authority formally engaged our Institute to try to resolve the problems disclosed, which were of socio-economic and psycho-social nature. Our objective was to demonstrate that a collaborative approach to implementing effective intersectorial health promotion works at county level and that there is a need for a new role for public health, working at county level. Numerous meetings of the inhabitants gradually developed into a community-wide dialogue, leading them to clearly define their requirements. Old people felt isolated and wished to remain in the village, rather than enter a nursing home elsewhere. Young families could not get established because of a lack of available housing and nonexistent day care facilities for children. Social links between people had diminished. Further difficulties arose from poor mobility. Given these findings the inhabitants drew together to develop a more equitable society, in a partnership between the authorities and our Institute. A participative intersectorial approach allowed a global program to be put together, which particularly united housing, urbanism, ecology and mobility. The project, driven completely by community participation, is now in its fourteenth year, its 40 million dollar budget adopted by community vote. One prominent aspect is the new village center, with its sheltered housing for the elderly, affordable accommodation for young families, child day care, a games library, shops and a restaurant as well as an intergenerational park and living space. The learning and experience gained in terms of community participation and of behavioral and social health determinants has been very important for all concerned.

A collaborative approach to implementing effective intersectorial health promotion works at county level and there is a need for a new health professional profile (the county practitionner).

13:20

Nune Truzyan and Varduhi Petrosyan

Lack of education might trigger multi-drug-resistant tuberculosis development in Armenia: knowledge evolution

ABSTRACT. Background: Approximately 47% of previously treated TB cases become multi-drug-resistant/rifampicin-resistant tuberculosis (MDR/RR-TB) in Armenia. The major known risk factor is the TB treatment ‘lost to follow-up’ (LFU) associated with the insufficient TB knowledge. The aim of this study was to assess whether the level of education received by TB patients and their families during inpatient treatment might influence the MDR/RR-TB development in Armenia.

Methods: In 2016 utilizing the International Accreditation and WHO TB Care Standards we evaluated the level of Patient and Family Education (PFE) standard compliance, applying a mixed method study design. Data exploring practices and the level of policies applied were collected through 15 in-depth interviews and a standardized checklist and analyzed using scoring system converted to percentages. We also looked at 5-year (2012-2016) treatment outcomes for the pulmonary drug-susceptible TB patients to disclose any trend between LFU, and ‘treatment failure’ (TF) as indicators of MDR/RR-TB development.

Results: Several processes were not standardized and consistent leading to meet the PFE standard minimally (26%). The trend analysis showed a strong relation between the treatment outcomes throughout the years. Decrease in LFU rates in 2012-2013 (12.6% - 8.9%) and continuous increase in 2013-2015 (8.9% - 12.6%) resulted in similar tendency for TF one year later: (1.5% - 1.1%) in 2013-2014 and (1.1% - 1.6%) in 2014-2016 conforming that those drug-susceptible TB patients who discontinued treatment, most probably had relapses in the following year and failed the drug-susceptible TB treatment because became drug-resistant.

Conclusion: Lack of education/counseling of drug-susceptible TB patients during their treatment might lead to higher rates of LFU and facilitate the MDR/RR-TB development in Armenia.

13:20

Nuntiya Somparn, Arunee Jetsrisuparb and Veerapol Kukongviriyapan

Adaptive response against oxidative stress due to iron overload in beta-thalassemia/HbE patients

ABSTRACT. Abstract Objective Oxidative stress due to iron overload is implicated in clinical manifestation of beta-thalassemia/hemoglobin E (beta-thal/HbE). In the present study, we investigated the cellular adaptation against oxidative stress in -Thal/HbE patients. Methods Twenty pediatric beta-thal/HbE patients and 20 healthy controls were recruited in the study. Oxidant status was determined by measurement of plasma lipid peroxidation, blood glutathione (GSH) and iron study. Expression of glutamate-cysteine ligase catalytic (GCLC) and a modifier (GCLM) subunit, heme oxygenase-1 (HO-1) and biliverdin reductase (BVR) were determined by Western blot analysis and reverse-transcription polymerase chain reaction. The electrophoretic mobility shift assay was performed to determine the role of Nrf2, a transcription factor involved in the cellular protection against oxidative stress. Results Blood samples from patients exhibited iron overload, elevation of lipid peroxidation and marked reduction of GSH. GCLC and GCLM was up-regulated about 3-4 fold when compared with controls. GCLC protein levels were correlated with serum iron. In thassemia. protein and gene expression of HO-1 were not difference from control whereas protein expression of BVR was increased. There was the enhanced binding activity of the oligonucleotide probe for Nrf2-driven antioxidant response element with nuclear protein from blood mononuclear cells of thalassemia subjects. Discussion The cellular response is operating in beta-Thal/HbE patients to defense with oxidant stress due to the iron overload. Such adaptive response is mediated by activation of Nrf-2 transcription factor, thereby up-regulates antioxidant enzyme GCLC and BVR to alleviate the stress.

13:20

Urarat Nanna, Linda Chularojanamontri and Seewaboon Sireeratawong

Effects of the Thumbergia laurifolia Lindl. Extract on Gastric Ulceration in Rats

ABSTRACT. Background: From the previous study in animals, Thumbergia laurifolia has been reported to possess anti-inflammatory effect. Its action might be similar to non-steroidal anti-inflammatory drugs, which commonly cause gastrointestinal side effects. Objective: To study the anti-ulcerogenic activity of T. laurifolia extract in animals. Materials and Methods: Male Sprague Dawley rats were used. Anti-ulcerogenic activity of T. laurifolia extract was tested by using four in vivo models including those the gastric ulcer was induced by HCl/EtOH, restraint water immersion stress, indomethacin as well as pylorus ligation model. Results: T. laurifolia extract at the doses of 100, 200 and 400 mg/kg caused the decrease of gastric ulcer formation induced by HCl/EtOH and restraint water immersion stress. Moreover, the extract at the doses of 200 and 400 mg/kg decreased the gastric ulcer formation induced by indomethacin. Regarding to the mechanism of anti-ulcerogenic action, the extract at the dose of 400 mg/kg decreased the gastric secretion as evidenced by the reduction of total acidity n the pylorus ligation model. Conclusion: The findings of this study indicates that the T. laurifolia extract possesses anti-ulcerogenic activity in animals.

13:20

Chi-Chang Chang, Chalong Cheewakriangkrai and Yixiang Zhang

Media Health Literacy Plays Critical Role of Shared Decision Making: Mediating or Moderating?

ABSTRACT. Media health literacy have proven to be associated with health information seeking and with health literacy may be predicted by patient’s Shared Decision Making. This study adopts a cross-sectional design to investigate whether the information ability has the mediating/moderating effects between health literacy and shared medical decision making. All participants completed the health literacy, ehealth literacy, and shared medical decision making questionnaires, respectively. The shared medical decision making index was used as an outcome measure. The mediation models and mediating hypotheses were tested by applying hierarchical multiple regression analyses. The results of this study show that female health literacy scores higher than male, ehealth literacy and shared medical decision making; medical students’ Health education manual score was significantly higher than that of non-medical students. The finding suggests that the college students’ e-health literacy has fully mediating effects between health literacy and shared medical decision making. Overall, it is important for health providers to consider the notion that more ehealth literacy may sometimes, but not always, be better. Discussion highlights the need to examine nonlinear as well as linear relationships.

13:20

Michael Yafi

The evolution of adult diseases into pediatric population: Pediatric obesity and its consequences

ABSTRACT. Background and Aim Childhood obesity remains the most important risk factor of developing type 2 diabetes, dyslipidemia and hypertension in children. In the U.S.A, the Center of Disease Control and Prevention (CDC) estimates that greater than one third of the children and adolescents were overweight or obese. In recent years, cases of pediatric type 2 diabetes in children have been diagnosed more frequently and at younger ages than previously seen. Pediatric obesity and type 2 diabetes are more likely to continue into adulthood. The objective of this study is to report the association of obesity in children 18 years old or younger with type 2 diabetes, dyslipidemia and hypertension.

Method The study population consisted of all patients seen in a pediatric endocrinology clinic. An analysis of ICD10 diagnosis codes was performed for a two year period from 2015 to 2016, to evaluate the association of diagnoses of obesity and abnormal weight gain with type 2 diabetes and other co-morbidities. Results: Of 250 overweight, obese or morbidly obese patients identified, thirty six patents (14%) had dyslipidemia, 26 (1%) had type 2 diabetes and 20 (less than 1 %) had hypertension.

Conclusion: The global pediatric obesity epidemic has allowed adult-type diseases to occur in children. Obese children may have the weight of adults and this has created the evolution of diseases which have been historically limited to adult population (ie: Type 2 diabetes) in children. All obese pediatric patients should be evaluated for comorbidities that include type 2 diabetes, dyslipidemia and hypertension. This screening should continue throughout life if obesity persists. The natural progression of comorbidity usually starts with dyslipidemia but often includes type 2 diabetes in adulthood. Early identification and therapy of these diseases in children can prevent their progression and complications.

13:20

Murtala Dahiru

SYNERGISTIC EFFECTS OF CHAMOMILE AND LAVENDER ESSENTIAL OILS FOR ANTIBACTERIAL ACTIVITY

ABSTRACT. Essential oils have been used for extensive applications of variety of wellness throughout documented history. With massive advancement in science, essential oils today have undergone numerous refining methods to give an improved effect. Determination of the antibacterial activities alone and in combination of lavender and chamomile essential oils is what the researched study explained. Three laboratory strains of cultured bacterial (Pseudomonas aeruginosa, ATCC 27858; Staphylococcus aureus, ATCC 6538 and Escherichia coli ATCC), were used in this analysis. The stock cultures were maintained at −20oC and the sub-cultured onto Tryptone Soya agar (TSA) was incubated at 37oC for 24 hours. The fractional inhibitory concentration index (FIC) was used in determining the oils interaction. The FIC was calculated by dividing the minimum inhibitory concentration (MIC) value of the combined essential oils with the MIC value of each essential oil placed in the combination. The ΣFIC was calculated by adding these two values. Lavender oil showed the greatest antimicrobial effect, with the lowest MIC values of 2mg/mL for both Pseudomonas aeruginosa and Escherichia coli and 4mg/mL for Staphylococcus aureus pathogens compared to chamomile oil when used individually. The combination of chamomile and lavender essential oils in various ratios indicated synergistic effect for all the nine ratios analysed. The minimum inhibitory concentration analysis indicated that these oils have favorable antimicrobial interactions when in combination, that are 100% and 70.4% synergistic and additive effects for the oils selected and this will offer potential for the common use of combining oils in achieving a greater therapeutic result.

13:20

Nitesh Pandey

Why we should be worried about pathogens with the “Killer move”?

ABSTRACT. Human pathogens need their host for survival and perpetuation. Some of these pathogens do not have any non-human reservoir and therefore killing humans is not considered in their long-term evolutionary interest. However, there are diseases like Human African Trypanosomiasis, Visceral Leishmaniasis, HIV, Ebola, and Tuberculosis which kill almost 100% to 50% of the untreated humans [1]. Pathogens that kill most of their host or cause severe sickness in the majority of the cases incur major cost in terms of transmission due to either host death or its immobility. This is one of the reasons why the spread of Ebola has been so limited [2]. But the diseases like Sleeping sickness, Visceral Leishmaniasis, HIV and TB have managed to not only kill their most of the hosts but have also thrived within the population. This could be understood by the “Killer move” hypothesis. These pathogens move into the body of their new human hosts much before they kill the primary infected ones. The cost that they incur from the death of the host gets significantly lowered due to the delayed virulence. This evolutionary balance has helped these deadly diseases to sustain themselves within the human population. This strategy is no lesser than a “killer move” and we should be worried of an emerging pathogen, which is inherently virulent and could be evolutionarily favoured for such a strategy. These types of pathogens have always been a major threat to humans.

References:

1. https://en.wikipedia.org/wiki/List\_of\_human\_disease\_case\_fatality\_rates 2. https://www.who.int/csr/disease/ebola/one-year-report/factors/en/

13:50-14:30 Session 10: Plenary Dan Lieberman

CHAIR: Barbara Natterson-Horowitz

LOCATION: Aula

13:50

Daniel Lieberman

Is Exercise Really Medicine? An Evolutionary Perspective.

ABSTRACT. It is widely appreciated that humans evolved to be physically active, and that physical activity is good for your health. But why and to what extent is exercise (that is, voluntary unnecessary physical activity for the sake of health and fitness) medicine? In this talk, I will make the case that a medicalized perspective on exercise (Exercise is Medicine®) excludes important evolutionary insights that have practical value for resolving widespread confusion and controversies over the relationship between exercise dose and type and chronic non-infectious diseases. Using heart disease and osteoarthritis as test cases, I will tackle four issues. First to what extent is physical inactivity a mismatch? Second, how and why does physical activity slow aging? Third, to what extent does exercise lead to trade-offs that potentially compromise health? I will conclude by exploring how an evolutionary perspective on exercise can help bridge the gap between evolutionary medicine as a field of academic inquiry and a practical tool to help prevent and treat disease.

14:30-15:00Coffee Break

15:00-16:20 Session 11A: Microbiome

CHAIR: Hinrich Schulenburg

LOCATION: Aula

15:00

Shauni Doms, Hanna Fokt, Leslie Turner and John Baines

Elucidating the genetic basis of gut microbial trait evolution in the house mouse subspecies complex and its relevance to understanding human disease

ABSTRACT. Understanding the forces that shape variation in host-associated bacterial communities within- and between host species is key to understanding the evolution and maintenance of metaorganisms, and importantly, recent studies indicate that coevolving microbial taxa are more likely to be associated with human disease. In this study, we used a combined approach to investigate evolutionary divergence in the gut microbiome between the Eastern Mus musculus musculus and the Western Mus musculus domesticus mouse subspecies. This includes (i) a survey of gut microbial variation across the geographic range of the two subspecies, (ii) QTL mapping of gut microbial traits in a cross involving hybrids of the two subspecies, and (iii) cultivation and bacterial genome sequencing of microbial traits identified in both (i) and (ii). Accordingly, indicator species analysis reveals taxa belonging to Bacteroides and Lactobacillus as potentially important microbial traits that differ between species. By performing QTL mapping in 320 second-generation hybrid intercrossed mice, we identified a total of 28 unique host loci involving 41 bacterial taxa, including the previously identified Bacteroides and Lactobacillus indicator taxa. Analysis of host candidate genes points towards circadian rhythms as an important trait, whose host genetic- and/or microbial basis may have diverged since the common ancestor of the two species. Given the emerging relationships between disturbances in circadian rhythms, the gut microbiome and metabolic disorders, an understanding of ongoing evolution of these traits in the mouse model system may provide important insight and potential targets for treating human metabolic disorders.

15:20

Hugo C. Barreto, Ana Sousa and Isabel Gordo

The Landscape of Adaptive Evolution of a gut commensal bacterium in Aging Mice

PRESENTER: Hugo C. Barreto

ABSTRACT. Aging is a complex process, with many associated time-dependent phenotypes. The gut microbiota has long been postulated as an important factor in shaping healthy aging. It is now known that the microbiota composition changes during aging, with taxa that are rare in adults becoming dominant in the elderly and shifting towards more beneficial microbes further occurring in centenarians. The observation that inflammation, associated with aging, can modulate and be modulated by the microbiota further supports the microbes as a key piece for the aging multifactorial process. The combination of the time-dependent inflammatory and ecological processes should lead to an altered pattern of evolutionary change of a gut commensal lineage. Aiming at testing this hypothesis we performed a genomic analysis of a labelled bacterial strain comparing the pattern and rate of evolution in cohorts of old and young adult mice, with controlled genetic and lifestyle factors. Overall, this study examines mechanisms of bacterial adaptation in aging mammals and will contribute to understanding the role of evolution to the diversity of the microbiota and its genetic structure in the context of aging.

15:40

Anke Kloock, Michael Bonsall and Kayla King

When to protect your master: Evolution of microbe-mediated protection in Caenorhabditis elegans

ABSTRACT. Microbes living with hosts can protect them against pathogen infection. Although microbes can have great evolutionary potential, the conditions under which they might evolve to protect their host remain elusive. It is hypothesized that a high risk of infection favours the evolution of protective traits by microbes, but infection is often temporally heterogeneous in nature (e.g., seasonality). We thus tested the effect of temporal heterogeneity in infection on the evolution of microbe-mediated protection. We experimentally coevolved protective microbes, Enterococcus faecalis, with populations of Caenorhabditis elegans nematode hosts, in treatments varying the infection frequency with virulent Staphylococcus aureus. Temporal heterogeneity involved pathogen exposure every host generation, alternating host generations, every fifth host generation or never, and we additionally investigated the effect of initial pathogen presence. Our results show that microbe-mediated protection evolved in those host-E.faecalis associations under constant or alternating generations of pathogen infection. Initial exposure to the pathogen did not influence the evolutionary outcome. Overall, our results indicate, that pathogen presence is required in sufficiently small intervals to drive the evolution of microbe-mediated protection. The results from this study illuminate the relationship between temporal variation in pathogen infection and selection for host-protection by an organism’s resident microbiota.

16:00

Irina M Velsko, James A Fellows Yates, Franziska Aron, Richard W Hagan, Laurent A Frantz, Louise Loe, Juan Bautista Rodriguez Martinez, Eros Chavez, Chris Gosden, Greger Larson and Christina Warinner

Microbial differences between dental plaque and historic dental calculus are related to oral biofilm maturation stage

ABSTRACT. Human microbiomes influence health and well-being in myriad ways, both beneficial and detrimental. The oral microbiome is associated with both local and systemic inflammatory diseases and poor oral health may indicate poor systemic health. Ancient dental calculus provides a unique opportunity to study an authentic human microbiome prior to introduction of industrialization-associated changes, such as high-sugar diets and antibiotic use, that are considered contributors to modern systemic inflammatory diseases. Data from such studies may reveal methods of adaptation by the microbiome that are discordant with host physiology and promote industrialization-associated metabolic disorders, and, further, may suggest microbiome-targeted therapies. Defining a historical normal oral microbiome is critical to identifying microbiome changes, and here we characterize historic dental calculus from a cohort of 48 Victorian-period British individuals and compare it to modern dental calculus and modern dental plaque. Dental calculus does not typically accumulate as much today as historically, and clinical oral microbiome research studies focus primarily on living dental plaque biofilm. However, plaque and calculus reflect different conditions of the oral biofilm, and differences in microbial characteristics between the sample types have not yet been systematically explored. Comparisons between microbial, protein, and metabolomic profiles revealed distinct taxonomic and metabolic functional profiles between plaque, modern calculus, and historic calculus, but not between calculus collected from healthy teeth and periodontal disease-affected teeth. Bacterial species co-exclusion was related to biofilm environment. Proteomic profiling revealed that healthy-tooth samples contain low levels of bacterial virulence proteins and a robust innate immune response. Overall, we find that there are there are systematic microbial differences between plaque and calculus related to biofilm physiology, and recognizing these differences is important for accurate data interpretation in studies comparing dental plaque and calculus.

15:00-16:20 Session 11B: Mixed session: cancer and methods

CHAIR: Charles Nunn

LOCATION: 217

15:00

Robert Noble, Katarina Bacevic, Michael Hochberg, Liliana Krasinska and Daniel Fisher

Spatial competition constrains resistance to targeted cancer therapy

ABSTRACT. Adaptive therapy (AT) aims to control tumour burden by maintaining therapy-sensitive cells to exploit their competition with resistant cells. This relies on the assumption that resistant cells have impaired cellular fitness. Using a model of resistance to a pharmacological cyclin-dependent kinase inhibitor (CDKi), we have shown that this assumption is valid when competition between cells is spatially structured. We generated CDKi-resistant cancer cells and found that they have reduced proliferative fitness and stably rewired cell cycle control pathways. Low-dose CDKi outperformed high-dose CDKi in controlling tumour burden and resistance in tumour spheroids, but not in monolayer culture. We have further used mathematical modelling to examine how tumour spatial structure can amplify the fitness penalty paid by resistant cells. This presentation will especially focus on the evolutionary theory that underlies AT, and on defining conditions under which the strategy promises to be most effective in the clinic.

15:20

Michael Hochberg and Andrei Akhmetzhanov

"You can pay me now or pay me later": evolutionarily sensible approaches to preventing cancers

ABSTRACT. In this talk I ask the question "can we optimize a life-style change or treatment against cancers, so as to both have minimal impacts on health and meet therapeutic objectives"? I present a general mathematical model that probe this problem and yield some surprising and promising findings.

15:40

Joseph W. Cauceglia, Derek L. Stark and Wayne K. Potts

The power of Organismal Performance Assays (OPAs) for detecting health declines due to any cause

ABSTRACT. The degradation of human health due to environmental exposures is likely greater than for any other cause of disease. Environmental exposures include environmental contaminants, dietary additives, pharmaceuticals and others. Unfortunately, many exposure-caused diseases are difficult to discover and predict, often being revealed only after decades of retrospective research. This problem highlights the great need for more sensitive methods to detect health degradation. We have developed such a methodology, called Organismal Performance Assay (OPA), which utilizes the extreme competition present in mouse societies to reveal health and performance differences between treatment and control mice competing in seminatural enclosure populations. We will overview published and unpublished data evaluating the efficacy of OPAs to reveal health degradation, where other modern assessment approaches have failed; examples include 1) health consequences of three recalled or blacklisted pharmaceuticals, 2) the genomic swapping of paralogous Hox genes, 3) the first demonstration of health degradation due to human relevant doses of dietary refined sugars, and 4) inbreeding depression. Since the major readout of OPAs is reproductive success (Darwinian fitness), the interpretation is clear, and allows direct comparison of insults; prompting questions such as: would you rather be on the American diet or have had your parents be first cousins? OPAs suggest it is a toss-up, as both result in a 35% loss of fitness. The toxicology community has embraced new sets of tools made possible by modern molecular approaches. We submit that in vitro and ex vivo approaches have proven insufficient, failing to detect adversity due either to having ambiguous measures of health or failure to stress-test the relevant systems. With ambiguous testing methods, and a policy of innocent until proven guilty, the bulk of the toxicity testing burden falls on the public. OPAs show promise of being an important contributor for fulfilling this public health demand.

