

Abstract Registration No: 1

Conference	ISEMP	ISEMPH
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Abstract no. 1
Abstract code
Title of abstract **NOD2 influences intestinal resilience and fungal signatures after antibiotic perturbation**

Author Moltzau Anderson, J.
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Co-Author(s) Nesse, R. Bharti,
Rehman, Kautz,
Paulsen, Rosenstiel,
Lipinski,
Pan,
Häsler,
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Topic Call for abstracts : ISEMPH conference

Abstract text In Crohn's disease, risk alleles on the NOD2 locus disrupt the NOD2 protein, which senses bacterial cell wall products and is highly expressed in intestinal epithelial cells. A disturbed resilience is hypothesized to be an environmental factor precipitating disease manifestation through this genetic variation. We aimed to investigate the resilience of the bacterial and fungal gut microbiota in response to antibiotic perturbation. Using a mouse model deficient in the Crohn's disease risk gene, NOD2, we administered broad-spectrum antibiotics and determined community composition with 16S and ITS1 sequencing. Additionally, the occurrence of resistance genes using qPCR was assessed. Antibiotics caused a significant increase in resistance genes and altered the microbial gut community in both genotypes. However, while bacterial diversity decreased, fungal diversity increased, and correlations between the bacterial and fungal microbiota were identified as co-occurrence or co-exclusion interactions. Interestingly, a phenotypic variation was observed, where the NOD2 genotype impaired bacterial resilience leading to delayed recovery. We demonstrate a complex relationship between gut bacteria and fungi, where antibiotic perturbation creates niche availability and the expansion of potentially opportunistic genera. Additionally, delayed recovery in the KO creates a 'window of opportunity', which may promote pathogen proliferation and the development of gastrointestinal inflammation.

Keywords NOD2

Keywords Resilience

Keywords Gut microbiome

Keywords Antibiotic resistance

Presentation pref. Oral presentation preferred (otherwise poster)

Additional file

Extra information

Presentation

Session Session 4B : Antibiotic resistance

Time 10:30 - 10:45

Date 20/08/2017

Location Red Room

Abstract Registration No: 2

Conference	ISEMP	ISEMPH
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Abstract no. 2

Abstract code

Title of abstract Antibiotic combination efficacy (ACE) network

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Co-Author(s) Rosenstiel,
Beardmore,
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Topic Call for abstracts : ISEMPH conference

Abstract text Fundamental evolutionary principles are key to alleviate the pressing challenge of antibiotic resistance. Rather than engaging in an open-ended arms race between compound discovery and resistance evolution, evolutionary thinking assists developing empirically-informed approaches with the double aim of minimizing resistance and extending the life span of existing drugs. Due to its enhanced potency and likelihood to reduce drug resistance evolution, the WHO has endorsed combination therapy as the first-line strategy to treat tuberculosis, malaria, or HIV. Yet for bacterial infections, current clinical guidelines do not factor in likely evolutionary trajectories towards resistance during treatment. Several novel antibiotic combination strategies, based on collateral sensitivities, high resistance costs, or antagonistic drug interactions, have been proposed recently to better mitigate resistance. We systematically assessed these by performing over 1800 evolution experiments complemented with network analysis. Our data indicates that combinations specifically composed by aminoglycosides and penicillins are consistently constraining antibiotic resistance evolution due to their strong synergistic interaction and the reciprocal collateral sensitivity among their components. Altogether our approach identified relevant evolutionary factors that enhance the predictability of drug resistance evolution.

Keywords Pseudomonas aeruginosa

Keywords Antibiotic resistance

Keywords Experimental evolution

Keywords Drug combinations

Presentation pref. Oral presentation preferred (otherwise poster)

Additional file

Extra information

Presentation

Session Session 4B : Antibiotic resistance

Time 10:15 - 10:30

Date 20/08/2017

Location Red Room

Abstract Registration No: 3

Conference	ISEMP	ISEMPH
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Abstract no. 3

Abstract code

Title of abstract **The Hypertension Pandemic: an Evolutionary Perspective**

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Co-Author(s) Bochud,
Devuyst,