16:00

Daniel Taub

The Potential of Broad-Audience Peer-Reviewed Literature for Disseminating Knowledge in Evolutionary Medicine

ABSTRACT. There is tremendous value in professionals in fields such as evolutionary medicine and public health sharing their expertise with a broad, general audience. However, systems of evaluation and reward for academics typically place a strong emphasis on publishing in peer-reviewed venues, while most publications for a general audience are not peer-reviewed. Several models have been developed for the publication of peer-reviewed papers that review scientific topics for a broad audience, however there have been few such efforts in evolutionary biology and related disciplines. I present analyses of a variety of article metrics, demonstrating that when this approach has been tried, these papers have been very well read and received. For example, every single “Topic Page” that has been published in PLOS Computational Biology and PLOS Genetics has received a greater number of views than the average research paper published in that journal during the same month. Even more telling, each of these review articles for a general audience has received a greater number of citations in peer-reviewed journals than the average research paper in the same journal. Reviews for general audiences in other publications, including the journal Genetics and the online publication Nature Knowledge similarly show high rates of being cited in peer-reviewed journals. This suggests opportunities for researchers to reach both professional and general audiences with broad-audience review papers. It further suggests that scientific journals can both disseminate disciplinary knowledge to a broad audience, and boost impact factors and other journal metrics by incorporating appropriate types of reviews intended for general audiences.

15:00-16:20 Session 11C: Symposium Paleopathology

CHAIR: Gillian Bentley

LOCATION: 204

15:00

Julia Gamble and Gillian Bentley

Palaeopathological Insights about the Developmental Origins of Health and Disease (DoHAD)

ABSTRACT. While most of the data on early life plasticity originate from longitudinal, epidemiological or anthropological studies of living people, bioarchaeology (the study of past populations in their archaeological context) can provide extensive insight into the developmental origins of health and disease from a deep time perspective. Through the study of human remains, we can collect information about patterns across the life course analogous to longitudinal analyses, considered the gold standard for studies of contemporary populations. Here, we provide an overview of the contributions bioarchaeology can make to evolutionary medicine using the DOHaD framework. We demonstrate insights that can be gained by leveraging evidence in three research directions that have made significant contributions to the field. These are: i) consideration of transition states (demographic, epidemiological, nutritional), ii) evidence of social inequalities, and iii) bioarchaeological studies of children and childhood. Through these three approaches and using case studies, we will explore the insights provided by bioarchaeology concerning the nature of individual frailty and stress responses as well as the influence of critical windows in growth and development on later life health experiences. We explore the nature of population responses to changing environmental conditions and provide a deep time perspective into how these responses have shaped health experiences in the past. In a world with increasing socioeconomic disparity, we also demonstrate how the bioarchaeological record, by drawing upon past contexts, can inform our understanding of the social determinants of health. While critically evaluating both the strengths and limitations of bioarchaeological data, we thus demonstrate the significant contributions that can be made to evolutionary medicine through the direct examination of osteological remains from archaeological populations, as well as the relevance of these contributions to current population adaptation and response.

15:20

Frank Rühli

Paleopathology and its impact on evolutionary medicine

ABSTRACT. Paleopathology is the study of ancient diseases. By using skeletal and mummified remains as well as indirect evidence such as images or other historical data pathologies are studied. Often - but not always - these studies are focusing on historic times spans only not on larger evolutionary timespans. Nevertheless, the established discipline of paleopathology can contribute to the field of evolutionary medicine; exemplary, since the evolution and secular trends of disease and its contributing factors can be very fast. The aim of this keynote lecture is to highlight not only the general impact and pitfalls of paleopathology as a discipline but with s specific focus on the evolution of disease. A major issue is the apparent lack of evidence is some paleopathological cases as well as the fact that often e.g., methodologies are not specifically tested for such ancient samples. Based on our long-term experience, challenges such as how to define undisputed criteria for providing sound paleopathological data will be presented. Disease load and its very specific impact on an individual both, purely physiologically but also functionally, are often difficult to assess retrospectively only. Therefore, some of our most recent studies used comparative well-documented case series to address this. Finally, in this presentation the need for an “Paleo-One Health initiative” will be outlined. With such evidence-based criteria and with the incorporation of holistic ecological data, paleopathology - as a discipline - shall be most beneficial for the advancement of the research field of evolutionary medicine.

15:40

Ella Been, Kimberly Plomp and Leonid Kalichman

Erect posture, bipedalism and spinal health

ABSTRACT. Humans are the only living hominoid that habitually stands upright and walks on two legs. The adoption of erect posture as habitual imposed substantial changes on spinal morphology and biomechanics. One of the major morphological changes is the increased curvatures found in the human spine. There is an ongoing debate about whether humans ''pay'' for becoming bipedal by suffering from a high prevalence of back pain and spinal pathology. In order to answer this question, we explored the relationship between sagittal spinal posture and spinal pathologies, back pain, and health-related quality of life. We found that spinal posture closely correlates with spinal pathology. Individuals with a well-aligned spine – within the neutral zone defined as moderate spinal curvatures and the line of gravity close to the acetabulum – have a better quality of life, less back pain, and less spinal pathology. Individuals out of the neutral zone, with accentuated or with decreased pelvic incidence and spinal curvatures, are at a higher risk for developing spinal pathology, back pain, and reduced quality of life. All of this indicates that adopting an erect posture and bipedalism has an impact on human's spinal health because variation in curvatures outside the neutral zone is associated with more spinal pathology, back pain, and lower quality of life, than those within this zone.

16:00

Elizabeth Uhl and Richard Thomas

Uncovering Tales of Transmission: An Integrated Paleopathological and Evolutionary Perspective on Shared Human and Animal Pathogens

ABSTRACT. The transfer of pathogens between animals and humans has occurred for millennia and remains a public health issue today. Although the focus has traditionally centred on pathogens transmitted from animals to humans (zoonoses), the reality is that the direction of transmission is just as often the other way (reverse zoonoses). This on-going cross-species transfer of pathogens is best understood through investigations of the environmental factors driving microbial evolution, in particular those affecting the transmission of a pathogen to a new host. The dramatic changes in domestic environments that occurred as human populations and their relationships with animals transitioned between hunting/foraging, herding/farming and urban/industrial had major impacts on pathogen evolution through the opportunities for transmission they provided, and on humans and animals by the resulting effects on pathogen virulence. These changes included crowding, often in unsanitary conditions, and the mixing of species whose interactions were much more limited than in their natural environments. Human induced environmental changes were often dramatic and both facilitated the evolution of new pathogens, i.e.: the morbilliviruses (canine distemper/measles/rinderpest), and expanded the transmission opportunities and host ranges of pathogens such as Mycobacterium spp and Burkholderia mallei. Although the challenges posed by the fragmentary nature of the archaeological record can make it difficult to definitively diagnose diseases in the past, an evolutionary perspective that considers how various domestic environments would impact pathogen transmission and virulence can provide important insights as to why specific diseases occurred when and where they did, and their potential for causing future outbreaks.

16:20-17:00 Session 12: Plenary Steve Frank

CHAIR: Michael Hochberg

LOCATION: Aula

16:20

Steven Frank

Mitochondria and male disease

ABSTRACT. Mitochondria usually pass from mother to offspring, whereas males rarely transmit mitochondria. Selection is, therefore, blind to male-specific mitochondrial phenotypes. A mutation with a strongly deleterious effect in males but only a weak effect in females is nearly neutral, because only the female-specific consequences can be selected. This sex-biased `selective sieve' inevitably causes deleterious mitochondrial mutational effects to accumulate more strongly in males than in females. But the actual force could in fact be weak and of little consequence. So, does this asymmetric selective sieve truly impose a burden on male health? Several studies suggest that the answer might be yes. However, not enough data have been collected to provide a definitive answer. Modern genetic techniques suggest several new studies that could tell us more clearly whether this sex-biased selective filter shapes observed patterns of disease.

17:00-18:00 Session 13: Business meeting

CHAIR: Randolph Nesse

LOCATION: Aula

18:30-20:30 Chocolate Event

LOCATION: Mensa B

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08:30-09:30 Session 14: Keynote Bernard Crespi

CHAIR: Jacobus Boomsma

LOCATION: Aula

08:30

Bernard Crespi

How evolutionary biology can frame a unified theory for understanding human mental illness

ABSTRACT. We need general, useful theory for how human mental adaptations relate to mental disorders. I have tried to develop such theory, focusing on human social and non-social adaptations, exemplified by a diametric, opposite nature to the psychotic-affective spectrum in relation to the autism spectrum. The theory is consilient with Marco Del Guidice's life history approach, with Simon Baron-Cohen's theories for autism, and with the bulk of genetic, neurological, and psychological evidence, barring mistakes and misinterpretations. I show how. The theory is based in evolutionary principles, and has direct implications for diagnosis, psychological therapies, and pharmacological treatments.

09:30-10:00Coffee Break

10:00-12:00 Session 15A: Life course

CHAIR: Gillian Bentley

LOCATION: Aula

10:00

Sean Byars, Steve Stearns and Koos Boomsma

Increased risk of digestive and genitourinary diseases but decreased risk of inflammatory bowel disease after childhood appendectomy: findings from a nationwide registry study

ABSTRACT. BACKGROUND Appendectomy is a relatively common pediatric procedure with little short-term negative impact. However, not much is known about long-term consequences beyond the perioperative risks. It is important to assess those consequences because this organ appears to have significant roles in maintaining appropriate gut biofilms for healthy digestive functioning and its lymphoid tissue might also play a role in the immune system. METHODS We tested the long-term health consequences of appendectomy by examining risk for 28 diseases within ~1 million Danish residents followed from birth to 30 years of age depending on whether appendectomy occurred in the first 12 years of life. Robust results were obtained by using stratified Cox regressions with sufficiently statistically-powered samples of cases (surgery) and controls. Our estimates of risk are adjusted for diseases occurring before surgery and for 18 covariates including parental history of the same diseases, birth metrics, and sex. RESULTS We found significantly elevated relative risks for many diseases, with the risks of various digestive (RR between 1.47-1.64) and genitourinary (RR between 1.30-1.72) diseases being particularly increased after appendectomy. The only decreased risk was found for inflammatory bowel disease (RR=0.58). Moreover, absolute risk differences suggest that effects on digestive tract (AR up to 2.81% increased) and genitourinary (AR up to 0.88% increased) diseases should be noticeable at the population level. CONCLUSIONS Our results provide evidence for longer-term health risks associated with appendectomy. This suggests that the appendix is important for the establishment of normal digestive and immunological function and that its removal may also be associated with other disease risks. These findings are consistent with the appendix having retained at least some of its ancestral functionality in modern humans. The decreased risk of IBD following appendectomy, previously found in other large epidemiological studies, remains puzzling.

10:20

Anna Grace Tribble

The Role of the UN Oil for Food Program in the Pathway between Fetal Malnutrition and Poor Adult Health among Iraqi Families

ABSTRACT. The Developmental Origins of Health and Disease (DOHAD) hypothesis suggests that negative exposures during prenatal and early life development can produce long-term health effects. One such exposure is fetal malnutrition which can lead to restricted growth and low birthweight. Food aid has been used since World War II to buffer pregnant mothers and other vulnerable populations from the effects of malnutrition. This project examines the efficacy of food aid in two respects. First, it estimates the effect of past maternal food aid receipt on food security among Iraqi mothers who were pregnant both before and after implementation of the United Nation’s Oil-for-Food program in 1996. Second, the study assesses the degree to which receiving food aid during pregnancy affects young adult health outcomes. Methods. The population-based survey includes a random sample of 40 families living in the Slemani governorate of northeastern Iraq. This retrospective survey collected data on mother’s food insecurity and food aid receipt during her pregnancies in the 1990s. Data were also collected on young adult chronic physical and mental health outcomes for the two children in the household born before (1994-1995) or after (1997-1998) the introduction of food aid. Health outcomes include depression, anxiety, stress, height, weight, waist and hip circumference, and blood pressure. Results. Analyses will compare the health measures of current young adults age 20-24 born before and after the UN Oil for Food program’s introduction conditional on the status of maternal food aid receipt. Each model will measure the average effect of maternal food aid receipt during prenatal development on young adult health outcomes. Discussion. The findings of this project further our understanding of food aid’s role in disrupting or perpetuating the pathway linking fetal malnutrition to poor adult physical and mental health outcomes.

10:40

Amara Finch

Developmental Origins of Health and Disease and Population Differences in Postnatal Growth Rates Among Premature Infants: Implications for Lifelong Health

ABSTRACT. Evidence suggests that postnatal growth patterns of preterm and small for gestational age infants are predictive of multiple pathologies during adulthood, including metabolic syndrome, diabetes, hypertension, and malignancy. Early life growth courses are influenced by a complex interplay of genetics, epigenetic programming, infant nutrition, and perinatal morbidity. Variations in perinatal growth are both reflective and predictive of adverse health outcomes, and it is unclear to what extent manipulating growth trajectories may modify associated long-term consequences.

African Americans living in the USA exhibit higher rates of both premature birth and specific adult pathologies when compared to white counterparts. Research has documented multiple social factors contributing to this pattern of health disparity, and has pointed to the role of psychosocial stress and racial discrimination in the pathogenesis of preterm birth and the development of poor neonatal and adult health outcomes. It is likely that both evolutionary history and lived experience are influential in programming fetal and postnatal growth.

While recently developed growth charts describe global trends in expected growth velocity of preterm infants, there is no documented data on the observed variation of postnatal growth between sub-populations of preterm infants in the USA. It would be surprising if there were not postnatal growth differences based on distinctive fetal growth and body composition patterns. The specific factors that may be associated with these differences remain to be clarified. My ongoing research seeks to characterize observed differences in postnatal growth patterns among preterm infants based on both ethnicity and maternal exposure to adversity.

Ultimately, knowledge of optimal growth rates for distinct populations of neonates will help guide clinical practice so that we may encourage healthy growth among all infants while remaining aware of population-specific growth goals.

11:00

Paul Turke

It's Better to Give than to Receive--Unless You're Young

ABSTRACT. Mismatch between ancestral and current environments has figured prominently in the field of evolutionary medicine, with changes in diet and physical activity leading the charge. Here, I argue that mismatch in the arena of social organization also has significant effects on our health and overall wellbeing, and I argue specifically that changes that distance young children from emotionally committed caregivers can be detrimental to both groups.

My hypothesis has three components: (1) throughout nearly the entirety of our evolution, children grew up in proximity to various categories of related older individuals; (2) Hamilton’s Rule predicts that these children would have been ‘worthy’ recipients of care (i.e., worthy in the sense of increasing a donor’s inclusive fitness); (3) there must have been coevolution of mechanisms that motivate and guide nepotistic transactions in adaptive directions. Most of these, I suspect, were emotional, and are still with us, implying that we’ll feel happy and fulfilled when we behave in ways that help our young dependents, and feel the opposite when we don’t. Thus, a major source of our discontent (e.g., 6.5 million of 35 million Americans aged 65 or older are depressed) could be a shortage of nearby investment-grade kin, combined with a plethora of seemingly desirable distractions that too often turn out not to comport well with our emotional design.

But there may be hope for us after all, if our helping-leads-to-happiness neural mechanisms are not overly specific. While it’s unlikely that watering the houseplants triggers a burst of happy feelings, helping puppies probably does, and so does helping children—all of them.

So, my advice is to be nice. You’ll be happier for it.

11:20

Gillian Bentley, Ben Bar-Sade, Reinhard Stöger, Khurshida Begum, Richard Emes, Or Eden and Philippa Melamed

Childhood Development and Epigenetic Effects on Reproductive Function

ABSTRACT. Earlier studies of migrant Bangladeshis showed that women who developed in Bangladesh have a different reproductive phenotype from Bangladeshi and European women who mature in the UK. Specifically, developing in Bangladesh (where infectious disease loads are higher and quality of health care is lower than the UK) lowers levels of reproductive hormones and shortens the length of the reproductive lifespan. However, child migrants to the UK have a modified adult phenotype that more closely matches that of women who grew up in the UK. In order to assess epigenetic modifications of the reproductive phenotype, we established a mouse model to replicate effects of infectious disease exposure in early life. Mice treated with Dextran sodium sulfate had a phenotype mirroring women who grew up in Bangladesh, including a later puberty, lower levels of progesterone and anti-Müllerian hormone, and lower numbers of primordial and primary ovarian follicles. Transcriptome analysis of ovaries from the treatment group revealed up-regulated genes that induce follicle growth, and down-regulation of genes promoting apoptosis. Repressed genes include Srd5a1 (encoding the enzyme 5α-reductase), down-regulation of which (through increased methylation) matched findings from Bangladeshi migrants obtained using cheek swabs. In mice, expression of Srd5a1 was also significantly reduced in the hypothalamus where neurosteroids direct central activation of both the HPG and HPA axes through binding and activating specific neuronal (GABA) receptors. Our studies link central changes in activation and functioning of the adrenal axis with possible epigenetic regulation of Srd5a1 expression during a crucial developmental window. Changes in activation of hypothalamic control centres (via reduced 5α-reductase activity) could provide a mechanism for changes in ages of puberty and adrenarche, as well as modified adult functioning of these axes. We reveal that epigenetic modifications comprise flexible, regulatory mechanisms mediating phenotypic changes through altered gene expression. Funding: ESRC/BBSRC, UK.

11:40

Luisa Rivera, Erik Ringen, Angela Narayan, William Harris and Alicia Lieberman

Prenatal PTSD is predicted by the interaction of hair cortisol, early life adversity, and current stress: implications for fetal programming

ABSTRACT. While rises in cortisol are likely adaptive response to normative stressors, chronic and/or severe stress during development may result in endocrine depletion and a subsequently ‘blunted’ phenotype that cannot mount appropriate responses to challenges. This blunting is thought to be a risk factor for post-traumatic stress disorder (PTSD). Perinatal PTSD is of particular concern, not only for maternal health but also because perinatal cortisol levels are thought to mediate life history tradeoffs via fetal programming of HPA axis. We explored the relationship between PTSD, early life adversity, current stressors, and hair cortisol in a cohort of 101 low-income pregnant women oversampled for current mood disorder drawn from a longitudinal study of perinatal mental health at an urban safety-net hospital. We found that lower levels of hair cortisol predicted greater PTSD symptoms in response to current stressors. We also found that lower hair cortisol moderated the effect between early life stress and PTSD, but that this effect was attenuated by the presence of higher levels of current stress. This research provides support for the HPA axis blunting hypothesis of susceptibility to anxiety disorders during pregnancy. We consider how HPA blunting could result in maladaptive fetal programming if highly stressed women express a mismatched endocrine milieu.

10:00-12:00 Session 15B: Mixed session: adaptations

CHAIR: Elisabeth Uhl

LOCATION: 217

10:00

John Martin and Gunter Wagner

The Origins of Megakaryocytes, Platelets and Eutherian Placentation are Linked

ABSTRACT. Invasive placentation with extended pregnancy is a shared derived characteristic unique to eutherian mammals which possess a highly effective system of hemostasis, platelets. These are found in all mammals but no other group of animals. We propose that platelets and megakaryocytes (which give rise to platelets) evolved from an ancestral 2N thrombocyte which became polyploid and then fragmented cytoplasm in the pulmonary circulation producing platelets. Possession of platelets enabled the evolution of invasive placentation, and allowed safe separation, without hemorrhage, of the placenta from the uterus at birth. This explains why invasive placentation is limited to mammals.

10:20

Sara Niedbalski

Novel genomic architectures for clinical traits evolved during the Beringian Standstill

ABSTRACT. A primary objective of medical genetics is to provide insights about disease etiology, including the complex interactions of both genes and environments. To this end, anthropological genetics offers a particular set of insights and tools with which to study signatures of environmental adaptation made by human populations experiencing novel or extreme environmental stimuli. Adaptations made during a period of extreme environmental circumstances may facilitate subsequent gene-environment mismatch when environmental pressures subside. The Beringian environment first encountered by the founding population of Native Americans in their migration from East Asia into the New World is a prime example. Previous research from our lab has identified a unique genetic architecture private to the Americas that dates to the period of Beringian occupation. Our dataset consists of high frequency SNP alleles (p > 0.30) identified from whole genome scans in the Thousand Genomes Project. Here we identify signatures of natural selection embedded within this American architecture, lending novel insights to the understanding of complex diseases and personalized medical trajectories. We generated novel software to annotate more than twenty thousand unique American SNPs with respect to four lines of evidence that are indicators of functional change related to adaptation: (1) genic or non-genic, (2) synonymous or non-synonymous, (3) ontological class, and (4) clinical significance. We compare the distributions for each category between the American SNPs and a set of matched randomly distributed SNPs in an American sample, which serve as a control. We identify multiple unique genic signatures related to human health outcomes within the American architecture that arose during the Beringian context and are now shared broadly by all extant Native Americans. Our work provides a novel set of candidate loci for investigating gene-environment mismatch in New World populations.

10:40

Stephen Corbett, Jin-Gun Cho and Evan Ullbricht

The Magic Mountain? Adaptations to altitude and susceptibility to Tuberculosis in Nepal and Tibet

ABSTRACT. Since 2006 there has been an influx into Sydney of 30,000 students and migrants from Nepal. We have documented high rates of activation of latent TB in this group, despite the absence of active TB being a condition for their emigration. This natural experiment parallels that of the 100,000 Tibetans who fled to Dharamshala in India following the 1959 Chinese occupation. These refugees and their children have some of the highest rates of TB in the world. Nepal and Tibet both have a moderate to high TB incidence rate of 120-150/100,000 per annum, with lower rates at higher altitudes. The prevalence of latent TB, however, in Tibetan refugees in the US is 90-98%. In the case of the Nepalese, causes of reactivation such as diabetes, poor immigration screening or recent contact with active cases in Australia are thought to be unlikely. Three environmental and evolutionary explanations are currently being considered. The first is that a return to normoxia, or in the case of Tibetans descending to Dharamshala, an increase of 25 mm Hg in ambient paO2, favours the growth of M tuberculosis, a largely aerobic organism. The second is that descent from altitude reverses the hypoxia related increase in cellular and innate immunity which accompanies activation of the Hypoxia Inducible Factor (HIF) pathway. HIF is the master regulator of the immunological and metabolic tissue and organismal responses to hypoxia. The third is that the proven adaptations to altitude of populations in Tibet and Nepal, which involve a lowered threshold for activation of the HIF pathway, permanently impair immunity and that this impairment, in concert with the first two explanations, amplifies the risk of tuberculosis upon descent. These observations are likely to have important implications for the prevention and treatment of tuberculosis and other infections in populations living at altitude.

11:00

Randolph Nesse

Adjustable defense response thresholds are inherently vulnerable to positive feedback dysregulation

ABSTRACT. Protective responses such as pain, vomiting and anxiety are regulated by evolved mechanisms that express the response when a threshold is exceeded for the intensity or duration of a cue correlated with the situation in which the response is useful. Such thresholds are heritable so natural selection shapes them to levels that tend to be optimal in general, but that may vary widely between individuals, presumably because environments vary substantially. Repeated expression of a protective response indicates that an individual’s response is inadequate for what is likely a very harsh environment and that a stronger, longer response to a lower threshold would increase fitness. Facultative adaptations that shift the threshold to greater sensitivity and the response to greater intensity and duration have been documented for pain and anxiety and may be common for other responses. Such systems are inherently vulnerable to slipping into a runaway positive feedback cycle. Such positive feedback is a recognized cause of chronic pain, although applications of this knowledge are still in development. Panic disorder can also result from positive feedback that lowers the response threshold. This presentation reviews evidence for the pathogenic process and describes other clinical conditions that may be explained by the same mechanism including pathological cough and vomiting. The results may be useful for strategies to prevent and treat syndromes of excess response in defensive systems.

11:20

Anne Lehner, Kaspar Staub, Lafi Aldakak, Patrick Eppenberger, Frank Rühli, Robert Martin and Nicole Bender

Fish consumption is associated with school performance in children in a non-linear fashion: results from the German cohort study KiGGS

ABSTRACT. Introduction: How the long chain fatty acids DHA and EPA in the diet permitted human brain evolution, and how much our brains need today to function optimally is still a hot topic for debate. DHA and EPA are considered as semi-essential because only insufficient amounts can be produced from other nutrients, such that they must be ingested with the diet. The Dietary Reference Intake (DRI) of DHA and EPA, or of food containing these fatty acids, has not yet been established, but consumption of fish is routinely recommended. Here we analyze data from a large cohort study to assess the association between fish consumption and scholastic performance in children and adolescents. Methods: We analyzed data from the German cohort of children and adolescent health KiGGS, which was conducted 2003-2006 and included more than 17,000 children. We applied ordered logistic regressions to test for associations between fish intake and school performance. We also included potential confounders in our models. Results: We found a statistically significant association between an intake of 8 g of fish per day and last grades in both German and mathematics. For the outcome German, higher levels of fish intake also had a positive effect. These relationships were not linear but tended to decrease again with higher intakes of fish. Discussion: Our result confirms previous reports of a positive association between fish intake and scholastic performance. Interestingly, this relationship was not linear but tended to decrease again in the highest categories of fish intake. We hypothesize that mercury or other pollutants in the fish could be detrimental at high levels. We recommend a minimal intake of 8 g fish per day for all children. Upper limits have yet to be established.

11:40

Virginia J. Vitzthum

The Fat of the Land: Is dietary fat a signal of environmental quality? Results from cross-populational studies of ovarian steroid concentrations.

ABSTRACT. Successful life history strategies depend in part upon an organism's ability to appropriately adjust reproductive investment in response to signals of current and/or future environmental conditions. In women, evidence suggests that reproductive investment is modulated by physiological mechanisms that vary ovarian hormone concentrations in concert with temporal changes in energy availability.

Some cross-populational studies have observed that lower average ovarian steroid concentrations are associated with lower average energy intake (but not with variation in populational or individual fertility). Moreover, because dietary fat and energy intake are typically highly correlated across populations, it has hitherto been difficult to determine the independent association of either macronutrient with cross-populational variation in ovarian steroids.

To break this degeneracy we measured and compared ovarian steroid concentrations from Central Asian pastoralists (high-fat despite low-energy diet), U.S. and German women (high-fat/high-energy diets), and Bolivian agropastoralists (low-fat/low-energy diet).

We found that ovarian steroid concentrations are greater in Central Asians than in US and German women (hitherto the populations with the highest known ovarian steroid concentrations). Bolivians had the lowest steroid concentrations.

We also compared ovarian steroid concentrations of women who grew up in East vs. West Germany during 1961-1989, when these genetically similar populations had different economic systems and resources (consequently East Germans were shorter). Nonetheless, our East German sample had significantly higher ovarian steroid concentrations than our West German sample. We hypothesize that this pattern may be due to the East Germans' higher dietary fat intake.

The findings of these two studies argue against energy intake alone as the major dietary factor in cross-populational variation in ovarian steroids, and suggest a significant role for dietary fat. These findings also suggest the hypothesis that temporal variation in dietary fat intake, like that in energy, may be an important signal of environmental quality that modulates an individual’s reproductive investment.

10:00-12:00 Session 15C: Symposium microbiome and neurologic disease risk

CHAIR: Molly Fox

LOCATION: 204

10:00

Joe Alcock

Microbiome as a Trojan Horse – how risky microbiomes influence brain and behavior

ABSTRACT. In the last decade, accumulating evidence suggests that the microbiome – the community of microorganisms inhabiting our bodies – has an important influence on brain activity, cognition and behavior. The bulk of the human microbiome resides primarily in the intestine, but microbes and their products have been increasingly identified in tissues previously assumed to be sterile, including the blood and the brain. One mechanism for microbial influence on behavior is low grade inflammation, including neuroinflammation, that may result in anxiety and depression-like behaviors. Also, the microbiome has been shown to have bidirectional effects on the stress response, memory, and social behavior. These effects appear to be microbe specific in some instances and raise the possibility of using microbial therapies to treat behavioral diseases. I outline the evidence for microbial influence on brain development, brain activity, mood and behavior that lay the groundwork for the potential microbial interventions for brain disorders. This presentation will explore the hypothesis that neurocognitive effects of microbes can be predicted by their status as mutualist, pathobiont or pathogen. Risk and reward from the microbiome may provide an explanation of why our brains are exquisitely sensitive to our resident microbes.

10:20

Jeffrey Gassen and Sarah Hill

Kombucha and the immune system: Implications for psychology and behavior

ABSTRACT. People have been consuming variants of kombucha, a sugared tea fermented with symbiotic bacteria and yeast, for thousands of years. Although kombucha is often consumed for its purported health benefits, there is currently a paucity of research examining a) whether kombucha does indeed improve health and b) the mechanisms through which this might take place. A growing body of research finds that the gut microbiota is an important regulator of immune function in the body. Moreover, administering probiotics that promote a healthy gut microbiome improves physical and psychological health by reducing excessive levels of inflammation. In the current talk, I will present the hypothesis that kombucha, through promoting a healthy microbiome and decreasing systemic inflammation, may yield a variety of benefits for physical and mental health. Further, I will present preliminary results of ongoing research conducted in our lab examining relationships between kombucha, immune function, and inflammation. I will close by discussing future directions for this research.

10:40

Gerard Clarke

What Lies Beneath: Microbiome-Gut-Brain Axis Dysregulation in Stress-related Disorders

ABSTRACT. The capacity of the gut microbiome to recruit signalling along the gut-brain axis in order to influence many core aspects of brain function and behaviour is increasingly appreciated. This includes a broad range of behaviours relevant to depression, anxiety and pain as well as host stress physiology. Exposure to psychological stressors in turn may impact substantially on the microbiome-gut-brain axis. This includes an impact on the structure and function of the gut microbiome itself as well as key neurotransmitters at both levels of this bidirectional communication system including serotonin and the metabolism of its amino acid precursor, tryptophan. Importantly, many of the behaviours influenced by the gut microbiota rely on intact serotonergic neurotransmission while other neuroactive agents produced via host-microbe interactions are also of important in this regard. Research efforts continue to identify the precise mechanisms underpinning these effects and to interrogate the translational relevance of a promising body of preclinical data derived from a variety of experimental approaches. Microbiota-deficient animals in particular consistently show alterations in the availability of tryptophan as well as serotonergic alterations in the gastrointestinal tract and the CNS. In this respect the gut microbiome may be necessary not only to determine the set point but may also prime the gut-brain axis for appropriate stress responses. Prototypical stress-related clinical gut-brain axis disorders such as irritable bowel syndrome are associated with aberrations in the stress response and tryptophan metabolism. Neuropsychiatric disorders, including major depression, are also now linked to compositional alterations in the gut microbiome which are associated with prominent symptomatic and neurobiological features. These translational insights will be critical as we move promising preclinical research towards mechanisms and therapeutic targeting of the gut microbiome in the clinical setting and advance towards a psychobiotic approach to managing stress-related disorders in the future.

11:00

Molly Fox, Delaney Knorr and Kacey Haptonstall

Symbiotic microbiota and Alzheimer's Disease

ABSTRACT. Microbiota of the human gut, oral cavity, nasal cavity, and brain may modulate Alzheimer’s Disease (AD) pathogenesis, and changes in the microbial composition of these body regions across human evolutionary history suggest escalation of age-matched AD risk. Dysbiosis in these body regions may promote immunoregulatory dysfunction, systemic inflammation, and epithelial barrier permeability. In turn, pro-inflammatory agents-- and occasionally microbes themselves-- may infiltrate the brain and promote AD pathogenic processes, modulated by APOE-genotype. Dysbiotic conditions throughout the body may influence AD susceptibility or pathogenesis by promoting peripheral inflammation and barrier permeability, which can facilitate neuroinflammation, reactive oxygen species translocation to the brain, and bacterial translocation to the brain. These processes, subsequently, promote beta-amyloid accumulation, microglial dysfunction, and neuronal damage. I will introduce these ideas and go into greater detail about the relationship between Alzheimer's and microbiota of the human nasal cavity. The subsequent two talks will discuss the oral cavity and gut symbiotic microbiota with relation to Alzheimer's.

11:20

Elizabeth Mallott and Katherine Amato

Metabolic contributions of the gut microbiome to the brain

ABSTRACT. The gut microbiome plays an essential role in host metabolism. Shifts in the gut microbiome both across evolution and within an individual’s lifetime may increase the energy available for brain maintenance and development. We see changes in the production of short-chain fatty acids (SCFAs) between nonhuman primates and humans. Specifically, we see a shift away from butyrate production in humans, a SCFA that is used by the gut epithelium for energy. Humans not only have fewer bacterial taxa associated with butyrate production, but also had significantly fewer butyrate-producing pathways present compared with other phylogenetic groups (humans=1.90±0.88 pathways, apes=3.00±1.41, Old World monkeys=3.03±0.76, New World monkeys=2.70±0.82, lemurs=2.27±0.59) (F=8.02, p<0.001). This decrease in butyrate production is likely associated with increases in the production of other SCFAs, acetate and propionate, which directly provide energy to the brain either directly or increase adiposity. We also see shifts in the gut microbiome related to energy production and lipid metabolism during pregnancy, lactation, and early development in both nonhuman primates and humans. In particular, we see increases in the relative abundance of Actinobacteria during pregnancy and the relative abundance of Proteobacteria during both pregnancy and lactation. Additionally, relative abundances of Proteobacteria are markedly higher during the first 8 months of human infant life. These changes in the metabolic functions of the gut microbiome both between and within species provide nutritional support for brain maintenance and may supply key nutrients for brain growth and development. However, these same gut microbial shifts are also associated with increased inflammation and risk of metabolic disorders, particularly in industrialized human populations. Thus, there may be a tradeoff between a metabolically-efficient gut microbiome that supports a large, energetically expensive brain and modern human health.

12:00-13:00Lunch Break

13:00-13:30 Session 16: Poster session II

All posters are exhibited during the whole congress, not just the ones listed in the specific session list.

LOCATION: Patio

13:00

James Mcnary, Michelle Blyth, Arnold DeCano, Finn Schubert, Audrey Ranson and Jeanne Carey

A Retrospective Chart Review of Emergent Antibiotic Use

ABSTRACT. The need for responsible antibiotic stewardship can be difficult to reconcile with the clinician’s task of preventing septic patients from progressing to severe sepsis and septic shock. Empiric antibiotics are typically administered before culture results, yet antibiotics carry non-trivial risks. The diagnosis of sepsis is often based on SIRS criteria, however they are nonspecific and frequently met by patients presenting with conditions other than bacterial infections.

This retrospective chart review includes 200 patients who were administered antibiotics while in the Emergency Department (ED) and admitted. From clinical documentation we are able to determine whether these patients met SIRS criteria and/or were deemed to have sepsis by the physician ordering antibiotics. Changes to, or discontinuation of, antibiotics by the admitting team are recorded as are final culture data, discharge diagnosis, and whether patients were prescribed antibiotics at discharge.

Our study finds that the majority of patients administered antibiotics in the ED of our academic community hospital do not meet SIRS or qSOFA criteria prior to administration of antibiotics and are formally documented as not having sepsis or septic shock. Most of patients in this study received vancomycin and piperacillin-tazobactam for a wide variety of suspected sources of infection. The overall mortality rate for this group during the admission was 4%, which was comparable to all-cause hospital mortality. Approximately 50% were found to not have an infection. Of note, about 40% had received antibiotics within 3 months of presentation.

These findings suggest that an opportunity exists for increased antibiotic stewardship in the emergency department in the management of patients who are being treated for possible sepsis and septic shock. Stable patients in whom infection cannot be definitively ruled out may benefit more from prompt, thorough evaluation by an admitting team prior to initiation of empiric antibiotics.

13:00

Benjamin Auerbach and Elizabeth Agosto

The Evolution of the Shoulder as a Functional Trait Complex with the Skull and Vertebrae

ABSTRACT. Shoulder evolutionary studies often focus on traits of the scapula alone. This approach makes an implicit assumption that the scapula evolves independently. However, the scapula shares both functional and developmental relationships with the basicranium and vertebral column. We hypothesize that these anatomical regions limit the ability of the scapula to evolve independently, and instead comprise a functional trait complex. In addition, the scapula also has analogous characteristics to the pelvis. Genetic covariances underlie all these relationships, and so accounting for the constraints imposed by these covariances is essential for accurate models of trait responses to selection.

To investigate this, we obtained linear dimensions in six primate taxa: humans, chimpanzees, macaques, tamarins, marmosets, and colobus monkeys. We examine if the functional and developmental relationships between the shoulder (scapula and clavicle) with the basicranium and vertebrae are reflected in genetic covariances among their morphological traits, that in turn would influence the ability of these elements to respond to selection. Pelvic dimensions are included as well, given developmental parallels between the limb girdles. Humeral dimensions not associated with the shoulder are also examined, as these traits do not have direct functional or developmental relationships with the other anatomical regions. All dimensions were standardized by measurement means within species. We calculated evolvability and residual covariances to assess our hypothesis.

Results show a consistent pattern among all six primate genera. The scapula is not evolutionarily independent from the basicranium or vertebrae with an equal magnitude as the scapula with the pelvis. The scapula is less evolvable with the basicranium, with vertebrae, and with the pelvis than with the humerus. We conclude that the scapula, vertebrae, and basicranium mutually limit each other in response to directional selection, forming a functional trait complex. This has important implications for models of shoulder evolution, function, and disorders.

13:00

Shantha Karthigesu, David Coall and James Chisholm

Intergenerational influences on breastfeeding behaviour in Perth, Western Australia

ABSTRACT. Background/Aims: Breastfeeding is a highly evolved biological mechanism with proven positive effects on the health status of mothers and infants. But it has been rendered complex in societies with a strong influence of western medicine and heavy marketing of infant formula. While the factors affecting rates of breastfeeding vary widely, grandparents remain a source of influence across time and cultures.

Method: A qualitative study of 73 adults from 17 focus groups was conducted in Perth, Western Australia. Different family member types were present in each focus group. Transcribed data from the focus groups were coded in vivo and analysed using an interpretative phenomenological framework.

Results: Grandparents’ breastfeeding experiences, beliefs and attitudes influenced parents’ expectation to successfully breastfeed. In cases where grandmothers failed to breast feed, mothers found it easier to justify formula feeding their infants. Grandparents, while agreeing that breast feeding was best for infants said as parents they were curtailed by the inability to feed in public. The lack of commercially produced infant foods was a source of anxiety for grandmothers when efforts to breastfeed failed, which often led to early introduction of solid foods. Grandparents’ experience contrasts with the challenges faced by parents today as mothers are forced to return to work, and the abundance of commercial infant food means failure to initiate and sustain breastfeeding has a relatively easier solution.

Conclusions: The intergenerational influence on breastfeeding seen in this study sample underscores the importance of breastfeeding education and support for parents and grandparents to ensure future generations benefit from this unique mammalian trait.

13:00

Sarai Keestra, Gul Deniz Salali and Victoria Male

Out of balance: evolutionary perspectives on the sex disparity in autoimmune disease

ABSTRACT. Autoimmune diseases (ADs), in which the immune system attacks the body's own healthy tissues, affect almost one in twenty and are the fourth leading cause of disability in women. Over the past century ADs have rapidly increased in Western, affluent societies, suggesting that changes in our ecology and lifestyle are driving this development. According to the hygiene hypothesis decreased early microbial exposure in modern environments is causing disruption to immunoregulation bringing about a surge in ADs. However, this explanation does not account for the observations that (a) 80% of autoimmune patients are female, (b) ADs co-occur more often in women than in men, and (c) the incidence of some ADs is increasing more rapidly in women. As we show, the female preponderance in autoimmunity is most pronounced from menarche onwards and decreases again around menopause, suggesting that the divergence in sex hormone levels during the reproductive years plays an important role in AD aetiology. After exploring the effect of the menstrual cycle, pregnancy, and contraceptive use on AD incidence and symptoms, we discuss how ovarian steroids can influence mechanisms for central and peripheral tolerance induction as well as the balance between cellular and humoral responses of the adaptive immune system. Using an evolutionary perspective, we suggest that tolerance induction as well as cyclical immunity in females have been shaped by natural selection to optimise the implantation and gestation of an allogeneic foetus, and suggest ways that trade-offs between immunocompetence and reproduction in different ecologies can affect AD development. We suggest that these immune mechanisms are currently out of balance because of a mismatch between the conditions that they evolved in and our modern lifestyles. Finally, we propose the novel hypothesis that current changes in AD prevalence and patterns are caused by increases in ovarian hormone exposure throughout a woman’s lifetime, which we relate to reduced immune challenges, increases in reproductive lifespan, changes in reproductive patterns, and enhanced positive energy balance, complementing existing theories on the role of obesity and changes in microbial exposure in AD aetiology.

13:00

Enrique Rayo, Giada Ferrari, Judith Neukamm and Verena Schuenemann

A novel non-destructive DNA extraction method for historical Ethanol-Fixed samples

ABSTRACT. Palaeomicrobiology has experienced significant advances based on the development of new and more efficient ancient DNA techniques, allowing the identification of pathogens and other bacterial genomes present in the analysed material. Soft tissues are often used as a source of ancient DNA, in particular in the form of fixed tissue specimens, but the sampling is still destructive and problematic for irreplaceable samples. However, to our knowledge, no prior study tried to extract biomolecules from the embedding liquid. For the storage of organs and tissues in medical collections, ethanol-based fixatives are often used as an embedding liquid Ethanol is less damaging to DNA than other embedding chemicals such as formalin. To test the potential of this source for historical DNA, we compared the metagenomes from tissues and from their preserving solution for 16 ethanol-preserved samples dated to between 1760 and 1889, with known diagnoses of tuberculosis, leprosy, syphilis and virus-induced skin tumours. In addition, we performed a mitochondrial enrichment to assess the proportion of endogenous DNA present in the fixative. We found similar communities in the extracts obtained from the tissue and from the preserving solution, and we successfully retrieved ancient mitochondrial sequences from the liquid component. This approach offers strong potential to analyse high-valued historical samples without destructive sampling.