Topic Call for abstracts : ISEMPH conference

Abstract text Hypertension is a highly prevalent multifactorial disease involving environmental and genetic factors together with risk-conferring behaviors. The hypertension pandemic has become the most critical and expensive public health problem. The ancestral susceptibility model postulates the positive selection of variant of salt retaining genes (<i>AGT</i> and <i>CYP3A5</i>) that confer a selective advantage in a salt scarce environment. During the neolithic the development of food preservation by salting made the ancestral alleles no longer confer protection but rather increase the susceptibility to hypertension. The rapid change (in terms of evolution) from a low salt to a high salt diet in most Westernized countries did not allow adaptation by selection of « salt-losing » genes (1). The other model postulates that, among environmental factors, pathogens have posed a major, if not the main selective pressure. This model is supported by the distribution of an ancestral frequent variant of the uromodulin gene (<i>UMOD</i>) associated with risk of hypertension. The dual role of uromodulin as a protective against infection and as salt retaining in the kidney may explain this observation.
(1) Rossier BC et al. Epithelial sodium transport and its control by aldosterone: the story of our internal environment revisited. <i>Physiological Reviews</i> 95: 297-340, 2015.

Keywords hypertension pandemics

Keywords angiotensin (AGT)

Keywords uromodulin (UMOD)

Keywords Renin-Angiotensin-Aldosterone-

Presentation pref. Oral presentation (no poster)

Additional file

Extra information

Presentation

Session Session 2A : Metabolic and cardiovascular diseases

Time 12:45 - 13:00

Date 19/08/2017

Location Round Room

Abstract Registration No: 4

Conference	ISEMP	ISEMPH
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Abstract no. 4
Abstract code
Title of abstract **Is cancer a side effect of evolution? Epidemiological and other evidence**

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Co-Author(s)

Topic Call for abstracts : ISEMPH conference

Abstract text Humans exhibit much high incidence of cancer, especially some special forms like breast and colon cancer, when compared with other mammals (even primates). Breast and colon cancer are associated with mutations in DNA repair genes. On 2014 I described an evolutionary procedure, explaining this high incidence. Accumulated genetic variation in DNA repair genes may be beneficial under extreme environmental conditions. Partially unstable DNA repair system raises mutagenesis rate and probability for an advantageous mutation to appear. Comparison of the last ice-age (extreme conditions) map with cancer incidence maps reveals high similarity. Human populations may have experienced extended group selection at the past, where sub-populations with less efficient DNA repair system survived. This phenomenon is known for years in bacteria. Under extreme conditions (eg starvation), "mutator" strains with mutated DNA repair genes (same genes found mutated in colon cancer) appear in cultures. Additionally, recent published data support the idea that there is increased genetic diversity in glaciation areas. I found also published evidence that many species that have evolved in not previously glaciated areas (Africa) have low incidence of cancer. Concluding, an evolutionary model is proposed for how populations escape extinction, exhibiting high cancer incidence long time after, an evolution "side-effect".

Keywords DNA repair genes
Keywords evolution and cancer
Keywords evolution under extreme
Keywords group selection
Presentation pref. Oral presentation (no poster)

Additional file
Extra information

Presentation

Session Session 4A : Cancer
Time 10:00 - 10:15
Date 20/08/2017
Location Room 4

Abstract Registration No: 5

Conference	ISEMP	ISEMPH
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Abstract no. 5

Abstract code

Title of abstract **Highly polymorphic loci through allelic division of labour: a mathematical model of heterozygote advantage**

Author Siljestam,
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Co-Author(s) Rueffler,

Topic Call for abstracts : ISEMPH conference

Abstract text Heterozygote advantage is a well-supported mechanism for the maintenance of single locus dimorphism. It is a biologically plausible mechanism acting in many highly polymorphic immune genes, such as the MHC genes. However, there is no theoretical support that heterozygote advantage is able to maintain high degrees of polymorphism, and other mechanisms are often acknowledged. Here, we present a novel mathematical model of allelic evolution in which the gene products of the alleles at a focal diploid locus are responsible for two or more tasks needed for survival, e.g., the induction of immune defence against different pathogens. In our model, a high degree polymorphism can evolve through evolutionary branching. If gene products are involved in two tasks up to 20 alleles can potentially coexist, while for five tasks the number of coexisting alleles can exceed 100. We conclude that heterozygote advantage alone has the potential to explain the high degree of allelic polymorphism found at e.g. MHC loci.

Keywords MHC diversity

Keywords Heterozygote advantage

Keywords Adaptive dynamics

Presentation pref. Oral presentation preferred (otherwise poster)

Additional file

Extra information

Presentation

Session ISEMPH abstracts during ESEB

Time 09:00 - 17:00

Date 21/08/2017

Location

Abstract Registration No: 7

Conference	ISEMP	ISEMPH
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Abstract no. 7

Abstract code

Title of abstract **Fitness-Reducing Cis- and Retrograde Trans-Generational Extended Phenotypes in Association with Autism**

Author Greenspan,
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Co-Author(s)

Topic Call for abstracts : ISEMPH conference

Abstract text In his 1982 book "Extended Phenotype," Richard Dawkins defined the concept of extended phenotype as a trait(s) attributable to a gene in one organism that is manifested in a second organism. A gene in a pathogen or parasite that influences the phenotype of a host provides an example of this phenomenon. Dawkins added the requirement that the extended phenotype must provide a fitness increment for the organism possessing the gene in question. I have observed that some parents of children affected by autism choose to have no additional children. There are now well over 100 genetic variants associated with conditions falling under the diagnostic umbrella of autism. In those cases where a genetic variant in a child (whether of standard parental origin or due to *de novo* mutation in parental germ cells or progeny) causes phenotypes in the child that in turn burden the parents, some parents may alter their reproductive plans by ceasing further attempts to procreate. In a sense, the phenotypes associated with a gene or genes in the progeny have, however indirectly, caused reduced parental reproductive fitness. Existing data are consistent with this perspective. I intend to initiate new studies with more definitive study designs.

Keywords autism

Keywords extended phenotype

Keywords transgenerational

Keywords gene

Presentation pref. Oral presentation (no poster)

Additional file

Extra information

Presentation

Session Session 3B : Cognition and aging

Time 17:00 - 17:15

Date 19/08/2017

Location Red Room

Abstract Registration No: 8

Conference	ISEMP	ISEMPH
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Abstract no. 8

Abstract code

Title of abstract Evolutionary nephrology: changing vulnerability of the kidney from birth to senescence

Author Chevalier,
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Co-Author(s)

Topic Call for abstracts : ISEMPH conference

Abstract text Evolutionary medicine has made significant contributions to the disciplines of infectious disease, immunology, and oncology, but nephrology remains comparatively neglected. Whereas chronic kidney disease (CKD) affects 10% of the world's population, current therapies are ineffective and based on physiologic adaptation by remaining nephrons: glomerular hyperfiltration resulting from nephron hypertrophy. These proximate causes ignore ultimate causes that can be explained by evolutionary adaptation of our ancestors from marine to freshwater to terrestrial environments. This evolutionary history resulted in energy-consuming mammalian nephrons surrounded by a hypoxic, hyperosmolar microenvironment vulnerable to ischemia and oxidative injury. Natural selection favors successful energy investment strategy: energy is allocated to maintenance of nephron integrity through reproductive years, but this declines with senescence. Risk factors for CKD include restricted fetal growth or preterm birth (tradeoff resulting in fewer nephrons), evolutionary selection for APOL1 mutations (tradeoff that provides resistance to trypanosome infection), and Western diet leading to diabetes and hypertension (mismatch). Marked variation in nephron number at birth, nephron heterogeneity, and changing susceptibility to kidney injury throughout life history result from evolutionary processes. Combined application of molecular genetics, evolutionary developmental biology (evo-devo), developmental programming and life history theory can yield new strategies for prevention and treatment of CKD.

Keywords Nephrology

Keywords Chronic kidney disease

Keywords adaptation

Keywords life history

Presentation pref. Oral presentation preferred (otherwise poster)

Additional file

Extra information

Presentation

Session Session 6A : Different topics

Time 15:30 - 15:45

Date 20/08/2017

Location Round Room

Abstract Registration No: 9

Conference	ISEMP	ISEMPH
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Abstract no.

9

Abstract code

Title of abstract

The Polycystic Ovary Syndrome and the Flexible Response Model of Human Reproduction

Author

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Co-Author(s)

Topic

Call for abstracts : ISEMPH conference

Abstract text

Polycystic Ovary Syndrome (PCOS), the most common cause globally of ovarian infertility, is a condition defined by the presence of polycystic ovaries, hyperandrogenism and infrequent menstruation and is strongly associated with obesity and insulin resistance. As a heritable cause of infertility it is an evolutionary paradox which has attracted much evolutionary speculation. Its origins have been ascribed to thrifty genes, and/or advantages for mothering, musculoskeletal development, reproductive longevity and childhood survival. More recently persuasive evidence has emerged that non adaptive evolution, genetic drift or sexually antagonistic selection, has allowed the trait to persist in human populations.