13:00

Caitlyn Placek and Kristen Syme

Choosing to fast rather than feast: Does behavioral immunity, signaling, or performance enhancement explain deliberate fasting in the ethnographic record?

PRESENTER: Caitlyn Placek

ABSTRACT. Fasting, the abstention from food or liquids for a prolonged period of time is a widespread practice that exists in cultures that vary in social complexity and access to resources. Evolutionary theories have primarily focused on explaining reactive fasting such that fasting evolved in response to fluctuations in resource availability. This theory, however, is unable to explain variation in deliberate fasting that exists across cultures.

Herein I propose and test three possible functions of deliberate fasting in humans: behavioral immunity, signaling, and performance enhancement. Regarding behavioral immunity, numerous human and non-human studies show that deliberate fasting increases longevity, delays the onset of chronic disease, and improves immune function. Some studies also show that fasters are less likely to consume toxic and pathogenic substances. Collectively, evidence suggests that fasting might function as a behavioral immune strategy, however systematic cross-cultural tests of this hypothesis are unavailable for confirmation.

Deliberate fasting could also function as a signal of in-group commitment through the display of fasting during public rituals that occur across the lifespan, particularly in the context of religious rituals. A third function of fasting is performance enhancement, whereby individuals use fasting to improve skills across a range of learned behaviors, such as hunting and shamanistic healing.

The current study tested these three functions of fasting in 129 cultures in the Human Relations Area Files (eHRAF). First, the term “fasting” was searched, and data were iteratively coded for type of fasting, function, and age category of abstainers. Although findings lend support for all three functions, signaling appears to best explain the function of deliberate fasting. This study concludes with a discussion of the evolutionary and public health implications of this research, and emphasizes the need for more biocultural research on fasting, particularly during vulnerable periods of human development.

13:00

Carina Polzer, Jacqueline Moltzau Anderson and Florian Horn

‘Evolutionary medicine’ neglects the pre-clinical phase

ABSTRACT. The application of evolutionary biological principles to clinical medicine represents an immense enrichment of medicine with a further, necessary explanatory background. However, evolutionary medicine largely skips an essential part of medical knowledge and medical education: the pre-clinical phase. Thus, there is a fundamental lack of awareness of the evolution of man himself that has taken place and is taking place – even without a clinical (pathological) context. In short: The evolution of the healthy human being is missing. The current main topics of Evolutionary Medicine (microorganisms, diseases of civilization, psychiatry) deal with problems, for which human history lies at its center. However, in this short period of time (in comparison to the environment and microorganisms), man’s evolution has been too slow. It is precisely at this point that there is a lack of awareness among physicians. An awareness that man can be placed in the greater history of evolution and its relevance for disease. Most of the contents of human evolutionary history are much older than man – rather they begin with life itself. The use of oxygen, for example, is the starting point for benefits (e.g. multicellular organisms), but also for problems that still characterize ageing and diseases (including tumors) today. The evolution of human organ systems (anatomy and physiology), supplemented by the molecular level, and thus the evolution of normal biochemical and genetic processes (biochemistry and molecular biology), are an urgently needed framework of content. For the timeframe, the basic features of phylogeny are, of course, indispensable. Altogether, this can be integrated into existing pre-clinical subjects, which can be used to pave the way for questions of evolutionary backgrounds in the clinic as early as the first semesters.

13:00

Basil Baccouche, Barbara Natterson-Horowitz and Nothirdauthor

Giraffe Myocardial Hypertrophy as an Evolved Adaptation and Natural Animal Model of Resistance to Diastolic Heart Failure in Humans.

ABSTRACT. Background: Hypertensive left ventricular hypertrophy (LVH) with reduced compliance due to myocardial fibrosis is a leading cause of human heart failure (Gradman & Alfayoumi, 2006; Talman & Ruskoaho, 2016). Adult Masai giraffe (Giraffa camelopardalis tippelskirchii) ventricles thicken in response to pressure but do not stiffen. This may be a natural animal model of resistance to diastolic dysfunction via fibrosis inhibition.

Purpose: To establish whether normal giraffe adult ventricles fibrose with hypertrophy and to identify pathways involved in pressure-responsive thickening without fibrosis.

Methods: Review of cardiac fibrosis peer-reviewed literature, veterinary databases, and privately-accessed data on 136 giraffe necropsies.

Findings: Minimal evidence of ventricular fibrosis was found in the necropsy reports, communications with DVMs, or veterinary literature. Within the developmental pathways related to cardiac fibrosis, three genes (TGF-β1, FGF23, and FGF2) with fibrosis-promoting and two (FGF21 and FGF16) with inhibiting effects were identified belonging to gene families with significant mutations unique to giraffes (Agaba et al., 2016; Itoh & Ohta, 2013).

Discussion: The hypertrophied giraffe myocardium lacks fibrosis seen in other mammals. Five candidate genes involved in cardiac remodeling (including one in the ACE pathway, which is uniquely adapted in giraffes) may play key roles in this adaptation (Wang et al., 2017). Hypertrophy without fibrosis likely evolved within the past 11.5 mya since divergence from a common ancestor with okapis (Agaba et al., 2016). Identification of these five genes and linked mechanisms has translational significance for models of human diastolic heart failure.

13:00

Devan Peterson and Barbara Natterson-Horowitz

Evolutionary and Comparative Insights Into Atherosclerosis: The Use of Systematic Review to Characterize the Phylogeny of Vulnerability to Atherosclerosis and to Generate Novel Non-Proximate Hypotheses for Atherogenesis and Vasculopathy.

ABSTRACT. Atherosclerosis is the leading cause of death in our species (Mozaffarian et al.). The vast majority of research focuses on proximate and hyper-proximate causes for atherosclerosis. Non-proximate hypotheses to explain potential adaptive benefits of vulnerability to atherosclerosis are infrequently advanced. One under-leveraged approach is to develop phylogenetic models of atherosclerosis vulnerability which can be used to:

1) Identify natural animal models of differential vulnerability 2) Identify selective pressures underlying evolved vascular vulnerability 3) Develop novel, testable hypotheses explaining adaptive bases for vulnerability to atherosclerosis

Our study features the use of systematic review to identify the taxonomic range of atherosclerosis occurrence and from these findings generate novel non-proximate hypotheses. Consulted databases included the BIOSIS Citation Index and Zoological Record databases within Web of Knowledge. We identified cases of non-induced atherosclerosis in 134 chordate species ranging from bluefin tuna to ostriches.

The appearance of spontaneously (naturally) occurring atherosclerosis in all vertebrate orders suggests a conserved, adaptive component of this vascular vulnerability. Potential hypotheses arising from our findings explaining the persistence of this vulnerability center on the antipathogenic features of vascular endothelium. One hypothesis is that atherosclerosis arose 540-510 million years ago with the evolution of the vascular endothelium, a ubiquitous trait among vertebrates that plays a key role in the initiation and development of the condition (Folcik et al.; Monahan‐Earley et al.). The collection and analysis of more necropsy data would likely reveal spontaneously (naturally) occurring atherosclerosis in numerous more vertebrates and would facilitate the formation and thorough examination of this and more such hypotheses.

13:00

Neil Isaacs

The hip as the first link in the rotary kinetic chain evolving concurrently with bipedalism.

ABSTRACT. Primates developed a diagonal foot placement involving rotating the pelvis and shoulders in opposite directions during the stride which also provides power in an elastic stretch shortening cycle in sport. Evolution of a valgus knee and elbow enabled efficient balance and weight bearing in an arboreal environment but also allows transfer of rotary momentum that may be linked to bipedalism in evolving simultaneously with advantages over other species.

Relatively shorter lower limbs in first hominids required a greater angle of inclination of the femur. The moment arms of Gluteus maximus(GM), previously underestimated, are altered by pelvic and femoral adaptations in bipedalism that also enable rotation of the pelvis that is the beginning of the rotary kinetic chain, similarly illustrated in comparative anatomy from the big toe to the thumb. The stronger biarticular connection of GM with greater moment arms as the hip flexes stabilizes the more flexible knee in transfer of increased torque in the coronal and transverse planes from hip to the lower leg.

This has great significance in sport performance and injuries in change of direction,hitting and throwing.

Changes in GM provide a link from the lower leg via the thoracolumbar fascia to the thorax and upper arm providing power, elastic energy and stability not only in locomotion but also the rotary kinetic chain.Research in injuries such as anterior cruciate ligament rupture and prevention programs has major relevance and may gain insight and solutions with new knowledge gained from studying evolution.

13:00

Nicholas Cavanaugh and Barbara Natterson-Horowitz

Use of Taxonomical and Comparative Analyses to Generate Novel, Testable, and Non-Proximate Hypotheses for Osteosarcoma

ABSTRACT. Background: Osteosarcoma is the most common pediatric bone malignancy. It is linked to periods of peak skeletal growth, increased bone cell turnover, and activation of the GH/IGF-1 pathways. Most osteosarcoma research has focused on proximate causes while potential adaptive components of vulnerability to osteosarcoma have received minimal research attention. Purpose: To develop non-proximate hypotheses for vulnerability to osteosarcoma by creating comprehensive taxonomies of non-human species with confirmed cases of spontaneous osteosarcoma and integrating these with life history and developmental information. Methods: Formal systematic review using PRISMA standards conducted to comprehensively identify species with confirmed cases of osteosarcoma. Life history characteristics of identified species were then mapped on to taxonomic findings from the systematic review. Results: Osteosarcoma is widespread across vertebral taxa with dynamic, environmentally-sensitive skeletal growth properties. Disproportionate occurrence during early-life peak growth periods and adolescence points to accelerated skeletal growth as a risk factor. Discussion: All taxa with vulnerability to osteosarcoma share environmentally-sensitive skeletal growth. Accelerated skeletal growth during critical life phases—gestation, early-life, and adolescence—enhance fitness through ecologically-influenced optimization of size and competitive advantage over conspecifics. Adaptive non-pathological accelerated bone growth and malignant osteoblastic transformation share GH/IGF-1 pathways. Experimental interference with GH/IGF-1 pathways may modify vulnerability to malignant osteoblastic transformation but would be predicted to also limit a growing organism’s ability to optimize size to environmental conditions. This study demonstrates how the integration of systematic review-derived taxonomy and life history information can generate a novel, testable non-proximate hypothesis for a high impact human cancer.

13:00

Gülfirde Akgül, Giada Ferrari and Verena Schuenemann

Using Museum Wet Specimens to analyze past pathogen genomes

ABSTRACT. Re-emerging infectious diseases are of worldwide significant importance, however survival mechanisms of many pathogens remain unclear. Studying historic pathogen genomes provides researchers with crucial information to identify and characterize past pathogens and also gives important information about the evolution and host interactions of these pathogens. Archival formalin fixed tissues could become valuable sources for retrospective molecular analysis. Museum collections provide researchers with well documented, and precisely dated sample data bases for genome wide analysis. However, the use of formalin fixed specimens is so far limited due to chemical modifications induced by formaldehyde. Thus, DNA recovery from these samples is challenging and new standards for processing and analysis need to be established. In this project we collected ten samples from the pathological collection in the Narrenturm at the Vienna Museum of Natural History. The samples are associated with diagnoses of tuberculosis, leprosy, and anthrax and originate from autopsy material collected between 1851 and 1936. To improve the DNA recovery, we tested three different extraction protocols with different digestion temperature and chemicals. To optimize the downstream work flow of DNA processing, we also compared double stranded and single stranded libraries for each sample. Our first results revealed that double stranded library preparation was not effective for our samples and most of the libraries were self-ligated adapters. Currently, we are testing our extraction protocols with the single stranded library method. DNA retrieval from formalin fixed tissues provides us with the opportunity to study the evolution of pathogens over the last few centuries and also helps us to analyse the progressing of diseases in natural conditions before the antibiotic-era.

13:00

Judith Neukamm, Saskia Pfrengle, Martyna Molak, Alexander Seitz, Michael Francken, Partick Eppenberger, Charlotte Avanzi, Ella Reiter, Christian Urban, Beatrix Welte, Barbera Teßmann, Alexander Herbig, Katerina Harvati, Kay Nieselt, Johannes Krause and Verena J. Schuenemann

2,000-year-old pathogen genomes reconstructed from mummies provide insights into the state of health of ancient Egyptians.

ABSTRACT. For many decades, the retrieval of ancient DNA from Egyptian mummies was considered challenging, due to issues surrounding the preservation and contamination of the extracted DNA. However, recent advances in ancient DNA methods, combined with next-generation sequencing, have enabled reliable retrieval of human mitochondrial and nuclear genomic data as well as metagenomic data. This opens up the possibility to also study the general health status of individuals, including pathogens that they might harbor. Here we analyze soft tissue and skeletal samples of 119 Egyptian mummies from different time periods using a metagenomic approach. First, Red Complex bacteria correlating with periodontal disease were identified in the oral microbiome. By screening the soft tissue and skeletal remains, the genomes of two ancient pathogens, a 2,200-year-old Mycobacterium leprae strain and a 2,000-year-old human hepatitis B virus, were successfully reconstructed. Our results demonstrate the suitability of Egyptian mummies as a source for metagenomic studies and give the opportunity to evaluate the health status of ancient Egyptian populations over time. Furthermore, the genomics data collected for M. leprae and hepatitis B virus helps to refine the current phylogeographic models of their previous distribution and spread.

13:00

Keith Mintzer

U.S. National Institutes of Health (NIH) staffer answers questions about how the NIH supports medical research

ABSTRACT. Do you have questions about how the NIH supports medical research? Come get answers from an NIH staffer who has worked at the NIH for the past sixteen years. Attendees will learn how the NIH is organized, how it supports biomedical research, and how peer review works. There will be ample time to ask questions about funding opportunities, peer review, and career development awards.

13:00

Jian Han, Anuoluwapo Odelade and Joseph Graves

Expressions of iron-responsive and oxidative stress genes in iron-resistant Escherichia coli

ABSTRACT. Iron is an essential micronutrient for all living things, including bacteria. However, excess iron can be toxic impacting numerous physiological systems. We have utilized experimental evolution to produce iron resistant strains of Escherichia coli K-12 MG1655. However, the molecular mechanism of how these strains handle iron resistance needs to be fully understood. To examine these mechanisms, we grew these strains and their controls in excess ferrous (Fe2+) iron medium. The mRNA expression of iron-responsive and oxidative stress genes was examined by Real-time PCR. The results showed that the mRNA expression of the iron storage gene (ftn) and iron regulatory gene (fur) both significantly increased in the Fe2+-resistant population compared to their controls. Iron uptake gene (fec A) mRNA expression significantly decreased in iron resistant populations in comparison to controls to reduce iron uptake in the excess iron environment. The mRNA expressions of oxidative stress genes, such as sodA (superoxide dismutase A) and soxR (superoxide regulator), were significantly upregulated in the Fe2+-resistant population in comparison to the controls. These two genes also increased their mRNA expression significantly when control populations are placed in toxic Fe 2+ medium. In summary, this study shows that iron resistant E. coli grown in excess iron medium have improved storage of excess iron as well as increasing sensitivity to ameliorate superoxide free radical damage thereby reducing intracellular oxidative stress.

13:00

Christian Urban, Jakub Kubacki, Jean-Michel Hatt, Claudia Bachofen and Verena J Schuenemann

Towards the understanding of zoonotic events in infectious diseases: Tracing animal reservoirs in Switzerland

ABSTRACT. Most emerging pathogens causing infectious disease in humans originate from interspecies transmission. In addition to introducing new pathogens to humans, animal populations can also serve as reservoirs for human pathogens. Thus, they play an important role in re-emerging and newly emerging infectious diseases as the latter mainly originate from animal wildlife. Europe is predicted to be one of the major hotpots for newly emerging zoonotic diseases in the future. Therefore, regular screening of pathogen prevalence in potential animal reservoir populations is strongly recommended. Here, we focus on pathogen screening in Swiss wild animal populations, particularly in European hedgehogs (Erinaceus europaeus). This species is well adapted to life in urban habitats, harbors multiple disease vectors and the detection of some human pathogens, like Salmonella spp., herpes viruses and the FSME virus, was described in previous studies.

To investigate on bacterial and viral pathogen prevalence in our samples we applied a metagenomic approach to analyze the microbiome and virome in hedgehog lungs: We used the MEGAN Alignment Tool for general screening of bacterial pathogens in shotgun sequenced DNA libraries and 16S amplicons of hypervariable region V3 and V4. Furthermore, tissue extracts were enriched for viral particles and used for viral pathogen screening.

Our results will contribute to the knowledge of pathogen presence in Erinaceus europaeus populations and therefore further elucidate their function as pathogen reservoir. As awareness is a crucial point to combat re-emerging and newly emerging disease, the general public health will directly benefit from our results.

13:00

Kristen Syme and Edward Hagen

An Anthropological and Evolutionary Critique of the Psychiatric Paradigm

ABSTRACT. During the 20th century, biomedicine rapidly reduced the global burden of infectious disease, which led to dramatic increases in life expectancy worldwide. In the 21st century, non-infectious diseases, including mental disorders, are responsible for most of the disease burden. The causes of mental disorders, however, are still mysterious. Worse, many pharmacological treatments, such as antidepressants and antipsychotics, have only moderate to weak efficacy, lack precision in targeting biological systems that underlie symptoms, and/or induce debilitating side effects. Unlike most biomedicine that bases diagnoses on recognizable dysfunctions and objective tests, psychiatric diagnoses are based on the number and types of symptoms, because too little is known about the biological bases of mental disorders to classify them based on causation. This leaves psychiatric diagnoses vulnerable to the influence of sociocultural norms and attitudes as opposed to evidence of dysfunction. Case-control investigations using DSM or ICD diagnoses as phenotypic measures are common in biomedical research. However, if our diagnoses have poor validity as natural entities (Hyman, 2010), this generates noise in genetics, neuroimaging, and other studies.

Critics from within psychiatry are calling attention to the failure of psychiatric research to improve public health and to rampant conflicts of interest that bias the research. There is an urgent need for a broader, more integrative approach to the study and treatment of mental disorders that incorporates cross-cultural data from a diverse range of societies and evolutionary theory.

We propose that combined insights from biological anthropology, a biological and social science that studies humans and their primate relatives, and evolutionary theory can help: 1) disentangle true disease states from conditions that are merely socially undesirable; 2) identify discrete psychiatric conditions; 3) determine the extent to which conditions vary across socio-ecological contexts; and 4) ultimately, develop a psychiatric taxonomy that corresponds to evolutionarily meaningful, universal phenotypes.

13:00

Alvaro Daschner, José-Luis Gómez Pérez and María-José Trujillo Tiebas

Necessary pluridisciplinarity in an Evolutionary Medicine Platform: our 10-year experience in Spain

ABSTRACT. Evolutionary medicine needs by definition pluridisciplinarity. We aim to describe our experience of an extra-curricular Evolutionary Medicine platform for research and diffusion in Central Spain. A pluridisciplinary core organization with a physician, a geneticist and an anthropologist, with endorsement of two Research Health Institutes and the National Museum of Natural Sciences made it possible to design and offer seminars and meetings over the last 10 years, inviting to all of them guest speakers from different disciplines. The annual meetings were held at University Hospitals and reached an audience between 69 and 162 participants. The seminars were intendedly held below 40 participants and were symbolically held both at the Hospital and at the National Museum of Natural Sciences. To each of the offered topics at least one physician and one biologist was invited. Over the years invited disciplines broadened to different specialties in Medicine, to Psychology, other Health Sciences, Philosophy and other. The interested audience was also composed of all the mentioned disciplines. A high interest in an evolutionary perspective of Health Sciences and the presence of several Universities and Hospitals in a 5 million inhabitants Madrid region was of advantage. In 9 annual meetings and 37 seminars, 112 different speakers gave 186 presentations. We have noticed a higher interest of Biologists in Health Sciences than Physicians in Evolutionary Theory. Within physicians, higher interest was perceived from specialties in the interface with Biology, such as Microbiology and Genetics. We were repeatedly motivated to offer written material, thus we began to publish and complete four volumes with 44 written contributions of selected topics. Summarizing, we notice a demand for an evolutionary perspective of health and disease, which converges in a necessary pluridisciplinarity as a necessary condition. Research interests and interesting diffusion topics emerge from putting together experts with different scientific background.

13:00

Danielle Katz and Barbara Natterson-Horowitz

The Phylogeny of Atrial Fibrillation(AF): The Power of Comparative Arrhythmology to Generate Novel Hypotheses on the Origin of Vulnerability to AF

ABSTRACT. Atrial fibrillation (AF) is the most common arrhythmia in humans and is associated with significant morbidity and mortality. The massive body of AF investigation has been focused nearly exclusively on proximate causation. Non-proximate explanations for the vulnerability remain essentially unexamined. Our study uses formal methods of systematic review to generate testable non-proximate hypotheses to explain human vulnerability to AF. Using taxonomies derived from systematic reviews, we created phylogenies of vulnerability to AF for chordates, horses, and dogs. Correlating the findings from these phylogenies with life history information, we developed non-proximate testable hypotheses for vulnerability to AF. The equine phylogeny demonstrated increased vulnerability in breeds with higher vagal tone, leading to the hypothesis that variations in autonomic tone may shift AF vulnerability. The canine phylogeny demonstrated vulnerability in larger breed dogs without structural heart disease, leading to the hypothesis that atrial mass, volume, and architecture may increase vulnerability. The chordate phylogeny demonstrated documentable AF only in mammalian species, leading to two hypotheses. First, the atrialization of the sinus venosus in endotherms and not ectotherms points to it as an element of vulnerability related to functional adaptation. Second, the reduced number of pulmonary veins and their separation from the left atrium in birds explain the absence of AF in this taxa. Further, this finding points to adaptive pulmonary vein architecture as a substrate for vulnerability. We conclude that identifying taxa with and without vulnerability to AF offers a pathway for the generation of novel non-proximate hypotheses. Finally, we present a roadmap for researchers to identify natural animal models of AF resistance and enhanced vulnerability which can facilitate the development expanded and evolutionarily-informed research agendas.