However this non adaptive scenario has two flaws. It rests on an assumption of invariance in the prevalence of PCOS among human populations and fails to adequately explain the strong association of PCOS with insulin resistance and Type 2 diabetes. When population based studies of PCOS prevalence which both include lean women and which scrutinise closely changes in prevalence with increasing BMI, ethnicity related differences are evident. The Flexible Response model of human reproduction provides a theoretical framework to explain how an insulin resistant metabolic and reproductive phenotype such as PCOS may under different conditions either decrease or increase fitness and lifetime reproductive success.

Keywords

Polycystic Ovary Syndrome

Keywords

Life History Evolution

Keywords

Type 2 Diabetes

Presentation pref.

Oral presentation (no poster)

Additional file

Extra information

Presentation

Session

Session 1B : Women's health

Time

10:45 - 11:00

Date

19/08/2017

Location

Red Room

Abstract Registration No: 10

Conference	ISEMP	ISEMPH
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Abstract no. 10

Abstract code

Title of abstract **The French or Mediterranean Paradox and Life History Evolution**

Author Corbett,
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Co-Author(s)

Topic Call for abstracts : ISEMPH conference

Abstract text The markedly lower rates of cardiovascular disease in France and southern Europe presented a major challenge to the prevailing dietary fat-heart hypothesis and led directly to the promulgation of the health benefits of the Mediterranean diet. What has been overlooked is another obvious factor which these countries all share -short stature. Human height is highly heritable and the observed European north-south gradient in height also has a strong genetic basis. At the same time economists or more precisely cliometricians know that human height is a summary measure of the standard of living, and varies with population density, nutrition and demographic expansion and contraction. The populations of each these countries share, at different times, a history of unremitting poverty extending over centuries due to vast income inequalities, mercantilist economies, land degradation and tenure arrangements dating back to Roman times, and high population densities. Under these conditions stunting may be a successful life history strategy to ensure sufficient energetic investment in reproduction and survival. The plastic and adaptive responses of human populations, and particularly of those involving insulin and insulin like growth factors may underpin the apparent immunity of Mediterranean people to cardiovascular disease in a world characterised by nutritional excess.

Keywords Stunting

Keywords The French Paradox

Keywords Insulin metabolism

Keywords Life History Evolution

Presentation pref. Oral presentation (no poster)

Additional file

Extra information

Presentation

Session Session 2A : Metabolic and cardiovascular diseases

Time 12:00 - 12:15

Date 19/08/2017

Location Round Room

Abstract Registration No: 13

Conference	ISEMP	ISEMPH
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Abstract no. 13

Abstract code

Title of abstract Behavioural deficiencies: the missing link in our understanding of complex disorders

Author Watve,
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Co-Author(s)

Topic Call for abstracts : ISEMPH conference

Abstract text Every behavior is associated with neuro-endocrine pathways through both causal and consequential links evolved to support a wide range of behavioral syndromes or personalities. Physically aggressive behavior increases the probability of injuries and therefore aggression related neuroendocrine processes enhance peripheral immunity and wound healing mechanisms including growth factors such as EGF, NGF, VEGF, FGF, BDNF, PDGF. Deficiency of growth factors is implicated in a variety of complex disorders. Insulin, leptin, cholesterol and cortisol have demonstrable cognitive and behavioral functions and therefore their expression is responsive to behavioral requirements of a lifestyle. The behavior associated brain monoamines have a role in determining bone strength and insulin sensitivity. An emerging concept is that many of the pathophysiological components of the complex disorders typical of modern urban life style are a result of deficiencies of specific evolved behaviors. Similar to dietary deficiencies it should be possible to treat behavioral deficiencies by appropriate supplementation. The role of exercise according to this concept is not burning calories but to supplement the deficient behaviors. Most active sports mimic hunter gatherer behaviors. Recognizing the role of behavioral deficiencies is likely to be the next major conceptual revolution in medicine after germ theory, dietary deficiencies and genetic disorders.

Keywords behavioral strategies

Keywords behavior-physiology interface

Keywords non-communicable diseases

Keywords life style

Presentation pref. Oral presentation (no poster)

Additional file

Extra information

Presentation

Session Session 5A : Theoretical considerations and animal models

Time 12:00 - 12:15

Date 20/08/2017

Location Room 4

Abstract Registration No: 14

Conference	ISEMP	ISEMPH
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Abstract no. 14

Abstract code

Title of abstract Disease Spread in Age Structured Populations with Maternal Age Effects

Author Clark,
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Co-Author(s) Garbutt,
McNally,
Little,

Topic Call for abstracts : ISEMPH conference

Abstract text Extrinsic mortality will determine population age structure, which in turn will influence disease spread when individuals of different ages differ in susceptibility, or when maternal age determines offspring susceptibility. Our experiments show that *Daphnia magna* offspring born to young mothers are more susceptible to the specialized parasite *Pasteuria ramosa*, than those born to older mothers. Previous observations show that susceptibility declines with age in this system. We used a Susceptible-Infected compartmental model to investigate how age specific susceptibility and maternal age effects on offspring susceptibility interact with demographic factors to affect disease spread. Our results show a scenario where an increase in extrinsic mortality drives an increase in transmission potential and so we identify a realistic context, in which age effects and maternal effects produce conditions favouring disease transmission. Ongoing experiments are investigating genotypic variation in age effects on parasite fitness.

Keywords Epidemiology

Keywords Age

Keywords Maternal Effects

Presentation pref. Oral presentation preferred (otherwise poster)

Additional file

Extra information

Presentation

Session ISEMPH abstracts during ESEB

Time 09:00 - 17:00

Date 21/08/2017

Location

Abstract Registration No: 16

Conference	ISEMP	ISEMPH
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Abstract no. 16

Abstract code

Title of abstract Evolutionary tradeoff theory of virulence and vector borne diseases

Author Pandey,
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Co-Author(s)

Topic Call for abstracts : ISEMPH conference

Abstract text Paul Ewald in his verbal model predicted that vector-borne diseases should be more virulent compared to directly transmitted infections. Diseases like Malaria, Dengue, visceral leishmaniasis, Yellow fever and sleeping sickness were cited in support of this argument. It was argued that vector-borne pathogens can be transmitted even from severely ill immobile hosts. Ewald also emphasised that immobile and sicker hosts are easy targets for mosquito bites compared to healthy moving host and this is what makes vector-borne diseases more virulent. However, I would like to present a counter view on this. In a case of diseases like Malaria, Dengue, Zika and Yellow fever almost 75% to 90% of the infections are asymptomatic and can still act as a reservoir for the disease transmission. There is ample data to suggest that it is the mobile and healthy host that transmit in a majority of the cases and not the sick ones. Diseases like Dengue, Zika, Yellow fever and Chikungunya cause self-limiting mild illness even in symptomatic hosts and a very small percentage of hosts get serious life threatening illness. We suggest reconsidering the conventional model of transmission mode and virulence for vector-borne diseases.

Keywords Vector-borne diseases

Keywords Dengue

Keywords Malaria

Keywords Zika

Presentation pref. Oral presentation (no poster)

Additional file

Extra information UMERIC

Presentation

Session Session 3A : Pathogens

Time 16:30 - 16:45

Date 19/08/2017

Location Round Room

Abstract Registration No: 17

Conference	ISEMP	ISEMPH
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Abstract no. 17

Abstract code

Title of abstract **Milder forms of obesity may be a good evolutionary adaptation: Fitness First'hypothesis'**

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Co-Author(s) Parakadavathu,

Topic Call for abstracts : ISEMPH conference

Abstract text The prevalence of obesity is increasing and is considered maladaptive. However, contrary to popular belief, recent studies have shown that people with milder grades of adiposity survive better (obesity paradox), both in normal and adverse conditions. Several new observations have been made on how insulin resistance accompanying obesity may be beneficial in selected situations. Insulin resistance operates at the post receptor level and selectively involves the P3K pathway controlling glucose metabolism while leaving the MAP kinase pathways intact, which promotes somatic growth. In insulin-resistant states, glucose is shunted away from the glycolytic pathways to the pentose phosphate pathway generating more NADPH for combating stress. Mild obesity improves survival probability but at the same time decreases fertility. Anthropological evidence shows that humans produce fewer children in resource-rich environments, leading to improved biological fitness of progeny. This attempt examines the situation of the obesity epidemic from a fresh evolutionary point of view, discusses and integrates the evidence from medicine, molecular biology, evolution and anthropology, and hypothesizes that milder forms of adiposity may be an evolutionary adaptation of humans to a resource-rich environment -a mechanism improving survival and promoting investment in fewer offspring, thereby improving the biological fitness of the race.