13:30-14:30 Session 17: Keynote Dario Riccardo Valenzano

CHAIR: Steven Austad

LOCATION: Aula

13:30

Dario Riccardo Valenzano

African killifishes shed light on the genomic basis of life history trait evolution in vertebrates

ABSTRACT. Whether adaptive evolution or genetic drift shape life history trait evolution across species has been for long an open question. African killifishes (oviparous Cyprinodontiformes) offer a natural experiment in life history trait evolution as they independently evolved short lifespan and rapid aging (annual life cycles) at least three times. Using a comprehensive whole-genome sampling of 46 species of African killifishes, we found that short-lived species, which evolved in dry climates, underwent genome expansion. Proliferation of transposable elements drove genome expansion in annual species, which also display higher gene family turn-over rates and relaxed selection in genes in known ageing pathways. Whole-genome re-sequencing in wild Nothobranchius populations showed bottle-necks and a genome-wide signature of relaxation of selection in populations from dryer climates. We found that ecology drove the evolution of short lifespan, associated with the genome-wide accumulation of tens of thousands of slightly deleterious mutations. Hence, drift, more than adaptive evolution, was the dominant signal underlying the evolution of short lifespan and rapid aging in annual killifish. The second part of my presentation will present our recent findings on how the gut microbiota plays a causal role in modulating ageing and lifespan and how understanding the interaction between adaptive immune system and the microbiota gives us novel insights into the biology of ageing and offers new possibilities for future therapeutic interventions.

14:30-15:00Coffee Break

15:00-17:00 Session 18A: Life history

CHAIR: Alejandra Nunez de la Mora

LOCATION: Aula

15:00

Melissa E. Thompson, Zarin P. Machanda, Alexandra Rosati, Martin Muller and Richard Wrangham

Do shorter lifespans in chimpanzees mean that they age less well than humans?

ABSTRACT. While short-lived animals have typically been selected as models in human aging research due to convenience, it has become increasingly clear that primates age differently than other taxa. Great apes are of particular significance due to their close phylogenetic relationship to humans and because they are long-lived. In order to better understand the evolution of the unusually long human lifespan, it is critically important to examine the forces that constrain lifespan in our closest extant relatives. Here, I synthesize research findings on aging among wild chimpanzees (Pan troglodytes schweinfurthii) from a 30+ year naturalistic study in the Kibale National Park, Uganda. This research used an unusually large sample of >25,000 biological specimens and a detailed daily record of activity and social behavior. While the maximum lifespan of chimpanzees exceeds 60 years, the average adult lives only about 30-35 years. We predicted that older chimpanzees would show senescent features commonly associated with degenerative aging in humans, and that rapid physiological aging would coincide with the ages of accelerated mortality. Indeed, chimpanzees exhibit age-associated increases in clinical signs of illness and in glucocorticoid levels, along with declines in muscle mass, respiratory rates, and certain aspects of activity. However, these changes were moderate and were associated with relatively little loss of function in what can only be described as a challenging physical and social environment. Rather than exhibiting frailty syndromes, individuals who survived to late ages exhibited unexpectedly robust physical condition and high levels of social participation and status. These data complement evidence from small-scale human societies that have pointed to a surprising rarity of the degenerative diseases that plague aging populations in the developed world. Early mortality selection, in combination with healthy lifestyle factors, in these populations reveal valuable samples of resilient individuals that could help expose the keys to successful aging.

15:20

Carina C. Kern, Hannah Morley and David Gems

A putative lactation reactivation syndrome triggered by menopause causing senescent multi-morbidity

ABSTRACT. The proposal by George Williams that natural selection can favour alleles that promote late-life disease due to antagonistic pleiotropy (AP)1 leaves open the question of how such alleles exert their pathological effects. One type of proximate mechanism was suggested by Misha Blagosklonny, particularly to explain major effects on ageing of growth-promoting pathways such as TOR (target of rapamycin): that AP affecting growth factors can in later life promote futile run-on of entire biological programmes. Because such programmes are senseless in fitness terms, yet promoted by wild-type gene function in a concerted fashion, Blagosklonny refers to them as quasi-programmes2.

Guided by our studies of generation of senescent pathologies by quasi-programmes in an animal model, the nematode Caenorhabditis elegans3,4, we have tentatively identified a quasi-programme-driven disease syndrome affecting post-menopausal women. In both invertebrates and vertebrates, reproductive females are capable of consuming their own biomass to increase production of yolk or milk to assure offspring survival, with resulting atrophy of source organs. For example, in many mammals during lactation bone is consumed to provide calcium for milk production, and this leads to transient osteoporosis. We postulate that in women the decline in oestrogen during menopause triggers a lactational quasi-programme, leading to irreversible osteoporosis and ectopic deposition of calcium. The latter manifests as vascular calcification, contributing to cardiovascular disease, chondrocalcinosis contributing to osteoarthritis, as well as other calcium deposition pathologies. The existence of this putative lactational reactivation syndrome is supported by a review of relevant literature examining correlations between osteoporosis and calcium deposition pathologies, sex specificity and timing of onset of pathologies and effects of hormone replacement therapy.

1. Williams,G. C. Evolution 11, 398 (1957). 2. Blagosklonny,M. V. Cell Cycle 5, 2087 (2006). 3. Ezcurra,M. et al. Curr Biol 28, 2544 (2018). 4. Wang,H. et al. NPJ Aging Mech. Disease 4, 6 (2018).

15:40

Alejandra Nunez de la Mora, Rosa Lilia Castillo-López, Diana Donaji del-Callejo-Canal, Margarita Edith Canal-Martinez and Maria Luisa Marvan

Inequalities, double burden of malnutrition and decline in age at menarche in 20th century Mexico: an evolutionary perspective

ABSTRACT. From an evolutionary perspective, age at menarche is considered as a life history trait that captures dimensions of an individual’s energetic experience during development. However, some elements of these relationships are rapidly being transformed as new global economic forces interact with nutritional shifts. The increasing number of reports in the literature on the association between high BMI and advanced age at menarche suggests that a trend towards earlier age at menarche may be a concomitant effect of the overweight/obesity epidemic. Mexico for its part, is in the midst of an obesity epidemic. A recent report highlights the worrying increase in the prevalence of overweight and obesity in young children alongside persisting under-nutrition, a scenario particularly marked in rural, poor and food-insecure groups. We use the findings of our secondary analysis on trends in age at menarche in 20th century Mexico and differences associated with area of residence, ethnicity and socioeconomic status, to advance some evolutionary hypotheses on the consequences of the double burden of malnutrition on age at menarche, the potential mechanisms and its implication for health.

16:00

Grazyna Jasienska

Life history perspective – the necessary tool for understanding energetic supplementation of women

ABSTRACT. Public health interventions aimed at improving infant birth weight, health and survival, often target mothers. Supplementation of pregnant and lactating women with additional energy and micronutrients has been a common practice, especially in populations with poor nutritional status. However, supplementation often has unexpected outcomes. Not only are improvements in infants health much smaller than expected but also the supplemented mothers experience faster resumption of ability to conceive again. Thus, supplementation of women leads to an undesirable increase in fertility. Reductions in women’s workloads brought about by labor-saving development initiatives have similar side effects on women’s reproductive physiology.

Using the framework of life history theory, I will discuss the impact of improvements in women’s energetic status via nutritional supplementation or reduction in physical activity. I will argue that in order to understand the effects of supplementations or labor reduction it is important to consider the long-term reproductive strategy, trade-offs in energy allocation to competing physiological functions and trade-offs between children’s quantity versus children’s quality. In addition, it is likely that supplementation will differently impact women depending on their prior developmental history (i.e. conditions experienced during their own fetal and childhood development). Therefore, evolutionary perspective suggests that public health interventions in the area of maternal and child health should be comprehensive and include not only short-term supplementations for women but also provide knowledge about family planning and access to contraception.

16:20

Erik Ringen, Adrian Jaeggi and Craig Hadley

Wealth, culture, fertility, and bargaining power: assessing competing theories of intimate partner violence in a large cross-national sample

ABSTRACT. Intimate partner violence (IPV) is a global public health problem that shows marked variability in prevalence and endorsement, which is often explained in terms of material (wealth, education) and ‘cultural’ (attitudes and norms) factors. We expanded upon this work with insights from the evolutionary behavioral sciences. Specifically, we theorized that post-marital residence patterns influence IPV risk by altering the availability of kin support, and thereby a woman's bargaining power. We also assessed whether fertility conflict (i.e., a husband who wants more children than his wife) increased a woman’s risk for IPV. To test these ideas, we applied Bayesian multilevel modelling to the Demographic and Health Surveys data from 11 countries and 42,000 couples, representing 476 ethnic groups. We found that wealth was associated with reduced risk and endorsement with increased risk of IPV. The effects of postmarital residence and fertility conflict were mediated via endorsement (i.e., attitudes towards IPV) and supported our predictions that women who leave their natal group for marriage are at greater risk of IPV, and that men who desire more children than their wives are more likely to perpetrate IPV. IPV risk (via endorsement) also differed between ethnic groups and countries, suggesting unmeasured socio-ecological factors and/or an influence of cultural history. In sum, our models support some predictions from evolutionary ecology (albeit with modest effect sizes), and extend previous work on this global health issue.

16:40

David Coall, Sonja Hilbrand, Ruth Marquis, Liz Wenden, Katrina Stratton, Denis Gerstorf and Ralph Hertwig

The costs and benefits of grandparental investment for grandparents’ health

ABSTRACT. Throughout human history it is likely grandparents supported the health of their families and communities. Evidence that grandparents have a positive impact on the health and well-being of grandchildren in contemporary industrialized societies, particularly in resource poor families, is growing. As some governments and communities can no longer support the needs of diversifying family types, grandparents are increasingly being recognized for the family and public health resources they contribute. There is little understanding, however, of the health consequences contributing resources to their families through childcare has for these grandparents. This paper will examine two extremes of the grandparent-childcare continuum by investigating the impact of non-custodial childcare (babysitting) by grandparents on their longevity and the health of grandparents who are raising their own grandchildren. This paper incorporates data from Europe and Australia to examine the potential costs and benefits of providing childcare for grandparents’ health. Using data from the longitudinal Berlin Ageing Study (n = 516), survival analyses show that help provided by grandparents, in the form of babysitting, is associated with increased longevity. Grandparents who provided childcare showed a mortality hazard that was 33% lower than among grandparents who did not provide help. Mediation analysis showed this association was only partially accounted for by health. At the other end of the care spectrum, data from a Western Australian study of grandparents who are raising their own grandchildren, shows negative health consequences of custodial grandcare. Survey data from 500 grandcarers illustrates the negative impact across eight domains of physical and mental health, compared to age matched community norms, as measured by the SF-36 Health Assessment. Understanding the diverse forms of grandparental help and the consequences they have for grandparental health will inform public health policy around healthy ageing and the targeted use of support services for grandparents and their families.

15:00-17:00 Session 18B: Immunology

CHAIR: Joachim Kurtz

LOCATION: 217

15:00

Joachim Kurtz, Robert Peuss, Kevin Ferro, Wentao Yang, Philip Rosenstiel and Hinrich Schulenburg

Evolution of alternative forms of immune memory

ABSTRACT. Evidence is recently accumulating that also innate immune systems can provide forms of immune memory, such as immune priming in invertebrates or trained immunity in vertebrates. Immune priming can even be specific. However, to date it is unknown whether and how the level of specificity in immune priming can adapt during evolution in response to natural selection. We tested the evolution of priming specificity in an invertebrate model, the beetle Tribolium castaneum. Using controlled evolution experiments, we selected beetles for either specific or unspecific immune priming towards pathogenic bacteria. After 14 host generations of selection, specificity of priming was not universally higher in the lines selected for specificity, but rather depended on the bacterium used for priming and challenge. The evolved differences in priming specificity were mirrored in the transcriptomic response, revealing an involvement of metabolic and transcription-modifying genes and pointing to similar mechanisms acting in vertebrate trained immunity. Our study shows that evolutionary studies in invertebrates could help to understand basic principles in immunity. Given the potential medical importance of trained immunity in humans, this bears large potential for the field of evolutionary medicine.

15:20

India Schneider-Crease, Randi H. Griffin, Megan A. Gomery, Thore J. Bergman and Jacinta C. Beehner

Evidence for parasitism as a cause of mortality in a wild primate

ABSTRACT. Parasites are considered to be drivers of primate evolution, but few studies have demonstrated fitness impacts of endemic helminth parasites on primates. While the simple life cycles of most parasites and pathogens may favor reduced virulence, parasites with other transmission modes may have higher virulence in some hosts. Parasites employing “predation-mediated transmission” have separate adult and larval stages infecting predator and prey species and depend on the transmission of the larval parasite from the prey host to the predator host for life cycle completion. Thus, parasites with trophic transmission that increase host mortality and predation risk in prey hosts should be favored over less virulent strains. We tested whether a parasite with this transmission mode influences mortality in wild gelada monkeys (Theropithecus gelada) in Ethiopia, where prevalence of infection with the larval tapeworm Taenia serialis reaches over 15%. Using survival analyses, we demonstrate strikingly higher mortality in both (1) geladas exhibiting the cysts characteristic of T. serialis infection and (2) the dependent offspring of female with cysts, relative to individuals that lack signs of disease. This research is among only a handful of studies to demonstrate explicit fitness costs of parasitism in primates and highlights the importance of using parasite evolution as a framework in which to evaluate infection dynamics in wildlife. Similar principles should apply to understanding parasites of humans, including related species in the genus Taenia.

15:40

Magdalena Migalska, Alvaro Sebastian and Jacek Radwan

Evolution of the number of MHC genes: testing the TCR depletion hypothesis

ABSTRACT. Major histocompatibility complex (MHC) genes encode proteins that initiate adaptive immune responses through the presentation of foreign antigens to T cells. The high polymorphism found at these genes, thought to be promoted and maintained by pathogen-mediated selection, contrasts with the limited number of MHC loci found in most vertebrates. Although expressing many diverse MHC genes should broaden the range of detectable pathogens, it has been hypothesized to also cause deletion of larger fractions of self-reactive T cells, leading to a detrimental reduction of the T cell receptor (TCR) repertoire. However, a key prediction of this TCR depletion hypothesis, that the TCR repertoire should be inversely related to the individual MHC diversity, has never been tested. Here, using high- throughput sequencing and advanced sequencing error correction, we provide evidence of such an association in a rodent species with high inter-individual variation in the number of expressed MHC molecules, the bank vole (Myodes glareolus). Higher individual diversity of MHC class I, but not class II, was associated with smaller TCR repertoires. Moreover, sex significantly affected the TCR diversity – males had smaller TCR repertoires compared to females. Our results thus provide partial support for the TCR depletion model, while also highlighting the complex, potentially MHC class-specific mechanisms by which autoreactivity may trade off against evolutionary expansion of the MHC gene family.

Reference: Migalska M, Sebastian A, Radwan J (2019) Major histocompatibility complex class I diversity limits the repertoire of T cell receptors. Proc Natl Acad Sci 201807864. doi: 10.1073/PNAS.1807864116

16:00

Mate Manczinger and Csaba Pal

Pathogen diversity and generalist human MHC alleles

PRESENTER: Mate Manczinger

ABSTRACT. Major histocompatibility complex (MHC) molecules mediate the adaptive immune response against pathogens. Certain MHC alleles are generalists: they present an exceptionally large variety of antigenic peptides. However, the functional implications of such elevated epitope binding promiscuity in the MHC molecules are largely unknown. According to what we term the pathogen-driven promiscuity hypothesis, exposure to a broad range of pathogens favors the evolution of highly promiscuous MHC variants. Consistent with this hypothesis, we found that in pathogen-rich geographical regions, humans are more likely to carry promiscuous MHC class II DRB1 alleles, and the switch between high and low promiscuity levels has occurred repeatedly and in a rapid manner during human evolution. We also show that selection for promiscuous peptide binding shapes MHC genetic diversity. In sum, our study offers a conceptually novel mechanism to explain the global distribution of allelic variants of a key human immune gene by demonstrating that pathogen pressure maintains promiscuous MHC class II alleles. More generally, our work highlights the hitherto neglected role of epitope binding promiscuity in immune defense, with implications for medical genetics and epidemiology.

16:20

Lafi Aldakak, Matthias Galipaud, Nicole Bender, Hanna Kokko and Frank Rühli

To Attack or Not to Attack: the evolution of immune defences and autoimmune diseases under precision tradeoffs

ABSTRACT. Autoimmune diseases are a major source of morbidity. Few studies have examined the evolutionary factors affecting the incidence of autoimmune diseases, but some new evidence indicates that it can be a byproduct of highly sensitive immune screening mechanisms. We modeled the evolution of the immune precision under the following assumption: high sensitivity confers better protection against pathogens but increases the risk of autoimmune incidents. We took eco-evolutionary feedbacks into consideration to account for the mutual effect of the risk of encountering pathogens and the average immune sensitivity in the population. The population density and the parasite transmission rate led to an increased prevalence of autoimmune pathologies. The pathogen's virulence, the lifespan of the host and the costs of autoimmunity define the evolutionary stable immune sensitivity and specificity. The outcome of immune evolution also depends on whether or not the host becomes immune to the same pathogen after recovery. Our findings show that the immune tradeoffs, population structure and immune memory affect the evolution of immune precision and the incidence rate of autoimmune diseases.

16:40

Robert Peuß

How decreased biodiversity impacts the immune system: Approaching “Old Friends” with the cavefish, Astyanax mexicanus

ABSTRACT. Reduction of parasite diversity in modern human populations is suspected to be a primary cause for the increase of autoimmune disorders. However, the long-term evolutionary consequences of decreased parasite diversity on the host immune system are not well understood. We used the cavefish Astyanax mexicanus to understand how loss of biodiversity, a hallmark of cave adaptation, influences the evolutionary trajectory of the vertebrate host immune system by comparing river with cave morphotypes. We show that cavefish display a more sensitive proinflammatory immune response towards bacterial endotoxins, which is characteristic to other vertebrate species inhabiting environments with decreased biodiversity. Surprisingly, cellular immune responses, such as phagocytosis, are drastically decreased in cavefish. Using an image-based immune cell phenotyping approach and single-cell RNA sequencing, we identified a shift in the overall immune cell composition in cavefish as the underlying cellular mechanism associated with altered immune responses. The shift results in an overall decrease of immune cells mediating inflammation and cellular immune responses such as phagocytosis (i.e. neutrophils and monocytes). Moreover, we find that immunopathological phenotypes in visceral adipose tissue are drastically reduced in cavefish. Our data indicate that a more sensitive immune system in cavefish is compensated by a reduction of the immune cells that play a role in mediating the proinflammatory response. These findings reveal that cavefish are an effective model system to study the evolution of auto-inflammatory processes.

15:00-17:00 Session 18C: Teaching Workshop

CHAIR: Jay Labov

LOCATION: 204

15:00

Jay Labov

Using Research about How People Learn and Effective Pedagogy as Guides for Developing Education Resources for Evolutionary Medicine

ABSTRACT. Many research scientists and educators in evolutionary medicine are seeking to develop resources that could be used by instructors at various levels of education to help students better understand the value and importance of evolutionary medicine or to use evolutionary medicine as a lens for learning evolutionary concepts more generally. Emerging research about how people learn can provide guidance about ways to make these resources more effective and ways to structure pedagogy to enhance learning experiences. This session will provide an overview of some of the research about how people learn and focus on an approach to effective pedagogy known as backward design. The goal of this session is to assist workshop participants in developing education resources for evolutionary medicine.

15:20

Daniel Grunspan, Randolph Nesse and Sara Brownell

The need for a learning framework for education about evolution and medicine

ABSTRACT. Momentum is growing for the inclusion of evolutionary medicine in classroom curriculum ranging from high school through medical school. Research in the learning sciences reveals that an important consideration for any curriculum is to have clear learning goals for students, alongside more specific and measurable learning objectives. To date, little information exists on what these goals are in existing evolutionary medicine courses, and no concerted effort has elicited what these goals should be. Creating a learning framework that outlines learning goals and associated objectives represents an important step for evolutionary medicine education. However, a ‘one-size-fits-all’ set of learning goals and objectives may not be appropriate or feasible in evolutionary medicine given 1) the multidisciplinary nature of evolutionary medicine, and 2) instruction of evolutionary medicine takes place across different educational levels and in different national systems of education. In this workshop, I will present on the structure and value of learning frameworks, what is known about learning objectives in evolutionary medicine, and lead a discussion about the potential creation of a learning framework in evolutionary medicine.

15:40

Michael Poulsen

How to teach evolutionary medicine effectively at European Universities

ABSTRACT. A variety of initiatives have been taken during the last decade to initiate graduate courses in evolutionary medicine. They appear to almost invariably have been within biology curricula, but no systematic evaluations have been done to answer questions like: 1. How many students sign up for these courses and what is their background? 2. How broad a course program do they get offered? 3. How useful (eye-opening) do students appreciate these courses to be? 4. What adjustment of course content might improve student interest in the future? 5. How much do answers to these questions vary across European countries and depend on whether evolutionary courses are taught under the auspices of a Natural Science or a Medical Faculty? Obtaining answers to questions like these may be particularly important because of the key differences between Europe and the USA in that European biology students almost never continue on a MD trajectory, but quite often obtain research positions in Medical Departments or hospitals. This may imply that optimal strategies for maximizing the impact of graduate courses in evolutionary medicine in Europe and the USA may not be identical. Here I intend to address and formulate tentative conclusions to the questions posed above, and engage in discussion with delegates to find out the best way to proceed with teaching evolutionary medicine in Europe.

17:00-18:00 Session 19: EMPH editorial board meeting

CHAIR: Charles Nunn

LOCATION: 220

18:00-21:00 Congress Dinner Swiss Fondue

LOCATION: Mensa B

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08:30-09:30 Session 20: Keynote Verena Schünemann

CHAIR: Anne Stone

LOCATION: Aula

08:30

Verena J. Schuenemann

Ancient DNA and pathogens: uncovering the past of human diseases

ABSTRACT. In recent years, advances in sequencing technologies and simultaneous improvements in the ancient DNA field have revolutionized our understanding of the evolutionary history of pathogens. Most notably, targeted DNA enrichment techniques have allowed to identify the causative agents of historic pandemics and to reconstruct their genomes, resulting in direct insights into the history and origins of these pathogens. We are now able to trace back the evolutionary and population dynamic processes of bacterial pathogens as well as their adaption mechanisms to various hosts throughout historical times presumed to be out of reach by prior methods. Here, we will use two examples, Mycobacterium leprae and Treponema pallidum to showcase the potential and variety of ancient pathogen studies and to discuss challenges and benefits arising from the current techniques for ancient pathogen DNA retrieval and analysis.

09:30-10:00Coffee Break

10:00-12:00 Session 21A: Infectious diseases

CHAIR: Sylvia Cremer

LOCATION: Aula

10:00

Selina Niggli and Rolf Kümmerli

Ecology and mechanisms of interspecies interactions between Pseudomonas aeruginosa and Staphylococcus aureus

ABSTRACT. Natural bacterial communities in the environment and in infections are typically diverse, yet we know little about the factors that determine interspecies interactions. Here, we apply concepts from ecological theory to understand interaction patterns between the two opportunistic human pathogens Pseudomonas aeruginosa and Staphyloccocus aureus, which often co-occur in polymicrobial infections. We focus on three ecological parameters potentially influencing bacterial communities. First, we predict that the spatial structure of the environment helps to physically segregate species from one another, thereby weakening competition and promoting co-existence. Second, we examine whether the genetic background of strains plays a role in competition. Third, we assess whether frequency-dependent dynamics occur. We tested our predictions by conducting competition assays between two P. aeruginosa and three S. aureus strains across three levels of spatial structures and three different starting frequencies. We found that increased spatial structure did not foster co-existence, but shifted the competitive dynamics in favor of P. aeruginosa. We further observed that the genetic background of both P. aeruginosa and S. aureus had a strong influence on competition outcomes, whereby both species can end up as winners depending on strain pair combinations. Finally, we found evidence for positive frequency-dependent selection showing that P. aeruginosa strains cannot invade populations when rare, but dominate when initially occurring at high frequency. Our findings have three potentially important implications for polymicrobial infections. First, interactions and pathogen dominance in infections are determined by strain background and might thus vary from patient to patient. Second, frequency-dependent selection might limit the opportunity of rare pathogens to invade an established infection. Third, a change in the physical structure at the infection site, possibly induced by treatment, might alter competitive dynamics. Altogether, our study highlights that ecological and evolutionary principles can help to understand polymicrobial infections.

10:20

Hélène Chabas, Sébastien Lion, Antoine Nicot, Sean Meaden, Stineke van Houte, Sylvain Moineau, Lindi Wahl, Edze Westra and Sylvain Gandon

Evolutionary emergence of infectious diseases in heterogeneous host populations

ABSTRACT. The emergence and re-emergence of pathogens remains a major public health concern. Unfortunately, when and where pathogens will (re-)emerge is notoriously difficult to predict, as the erratic nature of those events is reinforced by the stochastic nature of pathogen evolution during the early phase of an epidemic. For instance, mutations allowing pathogens to escape host resistance may boost pathogen spread and promote emergence. Yet, the ecological factors that govern such evolutionary emergence remain elusive because of the lack of ecological realism of current theoretical frameworks and the difficulty of experimentally testing their predictions. Here, we develop a theoretical model to explore the effects of the heterogeneity of the host population on the probability of pathogen emergence, with or without pathogen evolution. We show that evolutionary emergence and the spread of escape mutations in the pathogen population is more likely to occur when the host population contains an intermediate proportion of resistant hosts. We also show that the probability of pathogen emergence rapidly declines with the diversity of resistance in the host population. Crucially, we experimentally confirm these theoretical predictions using lytic bacteriophages infecting their bacterial hosts containing Clustered Regularly Interspaced Short Palindromic Repeat and CRISPR-associated (CRISPR-Cas) immune defenses as a model system. These results suggest effective strategies for cross-species spillover and for the management of emerging infectious diseases.

10:40

Michelle Blyth, James Mcnary, Finn Schubert, Audrey Renson and Jeanne Carey

Evolutionary Predictions and Understanding of Sepsis

ABSTRACT. Sepsis is a common, expensive, and often challenging diagnosis with the potential for high mortality and morbidity. Every year, approximately 1 million people in the United States are diagnosed with sepsis, with a mortality of 15-30% with similar statistics found in many other countries. However, accurately diagnosing and treating sepsis remains an elusive goal.

Sepsis, as defined by the 3rd International Consensus on Sepsis, is life-threatening organ dysfunction caused by a dysregulated host response to infection. On the surface, this definition does not seem to represent a particularly adaptive process; however, sepsis is a commonly encountered medical diagnosis. The high mortality rate of sepsis is canonically explained by the immune system causing self-harm disproportionate to the underlying infection. Evolutionary theory leads us to explain this paradox with one of these concepts: mismatch, tradeoff, constraint, or defense.

In order to further explore these questions, we performed a comprehensive chart review on 200 patients who received antibiotics in the emergency department of an academic community hospital prior to hospital admission. We performed data analysis in order to identify support for a mismatch, tradeoff, constraint, or defense explanation and applied a series of hypotheses in order to test these concepts. We compared various sepsis criteria and lab values among cohorts of patients based on comorbidities, infection status, and clinical outcomes. Further, in order to better understand the nature of sepsis as opposed to other acute medical conditions, we compared patients who were found to have an infection with those in whom infection was ruled out during their hospitalization. We also compared those with infection who presented with sepsis with those with an infection that did not present with sepsis. Using these tools, we hope to further the understanding of the pathology and evolution of the sepsis response to infection.

11:00

Sylvia Cremer

Sociality affects disease epidemiology and pathogen evolution

ABSTRACT. Social groups can fight disease collectively. Thereby, the individual defenses of each group member are complemented by jointly performed hygiene and mutual sanitary care. Social interactions can hence interfere with the course of disease in individual group members and transmission to group members. Ants and other social insects show particularly sophisticated cooperative disease defenses that protect the whole colony. We observed the social interactions of healthy ants and their pathogen-contaminated colony members and find that both, contaminated and healthy individuals, change their behavioral profiles and spatial preferences upon pathogen entry to the colony. This alters the colony-wide interaction network and reduces disease spread through the colony. We further tested whether the hygiene measures of the ants – pathogen removal by grooming and disinfection by antimicrobial compounds – exerts a strong selection pressure on their pathogens. To address this, we let fungal pathogens of ants evolve in the presence or absence of social defenses, that is, (i) in groups of ants or (ii) in single ants. We found that pathogens adapting to groups of ants showed higher production of new infectious stages and elicited altered sanitary care by the ants than pathogens that had evolved only with single ants. Our work reveals that the collective defenses of social insects have strong impact on disease transmission and pathogen evolution.

11:20

Saskia Pfrengle, Judith Neukamm, Sarah Inskip, Rezeda I. Tukhbatova, Ella Reiter, Nataliya Berezina, Alexandra P. Buzhilova, Stian Suppersberger Hamre, Vítor Matos, Maria Teresa Ferreira, Johannes Krause and Verena J. Schuenemann

Reconstruction of new ancient Mycobacterium leprae genomes from Europe

ABSTRACT. Leprosy is one of the oldest known diseases in human history with possible osteoarchaeological cases dating back till the Late Copper Age (3,650 BC) in Hungary. Molecular biological approaches, such as ancient DNA research focussing on the causative agent, Mycobacterium leprae, can greatly contribute towards understanding the evolutionary history of the disease. Previous genetic studies of ancient M. leprae genomes in comparison with modern strains have identified genomic continuity over the last 1,000 years and the existence of at least four lineages in medieval Europe. However, the ancient genomes published so far concentrate on certain regions of Europe which probably do not reflect the diversity of other regions. Here, we address this issue through the genetic examination of several medieval and post-medieval samples from so far unstudied regions. Up to now, three new ancient M. leprae genomes have been already reconstructed: two medieval genomes from Portugal (1,340 ± 48 AD) and Norway (1,328 ± 60 AD) and a genome from Russia dated to the 19th-20th century. Ongoing analysis is focuses on the reconstruction of additional ancient leprosy genomes in order to more fully capture the diversity of the ancient M. leprae strains in Europe. The phylogenetic analysis of the reconstructed genomes, including previously published modern and ancient genomes, reveals that the genomes from Portugal and Norway fall on branch 3. The genome from Russia is located on branch 2F and clusters with modern Ethiopian strains. Overall, our results contribute to a better understanding of the past diversity of leprosy in Europe by adding genomic data from so far unstudied regions.

11:40

Adele Crane, Kelly Blevins, Christopher Lum, Keolu Fox and Anne Stone

M. leprae genome variation in the Pacific

ABSTRACT. As one of the oldest known human diseases, Hansen’s disease or leprosy has left humankind a legacy of fear and social stigmatization, and it remains a public health concern in many places with almost 211,000 new cases worldwide in 2017, including 4084 in the Western Pacific, according to the World Health Organization. Most human leprosy cases are caused by Mycobacterium leprae, but a small number case are now known to be caused by M. lepromatosis, which is a sister taxon of M. leprae. At present, the pattern of genomic variation in leprosy strains around the world is not well understood, since there are relatively few genome sequences available for analysis. To address this, as well as to begin to investigate patterns of pathogen exchange across Polynesia, we extracted DNA from eight formalin-fixed paraffin embedded biopsy blocks dating to 2011-2015. We used targeted-capture and sequencing on the Illumina HighSeq 2500 at 2x100 to sequence the genome, obtaining a depth of coverage ranging from 2.5 to 95x. Our preliminary analyses indicate that these strains belong to basal lineages within the M. leprae phylogeny, specifically falling in branches 0 and 5. Further comparative and phylogenetic analyses of these strains will help to clarify the geographic patterning and evolutionary history of leprosy.

10:00-11:00 Session 21B: Symposium Pregnancy and Birth

CHAIR: Kenneth Buetow

LOCATION: 204

10:00

Angela Garcia, Heini Natri, Benjamin Trumble, Melissa Wilson and Kenneth Buetow

Evolved immune compensation due to pregnancy underlies sex differences in human diseases

ABSTRACT. Sex differences exist across a range of human diseases, that to date have been understudied and largely unexplained. For example, females in industrialized populations exhibit a higher prevalence of most autoimmune diseases than do males. By contrast, females have a lower risk of developing cancer, with nearly all non-reproductive cancers showing a higher incidence in males. Here we present the Pregnancy Compensation Hypothesis (PCH), which explains both the proximate and ultimate (evolutionary) mechanisms responsible for sexual dimorphism observed in human disease, as mediated by selection on the immune system due to pregnancy and placentation. We propose that because evolution has shaped the human immune system differently in males and females, under industrialized conditions that differ from the ancestral state, we expect sex differences in diseases to be more pronounced in urban, industrialized contexts.

Under the PCH, we propose that the evolution of eutherian placentation exerted significant sex-specific selection on immune function to tolerate fetal antigens while still defending the pregnant individual against parasites and pathogens. We theorize that this process is regulated proximately via hormones and mediated genetically by dosage on the sex chromosomes, and that today, the mismatch between an ancestral environment (being pregnant or lactating for the majority of adult reproductive years) and urban industrial environment (where common contraceptive use results in reduced pregnancies) interacts with this evolved compensatory immune regulation and results in the observed sex differences in disease risk. Finally, a sedentary lifestyle that affects reproductive hormone levels exacerbates these differences.

Here we focus on two disease classes with documented immune components that show sex differences in incidence and treatment: autoimmune diseases and cancer. We unpack the interrelated components of the PCH related to shifting reproductive states, parasite loads, and energetic availability, which are particularly relevant for sex differences in human disease.

10:20

Neerja Karnani

Human variation and health adversities: Insights from a modern birth cohort study

ABSTRACT. It is becoming apparent that changes in human exposures and behaviors are shaping future health adversities. The availability of big data and multi-omics technologies are now providing deeper insights into human variation and disease susceptibility. Using Singapore’s most deeply phenotyped and omics- profiled mother-offspring cohort, GUSTO (Growing Up in Singapore Towards healthy Outcomes), I will share how this study has helped to: (i) comprehensively map the molecular and phenotypic variability in Asians in both pediatric and adult populations, (ii) how this variability is linked with non-communicable diseases that are plaguing global health and economy, and (iii) how we can use these data for developing precision healthcare for future generations.

10:40

Kleber Jessivaldo Gomes Das Chagas, Marco Antonio Barbieri, Viviane C Cardoso, Heloisa Bettiol and Alexandre Ferraro

AN EVOLUTIONARY VIEW TO CESAREAN DELIVERY LATE CONSEQUENCES

ABSTRACT. Cesarean Section (CS) rate is high in developed and in developing countries. The optimal CS rate according to the WHO is around 10-15%. In Brazil, however, nearly 55% of babies are delivered by CS, suggesting a biased health system towards surgical birth. Delivery by CS has been associated with later life health outcomes. A recent meta-analysis of 28 studies found that children delivered by CS had a 34% greater risk [95%CI 1.18-1.51] of being obese during childhood and adolescence. Another meta-analysis, which included broader age groups, found that the association was present within different age strata. Similar findings were reported when highly different socio-economic settings were compared. Studies have also demonstrated links between delivery by CS and adult chronic diseases such as asthma and type I diabetes. We followed up 2020 individuals from birth to 25 years of age. CS was significantly associated with higher hypertension rates when compared with vaginal delivery (11.7 vs 7.7%, respectively). The risk for hypertension after adjusting for confounders was OR=1.49 (1.07-2.06). Evolutionary medicine allows us to look at this fact through a different point of view when compared to traditional clinical reasoning. Thus, we sought to analyze this situation using a clinical reasoning based on evolutionary medicine in an attempt to understand what are the long-term effects of CS. For that, a review of the literature on the subject was made and a theoretical model was developed that could explain this association. Given the burden of non communicable diseases, we highlight the importance of public incentives to promote vaginal birth in countries like ours.

10:00-12:00 Session 21C: Symposium One Health

CHAIR: Nicole Bender

LOCATION: 217

10:00

Stephan Schuster

Microbiomes of air, surfaces and dust as indicators of human health

ABSTRACT. Microbial communities inhabiting terrestrial and aquatic ecosystems have long been studied. With the onset of metagenomics, the degree of diversity and abundance of these communities has become apparent, even on a global scale. In contrast, the atmosphere, with its sizeable planetary volume, has largely been neglected as a habitat for microbial communities, despite providing means of transport with an intercontinental range. We have studied the occurrence of airborne microbial organisms in the tropical climate of Singapore and found robust and persistent assemblages, both on intra-day and a month-to-month time scales. Bacteria and fungi were the major constituents of the air microbiome, in addition to DNA derived from plants and insects. Besides conducting in-depth metagenomics studies that identified the diversity and abundance of airborne organisms, we have sequenced and assembled “100 genomes from air” using single-molecule sequencing (SMRT). These genome data from various indoor and outdoor settings, together with organismal and habitat information, are now enabling investigations of the impact of air environments on respiratory cohorts.

10:20

Jakob Zinsstag

What is One Health?

ABSTRACT. The inextricable linkage of human and animal health has been increasingly recognized in the past decades. However, human and veterinary medicine are often working so much in separation that human and animal health is affected. We define One Health (OH) as the added value in terms of human and animal health benefits, financial and other resource savings and improved environmental services compared to the two medicines working in separation. An integrated assessment of human and animal health requires methods capable of assessing effects on the animal – human interface. For example livestock mass vaccination against brucellosis is not profitable for the public health sector alone but becomes largely profitable from a societal perspective including all involved sectors. Dog rabies control in Africa by mass vaccination of dogs becomes less costly than human post-exposure prophylaxis alone after ten years. Other examples are provided from health services, integrated antimicrobial resistance surveillance and joint laboratory infrastructure. Conceptually OH is embedded in broader ecosystem approaches to health which can also be called health in social-ecological systems or health in human-environment systems which is also important for non-communicable diseases. In this way human and animal health improvements will be developed while considering social dynamics and sustained ecosystem services.

10:40

Jean-Michel Hatt and Verena J Schuenemann

Understanding the effect of urbanization of wildlife on health status, epidemiology and public health considerations

ABSTRACT. The current urbanization is one of the biggest environmental challenges and has led to a worldwide increasing number of wildlife species to conquer this new type of biotope. This results in novel communities of species that share a habitat that have mainly been selected based on their synantropism. Selection based on habitat parameters such as climate, diet, density is ongoing, while new species experience urbanization. Whilst multiple studies investigate the impact of abiotic parameters, the evolution of infectious agents in urban wildlife is widely unknown. Here, we describe what impact urban habitats can have on pathogens, their vectors, and hosts. Special attention is given to aspects linked to novel opportunities of cross species transmission, the effect of dim light at night and pollution. We propose to develop a network based on the One Health approach to study the ongoing evolution of infectious agents in urban wildlife, to compare the epidemiology with the species in the original habitat and to assess the impact of infectious agents with respect to conservation issues as well as possible public health concerns.

11:00

Barbara Natterson-Horowitz

Evolved Adaption and Natural Animal Models of Disease Vulnerability

ABSTRACT. All physiology, including vulnerability to disease, is the product of evolved adaptations. Exploring this vulnerability across the animal kingdom leads to: 1) an expanded understanding of disease causation 2) accelerated biomedical innovation and 3) identification of natural animal models of disease resistance. This lecture will explore methodology for developing comparative insights, generating novel hypotheses and conceiving of bio-inspired investigation.

11:20

Elizabeth Uhl

One Health: A Veterinary Perspective on the Integration of Human and Animal Medicine Through Evolution.

ABSTRACT. The One Health movement is based upon the recognition that human health is connected to animal health and the environment. While this movement is a good first step in raising awareness of the close connections between human and animal health, the focus needs to be expanded beyond the initial emphasis on animal diseases as threats to human health. An evolutionary perspective is critical for developing an integrated view of what is driving disease susceptibilities across species and how such susceptibilities in one species can inform those impacting another. In particular, an evolutionary perspective emphasizes how adaptations to the environment through modifications of common genetic pathways have resulted in species variations in susceptibility to disease. For example, the genes regulating calcium and phosphorus homeostasis evolved in fish. Expression and function of these mediators was repurposed during subsequent adaptation to various land environments, and it is these modifications that determine species difference in susceptibility to metabolic bone diseases (i.e.: rickets). An evolutionary based One Health perspective also removes two major obstacles to the full utilization of animal models: 1) the misconception that disease in animals is the same as in humans (i.e.: a mouse is a human), and 2) only animal models that exactly reproduce human disease are useful. No animal model perfectly replicates human disease phenotypes, however without evolution to provide a context to assess these species differences, they are often ignored. This also means that the basis for the differences between human and animal disease phenotypes, which have potentially important therapeutic implications, are generally not studied. Finally a cross-disciplinary evolution based approach to understanding the environmental factors impacting human and animal disease facilities a much deeper understanding of how human modified environments affect both human and animal health.

11:00-12:00 Session 22: Symposium The Normal and The Pathological

CHAIR: Paul Griffiths

LOCATION: 204

11:00

Maël Lemoine

Towards a model of age-related diseases

ABSTRACT. What is a disease? Philosophers of medicine have investigated the term's meaning and locked themselves in a “conceptual straightjacket” (Hesslow 1993) by priorizing a consistent rendering of common usage. Instead, they can explore contemporary science for concepts and theories of natural disease phenomena. This paper sketches one such possibility, starting with the observation that most cases of disease come with age, whatever the specific disease. A focus on theories and models of aging in contemporary biogerontology, biodemography and evolutionary biology, should help consolidate a biological concept or even a biological model or theory of ‘age-related diseases’ in general. Even if this would not determine what is common to all the things that we call ‘diseases’, it would help form a relevant and conceptually challenging concept of a core phenomenon associated with most diseases in human populations. The challenge is first to put together 3 basic theoretical frameworks, namely, Gompertz-Makeham models of the incidence of death in populations (biodemography), Medawar-Williams model of aging in evolution (evolutionary biology) and a consistent picture of the biological ‘hallmarks’ of aging (Lopez-Otin, 2013). The resulting model of aging should then feature as an explanatory factor in the etiology of age-related diseases, i.e., the most prevalent and/or deadly in a population. The final goal would be a general model of aging as a common cause to many diseases that are generally studied separately, despite the fact that aging is their major risk factor.