Keywords Obesity

Keywords Evolutionary origins of obesity

Keywords obesity paradox

Presentation pref. Oral presentation (no poster)

Additional file

Extra information

Presentation

Session Session 2A : Metabolic and cardiovascular diseases

Time 12:15 - 12:30

Date 19/08/2017

Location Round Room

Abstract Registration No: 18

Conference	ISEMP	ISEMPH
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Abstract no. 18

Abstract code

Title of abstract **Were language borders 'cultural' barriers for the spread of influenza 1889-94 and 1918-19 in the canton of Bern, Switzerland?**

Author Staub,
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Co-Author(s) Floris,
Bender,
Gemperle,
Rühli,
Staub,

Topic Call for abstracts : ISEMPH conference

Abstract text Airborne infectious diseases such as influenza spread where people meet and communicate with each other. However, historically stable language borders might keep people from intermix and communicate. It is well known that Swiss language borders serve as a historically stable proxy for diverse cultures and are an obstacle for population exchange. The presented preliminary results follow the hypothesis that language borders in Switzerland served as 'cultural' barriers for the spread of influenza in the bilingual Canton of Bern, Switzerland. Because influenza and other infectious diseases were widespread in 19th and early 20th century Switzerland the cantonal and national authorities kept detailed records to monitor these epidemics based on reporting obligations. For the canton of Bern, the severe influenza epidemics of 1889-1994 and 1918-19 are particularly well documented (weekly community data). We analyse the weekly spread of influenza (number of new infections and deaths) on the level of communities and compare the epidemics 1889-1994 and 1918-19. We take in account demographic as well as economic information on the municipalities as well as traffic route networks. Our results shall inform predictions of infectious disease spread in the light of modern population movements like travelling and migration where different language barriers are crossed.

Presentation pref. Oral presentation preferred (otherwise poster)

Additional file

Extra information

Presentation

Session ISEMPH abstracts during ESEB

Time 09:00 - 17:00

Date 21/08/2017

Location

Abstract Registration No: 19

Conference	ISEMP	ISEMPH
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Abstract no. 19
Abstract code
Title of abstract **Identifying genomic adaptations to rice-based diet in asian populations**

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Co-Author(s) Gnecci Ruscone, Bortolini,
Yu, Gentilini,
Landini, Di Blasio,
Abondio, Luiselli,
De Fanti, Pettener,
Sarno, Bortolini,

Topic Call for abstracts : ISEMPH conference

Abstract text Introduction of massive rice consumption in some pre-agricultural Asian populations and then in agricultural ones has plausibly represented one of the most relevant challenges for *H. sapiens* metabolism after the Out of Africa expansion. Among domesticated cereals, rice shows the highest carbohydrates content and glycaemic index, prompting rapid increase in glycaemia that makes its usual ingestion a potential risk factor for developing insulin resistance and metabolic diseases. This new selective pressure on insulin-related pathways may have triggered genetic adaptation of long-term rice-feeding populations against the dangerous side effects of their diet. To test such a hypothesis, we assembled a genome-wide dataset made up of 2,483 subjects from 129 South Asian/East Asian groups representative of human genetic variation observable at geographical areas where wild rice originated and was first domesticated. We used it to detect genomic signatures of natural selection and to test whether known candidate genes involved in modulation of insulin metabolism were enriched in the identified set of adaptive loci. The obtained results pinpoint some of the drivers of adaptive evolution occurred in Asian populations that are potentially responsible for maintenance of physiological glycaemia even after substantial rice consumption.
This work was supported by ?ERC-2011-AdG295733 to DP.