Griffiths, Paul E. and John Matthewson (2018) The British Journal for the Philosophy of Science 69: 301–27. Hesslow, Germund (1993) Theoretical Medicine and Bioethics 14: 1-14. López-Otín, Carlos et al. (2013) Cell 153: 1194–1217. Matthewson, John and Paul E. Griffiths (2017) The Journal of Medicine and Philosophy 42: 447–66. Nesse, Randolph M. (2001) Medicine, Health Care and Philosophy 4: 37–46.

11:20

Elselijn Kingma

Why medical dysfunction is (still) not selected effects dysfunction

ABSTRACT. Griffiths & Matthewson (2016) defend the so-called ‘selected effects account’ of dysfunction as the best candidate for a naturalist account of disease. Their paper is a welcome and important contribution to a literature in which, amongst naturalist position, undue focus has rested on Christopher Boorse’s the Biostatistical account of dysfunction/disease. Griffiths & Matthewson up-to-date-with-current biology account does much to strengthen and improve a position that so far has suffered from being mainly defended by people insufficiently attuned to the details of (evolutionary) biology.

This paper examines whether Griffiths’ and Mattewson’s improved selected effect accounts can survive the following problem: in those cases where traits and effects have been affected by organisms’ development in ‘new’ environments, can the account state whether these traits are functional or dysfunctional, and therefore healthy or disordered. ? This question builds on a general tenet of developmental biology, which is that traits and their effects do not exist in but are the result of the environment in which an organism develops. Immunesystems, for example, develop in and are primed by the environment.

Griffiths and Matthewson’s account is meant to accommodate such developmental plasticity. Nonetheless I argue that it lacks the resources to accommodate disorders that in some sense are the result of our developing in non-ancestral environments. And since many disorders are likely to be the result – in one way or the other – of our developing in ‘new’ environments, this spells trouble for the selected effects account of disorder – even in its most sophisticated form. The trouble may be avoided by significant revision of our concept of medical disorder. But that – I argue – takes us too far from the central interests of medicine to serve it appropriately.

REFERENCES Griffiths & Matthewson (2018), Evolution, Dysfunction, and Disease: A Reappraisal, BJPS, 69: 301–327.

11:40

Paul Griffiths

Disease and Evolution

ABSTRACT. Since J.B.S Haldane’s essay Disease and Evolution (1949) it has been widely recognised that disease is an important and distinctive factor in evolution. But in contemporary philosophy of medicine it is widely believed that ‘disease’ is value-laden term: whether a phenotype is normal or pathological cannot be determined without making value judgments. These two ideas are prima facie inconsistent. In earlier work I have defended evolutionary approaches to defining disease (Matthewson and Griffiths 2017, Griffiths and Matthewson 2018). Within evolutionary medicine authors such as Nesse (2001) have argued that, although evolutionary theory does not straightforwardly define disease, any definition should be informed by our best theories of why mortality and morbidity exist and are distributed as they are. In this presentation I defend an objective, biological distinction between normal and pathological phenotypes and show that this distinction is needed within biology, independent of any application to medicine. This biological understanding of pathology does not map perfectly onto how normal and pathological are distinguished in medical practice, and it may be that a distinct, medical understanding of pathology is needed. Whether or not that is the case, I argue that the biological understanding of pathology should guide the medical understanding of pathology as that understanding evolves in response to new biomedical findings.

12:00-13:00Lunch Break

13:00-13:30 Session 23: Poster session III

All posters are exhibited during the whole congress, not just the ones listed in the specific session list.

LOCATION: Patio

13:00

Alberto Vicens and David Posada

Ancient and recent selection on human cancer genes

ABSTRACT. Cancer is a disease generated by somatic mutations and clonal selection of cell lineages but also by the rapid germline evolution of genes that predispose to cancer. Indeed, several genes associated with cancer, also known as cancer or driver genes, show evidence of positive selection during the evolution of species, which could promote cancer risk as a secondary effect. Taking advantage of a list of 574 cancer genes collected in Cancer Gene Census database, we evaluated ancient and recent selective pressures on cancer genes using comparative genomics and population genetics approaches. We measured the role of purifying and positive selection in mammals applying the dN/dS ratio, on the human lineage after splitting from chimpanzee estimating branch-specific dN/dS and Neutrality Index, and on human populations applying polymorphism-based selection statistics (iHS, Fst and Tajima´s D) on 1000 genomes project data. We evaluate the global selective pattern of cancer genes with respect to a background of the human coding genome, compare the selective pressures among different functional categories of cancer genes, and explore functional enrichment of cancer genes subjected to positive selection across the three levels. Our study will provide insights onto the origin of cancer and have important implications for understanding the links between evolutionary forces, positive selection on cancer genes and increased cancer risk.

13:00

Paul Kubelac, Catalin Vlad, Ioana Berindan-Neagoe, Alexandru Irimie and Patriciu Achimaş-Cadariu

OVARIAN CANCER AS A MODEL FOR UNDERSTANDING TUMOR EVOLUTION IN SOLID MALIGNANCIES

ABSTRACT. Currently in Western societies solid malignancies represent one of the leading causes of death given the general decline in tissue structure and function associated with age. Ovarian cancer is the second most common gynecological cancer and the deadliest in absolute rates, with more than 280.000 new cases and 183.000 deaths predicted for 2020. Recent research based upon cost-effective whole genome data analysis has described ovarian cancer as a heterogeneous disease. Given it`s clinical features and pattern of carcinogenesis, ovarian cancer can be regarded as an evolutionary mismatch and can be used as a feasible model for studying tumor progression in solid malignancies. It shares with solid tumors features such as genetic diversity, clonal evolution, spatial and temporal genetic heterogeneity and development of drug resistance. There is growing evidence that dynamic interactions between ovarian cancer tumor cells and the host tumor microenvironment can actively influence therapeutic response. With this concept in mind, the multifaceted design of future basic, translational and clinical research and the development of predictive models for novel drug combinations represent a gateway towards tumor control in ovarian cancer and other malignancies.

13:00

Yuping Yang, Ruth Mace and Megan Arnot

The evolutionary ecology of menopause symptoms

ABSTRACT. Objective: Evolutionary anthropologists are unsure as to why selection would have ever favored menopause. Úbeda et al (2014) made a prediction about menopause symptoms: Consistent with the Grandmother Hypothesis, based on the intragenomic conflict, they find in populations with greater female-biased dispersal, women will experience a smaller degree of intragenomic conflict, shorter and less symptomatic peri-menopause and later menopause. There have been few studies testing it, and thus we propose to investigate the validity of the theory.

Methods: We use the Menopause symptoms Rating Scale (MRS) Questionnaire data from villages in Lugu lake and Zhaba in Sichuan province in China from 2 patrilocal populations and 2 matrilocal populations. The respondents' experience of the menopause was collected using the MRS that was developed by the Berlin Center, in which participants respond to statements (e.g. “I have hot flashes”, “I get heart palpitations”) on a 4-point Likert scale. For each individual, a ‘menopause symptoms score' (MSS) was created by summing the respondent's report of symptoms. This includes a total MSS, in additional to a vaso-motor MSS, a psychological MSS, and a physical MSS. Using these scores, we tested whether the residence pattern (matrilocal or patrilocal) of the individual is predictive of the severity of menopause symptoms. For the hypothesis to be supported, we would expect the matrilocal Mosuo and Zhaba to report worse symptoms than the patrilocal Han and the Yi.

Results: So far, according to the collected data, my conclusion is converse to the Úbeda‘s prediction. In my study, the primary results are: Whatever the female-biased dispersal is, the menopause timing is no difference; The Mosuo and the Zhaba females (smaller female-biased dispersal) have lower symptoms score than the Han and Yi (greater female-biased dispersal).

Conclusions: There is no evidence to support the intragenomic conflict hypothesis for the symptoms of peri-menopause.

13:00

H Neitzel, R Varon, S Chughtai, P Nürnberg, M Schweiger, D Horn, M Digweed, B Schulze and K Sperling

Mutations of the master regulator of centriole formation PLK4 cause primary microcephaly and severe transmission ratio distortion

ABSTRACT. The Polo-like kinase 4 (PLK4) is essential for centriole duplication, spindle assembly, and de novo centriole formation. Homozygous mutations in PLK4 lead to primary microcephaly. Here, we report a consanguineous, three generation family with 8 affected individuals, compound heterozygous for a novel missense variant of the PLK4 gene and a deletion of the other allele. The deletion was transferred to 14 of 16 offspring (P = 0.007). If individuals of other PLK4 families are included, there is a significant overrepresentation of affected probands (P<0.01). This also explains that among 24 informative offspring of heterozygote parents only a single individual was homozygous for the wild type allele. Thus, the deleted/mutated PLK4 alleles exhibit transmission ratio distortion (TRD) which cannot be explained by the known TRD mechanisms. Interestingly, a significant association has been reported between tripolar spindles and chaotic mosaic aneuploidies in cleavage stage embryos and a PLK4 linked haplotype (McCoy et al. Science 348:235-238, 2015). Under optimal conditions less than 30% of all fertilized human eggs result in a newborn. The vast majority of losses is due to meiotic and early mitotic aneuploidies. The highly error-prone mitotic divisions are controlled both by maternal gene products, including PLK4 and by paternal elements such as the centriol. Overexpression of PLK4 cause tripolar spindle formation. It is therefore assumed that PLK4 is normally overexpressed after fertilization, leading to mitotic aneuploidy and implantation failure to span the birth interval. Mutations/deletions of PLK4 could result in mitotic fidelity, more diploid embryos and hence preferential transmission of the deleted/mutated PLK4 alleles. Since the affected individuals have no children, this does not affect population fitness.

13:00

David Laloum and Marc Robinson-Rechavi

Evolutionary conservation of rhythmic gene expression

ABSTRACT. The rhythmic transcriptome is characterized by the set of genes that display rhythms in their mRNAs level which occur every 24 hours, i.e. which are nycthemeral. In baboon, 82% of protein-coding genes have been reported to be rhythmic in at least one tissue (Mure et al., 2018 Science 359: eaao0318). The nycthemeral rhythmicity of these transcripts can be driven by an internal oscillator clock, or by circadian behaviors such as food-intake, the light-dark cycle, sleep-wake behavior, or social activities. A common clock mechanism (transcription–translation feedback loop), driving the rhythmic expression of many genes, appears to be strongly conserved in evolution. This endogenous generated rhythm provides a time framework allowing organisms to anticipate environmental changes before they take place. Thus, many functions might benefit from this rhythmicity, and probably require it. Yet the evolution of the rhythmic transcriptome has not been studied so far, beyond core circadian genes. Here we have investigated the conservation of rhythmic orthologs, both as a starting point to study the evolution of rhythmicity, and to understand its functional role. Inter-species comparisons among vertebrates and among insects detect a high proportion of rhythmic orthologs with conserved rhythmic expression in the same homologous organ. This conservation of rhythmic expression is tissue-specific. For instance, within mouse-baboon orthologs which are rhythmic in baboon liver, 45% are detected rhythmic in mouse liver. This supports that rhythmicity at the mRNA level plays a functional role, subject to purifying selection. Furthermore, we find evidence that rhythmic orthologs are genes whose cost of expression, from gene to protein level, is higher than that of other genes. The rhythmic expression of these genes might be an evolutionary advantage, allowing a widespread reduction of costs of protein production.

13:00

R. Brooks Robey

Adaptive Metabolic Fitness in Cancer Selection

ABSTRACT. The recognition that accrual of genomic mutations is conducive to carcinogenesis has focused most cancer research on the promotion of oncogenic changes via mutagenesis. Much less attention has been paid to the specific determinants of cancer cell selection. At the most fundamental level, however, transformed cell phenotypes are unlikely to result in successful cancer establishment if not selected. Mutagenesis simply provides the genetic diversity that affords new selectable cell fitness advantages.

All cardinal features of cancer exhibit increased catabolic and/or anabolic support requirements. Cancer cells also encounter widely varying environmental conditions during carcinogenesis, cancer growth, and metastasis. As such, dysregulated intermediary metabolism – an established hallmark of cancer – is uniquely suited to serve as a major basis for selection.

Intermediary metabolism is neither a fixed property nor a unitary entity, and metabolic fitness can vary widely with changing substrate availability or conditions. As such, fixed metabolic phenotypes could disfavor the selection of cancer cells unable to optimally utilize available resources to meet prevailing cellular demands under changing heterotrophic conditions. In contrast, the ability to alter the metabolic gestalt in response to environmental changes could favor selection based on adaptive metabolic fitness.

Metabolic responses can be either adaptive or maladaptive across the spectrum of both physiological and non-physiological environmental conditions. Transformed cells with the intrinsic phenotypic plasticity to adapt to broad variability in both the types and amounts of available nutrients may be better suited for survival than cells with any particular fixed metabolic characteristic. The ability to adapt to mesotrophic or oligotrophic conditions may also obviate metabolic bottlenecks and provide competitive growth advantages that promote selection. A corollary of such relationships would assert similar selection advantages during rapid clonal expansion, tissue invasion, and metastasis. Such behavior could also help explain observed deviations from modeled tumor development and spread.

13:00

Ana Clara Cruz Nadim and Alexandre Archanjo Ferraro

Sexual dimorphisms in response to pre-natal violence in humans: an evolutionary perspective

ABSTRACT. Many studies have found an association between child's health and maternal stress during pregnancy, such as domestic violence. Identifying these cases can be difficult and biomarkers of chronic stress, such as capillary cortisol, may be helpful. In a population-based birth cohort from the outskirts of the city of São Paulo, it was found a causal association between stress in pregnancy (violence and capillary cortisol levels) and intrauterine growth restriction (IUGR) in female neonates and cognitive delay in male infants of 6 months of age (n=183). In order to understand if there are selective pressures favoring such sexually dimorphic response, as well as which they could be, we revisited great evolutionary processes that determine and condition sexual reproduction. A particularly important concept approached here is the dichotomy between r and K reproduction strategies, the first one being more interested in quantity in the offspring, whilst the second one values quality. We hypothesize, in accordance with previous findings, that the observed dimorphisms may have an adaptive value in contexts of environmental instability, along with a higher inclination towards polyandrogyny in its mating system, and an increased competitivity amongst males in order to gain access to fertile females. Our hypotheses imply the existence of polymorphisms that are maintained in the population through variability generating mechanisms, which accompany female choice. This can entail important consequences for public health, since low birth weight has been associated with early puberty, higher fertility rate, less paternal involvement in parental care, maternal withdrawal from work and, eventually, scarce human capital in adulthood. Finally, we suggest ways to test some assumptions presented in our hypotheses by comparing evolutionary rates in genes involved in the determination of social grouping, affectivity, stress signaling through the placenta and mutation rates.

13:00

Lynnette Sievert

The evolution of menopause and post-reproductive life: a phylogenetic perspective

ABSTRACT. Menopause is the permanent cessation of menstruation and/or the irreversible loss of the ability to produce offspring due to the cessation of ovarian follicular activity. Menopause results from a particular pattern of oogenesis. Mammals and birds generate hundreds, thousands or, in the case of humans, millions of eggs early in the lifespan, and oogenesis is complete before, or just after, birth or hatching. In these species, there is a gradual loss of oocytes through ovulation and follicular atresia across the lifespan. With the exception of humans and various species of whales, most females die before the complete exhaustion of ovarian follicles. However, menopause has been observed among some individuals in dozens of mammalian species. Menopause and post-reproductive life can only occur in species that end the production of gametes. Fish, amphibians, and most reptiles cannot demonstrate a menopause because oogenesis continues across life. Monotremes share the same pattern of oogenesis and oocyte loss as demonstrated in all other mammals. Therefore, it appears that the shift from a fish-like pattern of continuous oogenesis to a mammalian and bird-like pattern of abbreviated oogenesis occurred within the reptiles, but evidence for this has been difficult to find. This presentation will present evidence that the capacity for menopause and post-reproductive life evolved more than 200 mya. One reptile group in particular provides clues to explain when and why the female (but not male) pattern of gametogenesis changed. From this phylogenetic perspective, human menopause and post-reproductive life are byproducts of this much earlier change from one stable pattern of continuous oogenesis to a new stable pattern of constrained oogenesis and oocyte loss. The new pattern brought about the loss of ovarian follicular activity with age, resulting in menopause.

13:00

Martin Haeusler, Sabine Landis, Bernhard Zipfel, Viktoria Krenn and Cinzia Fornai

Evidence for adaptation to malaria in the human ancestor Australopithecus africanus, 2.6 million years ago

ABSTRACT. The MLD 46 Australopithecus africanus proximal femur from Makapansgat, South Africa, represents the earliest known case of hip osteoarthritis in the human fossil record. Dated to 2.6 million years ago, it long predates the second oldest fossil with hip osteoarthritis a 50-000-year-old Neanderthal. Based on its large size, MLD 46 probably belonged to a male individual, while the closed epiphyses and the generally low life expectancy in the Plio-Pleistocene indicate a young adult age. MLD 46 shows extensive marginal and medial osteophytes, without collapse of the head. This suggests that the severe hip osteoarthritis resulted from acetabular protrusion, which in young adults is often associated with bone marrow expansion due to haemoglobinopathies such as sickle-cell disease and thalassemia. A large piece of bone was flaked off from the femoral head anteriorly, revealing various subchondral cysts and a large cone-shaped sclerotic zone in the medial sector of the head. This sclerotic zone was confirmed by micro-CT examination. Its differential diagnosis includes a bone island, a tumour metastasis, or, most likely, osteonecrosis. Osteonecrosis represents a common complication of sickle-cell disease. Other aetiologies of osteonecrosis including corticosteroid medication and alcoholism are less likely in prehistoric times. In addition, the micro-CT images revealed clogging of various fine branches of the medial femoral circumflex artery at the tip of the osteonecrotic area. Osteonecrosis due to infarction of the proximal femoral epiphysis is characteristic of sickle-cell disease. Because sickle-cell disease offers protection against malaria tropica, the earliest human ancestors must already have evolved adaptations against Plasmodium falciparum infections. So far, malaria tropica was thought to have originated in humans when forests were destroyed at the agricultural transition, thereby facilitating a cross-species transmission of Plasmodium parasites from gorillas. Yet, our findings suggest that the origin of malaria dates back to the earliest times of human evolution.

13:00

Cinzia Fornai, Előd Úry, Daniele Togni, Michael Kundi and Eva Piehslinger

Evidence-based relationship of occlusion and temporomandibular disorders

ABSTRACT. The dissociation between the evolutionary adaptation of the human masticatory apparatus and the actual functional needs in modern societies has been proposed as a major factor for increased prevalence of malocclusion and retrognathism. The role of deviating occlusal patterns in the development of temporomandibular disorders (TMDs) is controversial. TMDs likely originate from multiple etiological factors such as occlusion, parafunction, emotional stress, and trauma. Numerous dental studies have tried to test whether there exists a quantifiable relationship between the morphology of the masticatory structures and TMD. These works are heterogeneous and deliver contrasting outcomes, hampering a clear interpretation of the clinical literature. In order to decipher the signal stemming from the evidence-based literature, we performed a meta-analysis of the available clinical literature on occlusion and TMD, considering articles in which patients are thoroughly clinically examined. We excluded studies focusing on children, senile or edentulous individuals, or applying interventional approaches (e.g., orthodontic and prosthetic). We analysed a total of 43 articles out of 201 screened, considering a total of 61 occlusal features relative to the different TMD diagnoses (except for headache aggravated by mastication). Studies using international guidelines for TMD diagnosis were analysed separately from those using sets of signs and symptoms. Our analyses revealed a significant association of the considered occlusal features with TMD in about 30% of the cases. These included sagittal deviations from dental and skeletal class I, posterior open bite, and alteration of jaw dynamics caused by medio- and laterotrusive interferences. We found that articles applying international guidelines for TMD diagnosis were less heterogeneous than those using sets of signs and symptoms. Our outcomes lay the bases for future research investigating the influence of the skeletal and occlusal form on TMD. Understanding this relationship will fundamentally change treatment planning in many clinical settings.

13:00

Nicole M. Webb, Falk Mazelis and Martin Haeusler

New Insights Into Caesarean Section Risk Prediction Using Machine Learning

ABSTRACT. The steady rise in global Caesarean rates presents a mounting challenge given the associated health risks and high costs. Here we utilize a Centers for Disease Control and Prevention vital statistic public dataset with detailed accounts surrounding the total live births recorded for the United States in 2017 (n=3,864,754). The data include variables about each parent, maternal prenatal care/medical history and information about the fetus and the birth circumstances. Caesarean sections accounted for 32% of all births in this sample, which exceeds the WHO’s recommendation of a 10-15% section ratio. Therefore, this dataset provides an opportunity to explore the role of maternal phenotypic and socioeconomic variables in assessing Caesarean risk in a population with elevated rates. We explore these predictor variables via machine learning (ML) algorithms due to their efficient application to large datasets.

We used a binary decision tree intended for multiclass classification to train a model to predict vaginal versus Caesarean delivery outcomes. Our birth classification model produced accuracy recalls of over 82% and a precision rate of 93%. Increased Caesarean risk was associated with the time of day, previous Caesarean sections, fetal presentation at birth, and pregnancy with multiples. These results corroborate known predictor variables and correspond with those of a pilot birth classification ML study. Yet, our integration of significantly more data points and different variables provide additional insights into individual predictor influence. Specifically, depending on the percentage of data included in model training, predictor importance differed notably, thereby suggesting that sample size may explain correlations promoted in previous studies. This includes the role of maternal height and education level, which diminished in contribution once larger training samples and more variables were utilized in our analyses. This study demonstrates that models trained via supervised learning offer novel predictive potential for Caesarean section risk assessment.

13:00

Karolina Milkowska, Andrzej Galbarczyk and Grażyna Jasieńska

Does meat consumption change across menstrual cycle?

ABSTRACT. Objectives. The compensatory prophylaxis hypothesis (CPH) proposes that evolved psychological mechanisms enhance the avoidance of potential contaminants during periods of reproductive immunomodulation (such as luteal phase of menstrual cycle) in order to decrease a chance of infection. Meat has been one of the primary sources of foodborne pathogens throughout human evolutionary history, as animals carry pathogenic endosymbionts and parasites, and many microbes proliferate on meat. Therefore, the aim of the study was to analyze differences in meat consumption among healthy, regularly menstruating women. Method. The participants of our pilot study were 34 women aged 18-45. Participants were asked to complete four daily surveys: 1) in the follicular phase on days 3rd and 8th of the cycle, 2) in the luteal phase on days 18th and 23rd. Survey items included questions about the number and size of servings of specific types of meat eaten. Women were also asked to conduct ovulation-detection LH tests from day 10 to 20 of their cycles (counting from the first day of menstrual bleeding) or until a test indicated an ovulation. Results. Women consumed less meat per day in the luteal phase than during the follicular phase (198 grams vs. 244 grams, respectively), but this difference was not statistically significant (p=0.21). Conclusions. Results of the study did not prove any differences in meat consumption among follicular and luteal phase, which is consistent with findings of some previous studies in that field. The meat-borne pathogens widely differ in time of their incubation and, therefore, cyclic alterations in meat consumption might not provide protection from meat-borne infections. Thus, it is possible that alterations in prophylactic behaviors are not related to dietary exposure to pathogens.

13:00

Vitor Matos, Carina Marques, Daniela Pacheco and Ana Luísa Santos

Co-infection or cross-immunity? New palaeopathological evidence for two debated hypotheses regarding the co-evolution of leprosy and pulmonary tuberculosis

PRESENTER: Vitor Matos

ABSTRACT. There is scarce evidence of leprosy and tuberculosis co-occurrence in past human populations and two long-debated hypotheses regarding their co-evolution exist: cross-immunity versus co-infection. This study presents new palaeopathological evidence, namely periosteal new bone formation (PNBF) on the visceral surface of ribs – a proxy to pulmonary pathological conditions, including tuberculosis infection –, in two medieval/modern (13th-17th centuries) cemeteries, from Odense, Denmark. The palaeoepidemiological importance of these skeletal lesions for the understanding of the co-evolution of leprosy and tuberculosis is discussed. We analysed 292 human skeletons – 235 adults from both sexes and 57 non-adults – housed at the University of Southern Denmark (ADBOU), namely: 191 from the St. Jørgen’s leprosarium cemetery [SJG] and 101 from the Blackfriars monastery cemetery [BFM]. Ageing and sexing of skeletons, and macroscopic observation of bones followed standard bioarchaeolological methods. PNBF on the visceral surface or ribs was found in 5.8% (10/173) and 7.3% (7/96) of the skeletons with well preserved ribs from SJG and BFM, respectively (OR=1.282; IC95%: 0.472-3.484). Few of the 4150 ribs observed (59.2% of the total 7008 expected) were affected: 0.9% (22/2504) for SJG and 1.5% (24/1646) for BFM (OR=1.669; IC95%: 0.933-2.987). None of these proportions differed significantly between cemeteries (p>0.05). These findings suggest a low prevalence of pulmonary tuberculosis in the medieval/modern population of Odense. PNBF on ribs was found both in skeletons with (8.1%) and without (5.6%) leprosy related bone lesions (p=0.64), challenging the assumption of a differential mortality in leprosy patients due to pulmonary tuberculosis. The (dis)advantages of palaeopathological approaches to understand leprosy and tuberculosis co-evolution in past human populations will be addressed. Funding: This research was financed by national (POPH – Programa Operacional Potencial Humano) and European (European Social Fund) funds through the FCT – Fundação para a Ciência e Tecnologia: project references UID/ANT/00283/2019 and IF/00186/2014.

13:00

Bethany Usher

The evolution of courses in evolutionary medicine

ABSTRACT. Evolutionary perspectives on disease first began to be formally introduced in courses in the 1990s, with the publication of Why We Get Sick (Nesse and Williams, 1994), although medical anthropologists have been taking a biocultural approach towards studying health since at least the 1960s (medanthro.net) and biological anthropologists formalized paleopathology as a field in 1973 (paleopathology-association.wildapricot.org). The author began teaching an undergraduate course, Humans, Disease, and Death (HDD), that included foci on evolutionary medicine, paleopathology, and demography in 2002. That course has evolved into two courses that have been taught almost continuously in three different institutions. These courses are now offered at undergraduate and graduate levels, and serve as electives for students in anthropology, biology, public health, and nutrition programs. The HDD course now uses the principles of evolutionary medicine (Gluckman, Beedle, and Hanson, 2016) and anthropological perspectives to study genetic, infectious, and chronic diseases. The emphasis on evidence of disease in the past as well as the past’s influence on modern health, is inherently anthropological - holistic, cross-cultural, evolutionary, and ecological. In 2013, another descendent course emerged to fill a niche of student and faculty interest in Food and Human Evolution (FHE), concentrating on the role that nutrition and cooking have played in the evolution of modern humans. FHE uses the interaction between culture and biology to examine the role diet plays in adaptation, fitness, and health. As a part of George Mason’s University’s focus on undergraduate research, both are taught as “Inquiry” courses, actively involving students in examining primary literature, conducting data analysis, and giving presentations. Assessment shows that students successfully identify major concepts, are confident in their research skills, and have positive attitudes and opinions about the value of science.

13:00

Patricia Brito

Evolution of chaperon-usher pili in Escherichia coli

ABSTRACT. In pathogenic bacteria surface pili or fimbriae are crucial virulence factors that mediate attachment and infection of host epithelial cells. Among the different fimbrae produced by gram-negative Bacteria, the chaperon-usher (CU) are among the most well studied, in particular in Escherichia coli where each strain may harbor up to 16 different CU operons in its genome. These organelles are key targets for the development of vaccines but without a proper understanding of the mechanisms that generate and maintain diversity in this system, the development of effective vaccines may be hindered. In this study, we characterize the CU operons present in E. coli genomes isolated from clinical samples and associate their patterns of evolution to modes of infection. We show a complicate dynamic of fimbriae evolution with events of whole-operon duplication and lateral transfer, and distinct patterns of protein evolution. Some operons are highly conserved within E. coli with genes under purifying selection, while others show a remarkable rate of evolution with main structural genes showing patterns of polymorphism driven by recombination. These results are likely a consequence of ongoing bacterial-host interactions leading to the acquisition of host tissue adaptation.

13:00

Andrzej Galbarczyk, Magdalena Klimek, Ilona Nenko and Grazyna Jasienska

Number of sons and inflammaging among postmenopausal women

ABSTRACT. Sons and daughters differently influence maternal physiology in older age. The higher number of sons, but not the number of daughters, may negatively influence maternal health and may be associated with a shorter life span of mothers. Number of sons may also contribute to increased inflammaging, a chronic sub‐clinical systemic inflammatory state. Inflammaging is characterized by elevated levels of serum inflammatory mediators such as C‐reactive protein (CRP). The aim of this study was to determine the impact of number of children, and number of daughters and sons on serum CRP concentration among older women. This study was conducted amongst a rural Polish population. Serum CRP level was measured in 414 women, aged 45-92 (mean 61.8, SD 11.00), who had 4.0 (SD 2.15) children, including 2.1 (SD 1.49) sons and 1.8 (SD 1.43) daughters on average. Since CRP had a positively skewed distribution gamma regression models were used. There was no significant relationship between serum CRP level and the total number of children (β=1.03, p=0.338), after controlling for women’s age. However, serum CRP concentration was positively associated with the number of sons (β=1.13, p=0.027) but not with number of daughters (β=0.98, p=0.670), after adjusting for women’s age. During pregnancy sons are more energetically demanding and can induce an immune-response in the mother against the male-specific transplantation antigen (HY) which may persist for many years. Our results confirm that sons may have more pronounced immunological impact on the mother also in later life. The vast majority of the studies investigating trade-offs between reproduction and women’s health focus only on their lifetime reproductive effort, namely the total number of children born. Here we present another piece of evidence suggesting that number of children of each sex should be taken into account.

13:00

Francy Johanna Pérez Llanos, Doreen Beyer, Stefan Niemann and Susanne Homolka

Impact of host -pathogen mismatch in tuberculosis infections: Insights from a new infection model employing M. africanum and bovine macrophages

ABSTRACT. The causative agent of tuberculosis, M. tuberculosis complex (MTBC) strains has co evolved with the human populations since their migration out of Africa and subsequently with historic human migration events to become a globally successful pathogen. However, during these speciation process distinct lineages expanded globally (i.e. M. tuberculosis) and others like M. africanum (Maf) are restricted to the West African (WA) region with evidence of a reduced disease susceptibility in African people. It is hypothesized that Maf takes over the role as a specialist that is very well adapted to a particular host population and M. tuberculosis as generalists that can successfully transmit between genetically diverse host populations. Less is known how an evolutionary host-pathogen mismatch impacts on the pathobiology and transmissibility of MTBC bacteria. This study evaluate the genetic diversity and pathobiology of Maf-WA compared to other M.tuberculosis clinical isolates in a bovine macrophage model. So far, reproducibility of the infection in the microenvironment of the bovine macrophage was successful as well as different intracellular survival patterns were found. This study not merely set the foundation of a novel infection model but also gives insights to better understanding into overall successfulness of MTBC bacteria along with the evolutionary signatures of disease susceptibility.

13:00

Peter Takacs and Joshua Christie

Selected Effects Accounts of Dysfunction

ABSTRACT. A much-criticized view in the philosophy of medicine defines a pathological phenotype as one that fails to perform the function that it was selected for by evolution. Here we sidestep issues regarding whether this “selected effects” approach is a useful heuristic for characterizing pathological states and instead consider a more fundamental problem. The evolutionary definition presumes that when a phenotypic trait evolves by natural selection, some activity or activities of that phenotype, in interaction with ancestral environments, explains why ancestors with the phenotype proliferated or persisted. Selected effects accounts have recently been proposed for mental disorders, such as depression and generalized anxiety disorder. Two distinct approaches and seemingly inconsistent conclusions have subsequently emerged. One approach maintains that common mental disorders are objectively dysfunctional in an evolutionary sense and therefore focuses on elucidating the genetic mechanisms which maintain susceptibility. Others have argued that at least some common mental disorders might be developmental mismatches due to phenotypic plasticity and, although genuine disorders, are not dysfunctional from an evolutionary perspective. We introduce the early results from an interdisciplinary project that applies philosophical analysis and quantitative modeling to clarify how phenomena, such as mental disorders, are subject to the selected effects account of dysfunction.

13:00

Bria Dunham and Sara Hall

Robot Placentas in the Simulation Lab: The Shortcomings of Maternity Simulation Manikins in the Education of Advanced Practice Nursing Students

ABSTRACT. Popular maternity simulation manikins used in advanced practice nursing programs replicate a number of pathologies and processes using high-tech programming, but fall short at modeling physiologically normal, low-intervention birth in a naturalistic manner due to the mechanical limitations of the manikins along with the priorities of the designers and manufacturers. While these manikins can simulate postpartum hemorrhage, seizures, shoulder dystocia, and delivery of a cyanotic infant, they cannot be moved into squatting or sitting postures, be shown to walk around in labor, or get into a birth tub filled with water. By emphasizing technology over a full range of postures and labor support strategies, the design of these mannequins reinforces a passive role for laboring bodies and the notion that health care providers are really the ones who deliver babies—in opposition to an evolutionary perspective that emphasizes the human anatomical, physiological, and behavioral adaptations for birth, including the value of a dedicated care provider for physical and emotional support. This failure to model physiologically normal, low-intervention birth scenarios conditions advanced practice nursing students to expect that birth occurs exclusively or by default in the lithotomy position, pointing to a clear need for insights from evolutionary medicine in nursing education.

13:00

Stanislav Kotlyarov and Aleksei Bulgakov

Cholesterol regulation of innate immune system and its disorders due to smoking

PRESENTER: Stanislav Kotlyarov

ABSTRACT. Cholesterol is one of the most important biochemical parameters for humans. A number of recent researches suggest that reverse cholesterol transport (RCT) regulates not only the homeostasis of cellular cholesterol, but also innate immunity. Involvement of cholesterol in the innate immune response is mediated by ATP-transporter ABCA1, regulating RCT. By regulating the content of cholesterol in lipid rafts, it is involved in the activation of TLR, phagocytosis and regulation of apoptosis. ABCG1 plays an important role in atherogenesis. Objective: study the expression of genes ABCA1, ABCG1 in smoking. The analysis was carried out on previously studied data sets (gene sets) derived from Genes Expression Omnibus (GEO). Researching of alveolar macrophages in smokers (sets GSE2125, GSE8823) showed a significant decrease in the expression of genes ABCA1, ABCG1 compared with non-smokers. Researching of monocytes in patients with COPD (set GSE8808) showed a significant decrease in the expression of ABCA1 compared with healthy individuals, which emphasizes changes in the activation of monocytes in peripheral blood. This can serve as a mechanism of trained innate immune response in atherosclerosis in COPD patients. Genes expression in the airway epithelium in smokers showed conflicting results. There were not significant changes in the gene expression of ABCB1, ABCG1 in sets GSE4498, GSE994, GSE11906, though in sets GSE76324, GSE18385, GSE11784 gene expression of АВСА1 increased. Expression of ABCA3 significantly increased in smokers in sets GSE76324, GSE18385, GSE63127, GSE64614, GSE11906, GSE11784. Gene expression in alveolar epithelial type II cells in patients with COPD compared with healthy individuals (set GSE29133) showed a significant decrease in the expression of genes ABCA1, ABCG1. Thus, smoking disrupts the RCT in monocytes, macrophages and respiratory epithelium, which probably serves as a mechanism of progression of local and systemic inflammation through the mechanisms of the innate immune system.

13:00

Julia Kloos, João Gama, Joachim Hegstad, Ørjan Samuelsen and Pål Johnsen

Evolution towards reduced burden of clinical antibiotic resistance plasmids

ABSTRACT. The spread and maintenance of multidrug resistance plasmids (MDR) in clinical settings is a challenge to modern medicine and a puzzler to evolutionary biologists. The impact of resistance plasmids on host fitness is often detrimental, but adaptation processes during experimental evolution reduce plasmid cost. Various mechanisms compensate high-cost plasmids by improving and stabilizing host-plasmid relationships. We aimed to describe adaptive routes for a clinical low-cost carbapenemase-encoding plasmid from Klebsiella pneumoniae when introduced into an uropathogenic Escherichia coli isolate. We performed experimental evolution, fitness assays and whole genome sequencing (WGS) to understand compensation of the plasmid cost. After evolution we identified a clone where the cost of carrying a blaVIM-1-encoding plasmid was ameliorated. No mutations were found on the evolved plasmid. A cpdA non-synonymous mutation previously associated with media adaptation was identified in the chromosome. This adapted host also reduced the cost of an unrelated blaNDM-1-encoding, clinical plasmid. Three chromosomal target genes for adaptive changes, cpdA, arcA and crp, were identified at the population level. This was true for evolved plasmid-carrying, as well as evolved plasmid-free populations suggesting that these mutations occurred independently of plasmid carriage. Stability of MDR plasmids in new hosts depends on the adaptability of plasmid and host. We show increased fitness effect of a general media adaption on a plasmid-host relationship. The underlying mechanism leading to reduced plasmid cost requires further investigation, since it facilitates the persistence and spread of resistance plasmids.

13:30-14:00 Session 24: G.C Williams Prize winner Jessica Marie Hoffman

CHAIR: Randolph Nesse

LOCATION: Aula

13:30

Jessica Hoffman

Is antagonistic pleiotropy ubiquitous in aging biology?

ABSTRACT. Over 60 years ago, George Williams developed the idea that a major contributor to the evolution of senescence was antagonistic pleiotropy, a genetic mechanism by which alleles that increase early life fitness with deleterious effects in later life could be favored by selection. At the time, the idea was speculative in that no real-world examples of such alleles had been discovered. However, in the past twenty years, molecular biologists investigating mechanisms of aging have uncovered many such genes without generally realizing that they were relevant to a major theory of aging. Here, we present a brief review of specific examples of antagonistic pleiotropy in both wild and laboratory organisms. We find that whenever antagonistic pleiotropy has been searched for in earnest, it has been found. Interestingly, the pleiotropic effects are not always directly in the form of tradeoffs between reproduction and longevity but can include impacts on developmental timing and stress resistance as well. Overall, antagonist pleiotropy is common if not ubiquitous in aging biology with the implication that molecular mechanisms of aging are likely to be widely shared among organisms.

14:00-14:30 Session 25: Gilbert Omenn Prize winner Roderich Römhild

CHAIR: Isabel Gordo

LOCATION: Aula

14:00

Roderich Römhild

Hysteresis treatments: Exploiting cellular memory to prevent resistance evolution

ABSTRACT. Antibiotic resistance is a growing challenge. Resistance can rapidly emerge during treatment, due to the high potential of bacteria for rapid evolutionary adaptation. One approach to sustain the efficacy of antibiotics is to develop treatment strategies that inhibit resistance evolution. This talk will show an example of a new treatment strategy - hysteresis treatments - that inhibits resistance evolution by using available antibiotics in a new way. Hysteresis treatments exploit cellular phenotypic memory, which refers to long-lasting changes in cellular physiology induced by previous antibiotic exposures. Antibiotics can act as signals, and induce specific and long-lasting cellular responses, such as heat-shock response, motility and changes in membrane permeability. Bacterial responses are stabilized across generations and can have pleiotropic effects for treatment with other antibiotics. Cellular memory can harm bacteria, when they are treated with appropriate sequences of antibiotics. Using evolution experiments, mathematical modelling, genomics, and functional genetic analysis, we demonstrate that hysteresis treatments are highly efficient - they cause extinction at sub-MIC concentrations - and inhibit the evolution of resistance. Hysteresis treatments impose specific selective pressure on the bacteria that does not favour resistance mutations, but rather mutations causing cellular ignorance behaviour, or a loss of memory. Cellular hysteresis can be harnessed as a novel principle to optimise antibiotic therapy, in order to achieve both, enhanced bacterial elimination and reduced resistance evolution.

14:30-15:00 Session 26: Plenary Detlev Ganten

CHAIR: Frank Rühli

LOCATION: Aula

14:30

Detlev Ganten

Lessons learned from Evolution for the Implementation of the Sustainable Development Goals and Better Health for All

ABSTRACT. The cardiovascular system developed in multicellular organisms about 500 million years ago. Now cardiovascular diseases (CVD) present the most important burden of the non-communicable diseases worldwide. CVD are particularly suited for a holistic approach to health and disease based on our increasingly precise molecular understanding of evolution: genetic causes have been identified, basic mechanisms are elucidated and there are unique opportunities for treatment and prevention. Evolutionary medicine can make major contributions at all levels: research, treatment, prevention. Factors important for health and CVD in addition to our biology can be summarized as environmental (e.g. climate, poverty, hunger, pollution, urbanization, socio-economic factors) and lifestyle (e.g. education, nutrition, physical Activity). Epigenetic effects are increasingly recognized. They all contribute to, or are risk factors for, cardiovascular diseases such as hypertension, obesity, metabolic and kidney diseases, diabetes, heart failure.

This supports the lessons learned from evolution that biology, survival, reproduction, life and death cannot be understood if we do not include and consider the lifestyle and the environment. The 17 Sustainable Development Goals SDGs of the United Nations can be subdivided in exactly these 3 evolutionary categories: biology, environment and lifestyle. SDG 3 “Health and Well-Being for All” and the Action Plan of the World Health Organization (WHO), proclaimed at the World Health Summit 2018 in Berlin, are a milestone in this direction. It must be our collective goal to make a significant contribution. The holistic concept of Evolutionary Medicine can provide orientation for research and translation into better health for all.

15:00-15:15 Session 27: Closing notes

CHAIR: Randolph Nesse

LOCATION: Aula

15:30-17:00 Session 28: Cancelled--ISEMPH Executive Committee Meeting--Cancelled (no need for this meeting now)

CHAIR: Randolph Nesse

LOCATION: 203

16:00-17:00 Wax Moulages Museum guided tour

Please register on site at the registration desk. Places are limited.

18:00-22:00 Farewell Dinner University Tower

21:00-23:00 City night tour

There will be two groups, one starting at 20.45, one starting at 21.45

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