Keywords Asian Populations

Keywords Rice-based Diet

Keywords Metabolic Risk

Keywords Natural Selection

Presentation pref. Oral presentation preferred (otherwise poster)

Additional file

Extra information

Presentation

Session Session 6A : Different topics

Time 15:15 - 15:30

Date 20/08/2017

Location Round Room

Abstract Registration No: 21

Conference	ISEMP	ISEMPH
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Abstract no. 21

Abstract code

Title of abstract **The influence of omega-3 fatty acids on the development of human cognition: systematic review and meta-analysis**

Author Bender,
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Co-Author(s) Lehner,
Staub,
Häusler,
Rühli,

Topic Call for abstracts : ISEMPH conference

Abstract text Scientific research points to a possible role of fish and other aquatic food in the development of the brain in hominin evolution on the one hand, and for the development and health of today's human brains on the other hand. In fact, omega-3 long-chain polyunsaturated fatty acids (LC-PUFA), especially eicosapentaenoic acids (EPA) and docosahexaenoic acids (DHA), seem to play a role in human learning capacity and behaviour. In recent years, several systematic reviews and meta-analyses were done about cognitive development in toddlers and school-age children after fish oil supplementation in their mothers during pregnancy and/or lactation or later during childhood, all with an unclear result. To clarify this question, we perform a systematic review and meta-analysis on these associations, including recent studies and additionally assessing the relevance of the $\omega_6 : \omega_3$ ratio, the ratio of PUFA to saturated fatty acids in the diet or supplementation, the basic level of ω_3 in the mothers or children before the intervention, and the time point of supplementation during brain development. The results will be interpreted in the light of hypotheses on human evolution that discuss the association between food resources and brain development in different environmental contexts.

Keywords Nutrition

Keywords Cognition

Keywords Omega3

Presentation pref. Oral presentation preferred (otherwise poster)

Additional file

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Presentation

Session Session 3B : Cognition and aging

Time 16:30 - 16:45

Date 19/08/2017

Location Red Room

Abstract Registration No: 22

Conference	ISEMP	ISEMPH
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Abstract no. 22

Abstract code

Title of abstract Care as Human Condition - An Evolutionary Psychology of Sickness and Healing

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Co-Author(s)

Topic Call for abstracts : ISEMPH conference

Abstract text Care of the sick has been a crucial part of human social life since Paleolithic times. Certainly, ancient care did not involve modern means such as injections, x-rays, and medical machinery, but was based on extensive support from the group, such as sharing food with sufferers, absolving them from duties, and simple medical procedures. Even though these early precursors were not as effective as modern healthcare, they could still make crucial contributions to the chance of survival and recovery. The long existence of healthcare encounters and the fitness relevance of their outcome suggests that humans developed adaptations for problems incorporated in the sick role and the helper role. As the talk proposes, such "sickness-healing adaptations" could offer evolutionary explanations for important phenomena in medical research. The talk integrates recent empirical findings and theoretical developments on heterogeneous topics such as pain modulation and pain empathy, disgust and the behavioral immune system, overmedication, racial discrimination in treatment, therapeutic effects of compassionate care and the placebo effect. The talk develops an evolutionary framework for the understanding of healthcare encounters and, thereby, points out how evolutionary medicine could study not only disease, but also healing.

Keywords therapeutic encounter

Keywords patient-practitioner relationship

Keywords placebo effect

Keywords evolutionary psychology

Presentation pref. Oral presentation (no poster)

Additional file

Extra information

Presentation

Session Session 2B : Culture, gender and sexual health

Time 12:00 - 12:15

Date 19/08/2017

Location Red Room

Abstract Registration No: 24

Conference	ISEMP	ISEMPH
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Abstract no. 24
Abstract code
Title of abstract **The genomic basis of experimental evolution of aging in Drosophila: how individual SNPs affect lifespan**

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Co-Author(s) Seddon,
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Keller,
Zwaan,
Flatt,

Topic Call for abstracts : ISEMPH conference

Abstract text Both diet and reproduction are known to have a strong influence on lifespan and aging in a wide range of animal species. We study a unique set of experimentally evolved (EE) *Drosophila melanogaster* lines that have adapted their life history in response to selection for postponed reproduction and/or coping with developmental over- or undernutrition. In particular, the lifespan phenotype has evolved, which includes increased longevity in late reproducing lines and interactions with the nutritional environment. Our genome analyses have revealed consistent differences in SNP allele frequencies that correlate with this differentiation in lifespan. To test how alternative SNP alleles affect lifespan, we reconstituted outbred populations that differ consistently only at the specific SNP position of interest by using lines from the *Drosophila* Genetic Reference Panel (DGRP). We used this approach to test five SNPs in genes from different genetic pathways: the insulin/TOR signalling pathway member *hppy*, the LAMMER protein kinase *Doa*, the nuclear hormone receptor *Eip75B*, and the immune gene *sickie*. Our experiments demonstrate that individual SNPs have strong and consistent effects on adult survival, can either extend or shorten lifespan and be sex-specific. We discuss our results in the broader context of the correlated evolution of life history traits.

Keywords Aging

Keywords Genome

Keywords Life History

Keywords Experimental Evolution

Presentation pref. Oral presentation preferred (otherwise poster)

Additional file

Extra information

Presentation

Session Session 3B : Cognition and aging

Time 17:15 - 17:30

Date 19/08/2017

Location Red Room

Abstract Registration No: 26

Conference	ISEMP	ISEMPH
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Abstract no. 26

Abstract code

Title of abstract **In utero sensitization and induction of tolerance to parasite antigens: Is transplacental immunization a mechanism for the inheritance of immunological strategies?**

Author Blackwell,
University of California - Santa Barbara; United States of America; Tel: +18052532796, blackwell@anth.ucsb.edu

Co-Author(s)

Topic Call for abstracts : ISEMPH conference

Abstract text Infants born to parasite infected mothers can mount an immune response to parasite antigens, as if they had themselves been exposed to these parasites, despite very few cases of actual infection across the placental barrier. Because the transplacental transmission of antigens can induce tolerance to parasites in infants, and subsequently greater odds of becoming infected, many researchers have considered this transmission to be a non-adaptive byproduct of maternal infection. However, a reassessment of the evidence suggests this may not be the case. Transmission of antigens across the placental barrier is both ubiquitous across parasite infections and an active processes, requiring specialized mechanisms to transport antigen and suggesting adaptive design. Additionally the outcome of exposure in infants is variable, with some infants developing immunity and others developing tolerance. Despite higher rates of infection, tolerance may actually be optimal in many circumstances, for example when pathology is caused not by infection but by over-exuberant immune responses, or when resources are limited and immune responses are costlier than they are effective. These observations suggest that mechanisms may exist that allow for the non-genetic transmission from mother to infant of not only antigens, but immunological strategies for dealing with particular types of infection.

Keywords immune function

Keywords pregnancy

Keywords non-genetic inheritance

Keywords parasites

Presentation pref. Oral presentation preferred (otherwise poster)

Additional file

Extra information

Presentation

Session Session 5B : Microbiome

Time 12:00 - 12:15

Date 20/08/2017

Location Red Room

Abstract Registration No: 29

Conference	ISEMP	ISEMPH
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Abstract no. 29

Abstract code

Title of abstract Host-parasite coevolution: from experimental evolution studies to evolutionary medicine

Author Kurtz,
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Co-Author(s)

Topic Call for abstracts : ISEMPH conference

Abstract text Parasites and pathogens are important determinants of human health and have shaped the evolution of our immune system. Understanding the evolutionary processes underpinning host-parasite coevolution is thus of major importance also for medical research, but difficult to address in human hosts. In this contribution, I will present findings from experimental systems that can be studied in the lab, such as the red flour beetle as a host and bacteria as micro-parasites. Understanding the genetic processes underlying bacterial rapid adaptation and host immune system evolution might also be of medical relevance. As an outlook, I will briefly explore the potential value of invertebrate hosts for experimental studies of evolving bacteria in human hosts.

Keywords host-parasite coevolution

Keywords immunity

Keywords bacteria

Presentation pref. Oral presentation preferred (otherwise poster)

Additional file

Extra information UMERIC

Presentation

Session ISEMPH abstracts during ESEB

Time 09:00 - 17:00

Date 21/08/2017

Location

Abstract Registration No: 30

Conference	ISEMP	ISEMPH
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Abstract no. 30

Abstract code

Title of abstract Evolution of human immunity during last several millennia

Author Morozova,
Institute of Evolutionary Medicine, University of Zurich; Switzerland; Tel: +41 44 635 05 2,

Co-Author(s) Bruskin,
Chekalin,
Rühli,

Topic Call for abstracts : ISEMPH conference

Abstract text One of the key points for understanding of human defense mechanisms and for proper treatment of patients is the knowledge of immune system evolution. Using comparative genomics, we traced the transformation of human immune system during last several thousand years. Analysis of biochemical and signaling pathways directly indicating selection signals allowed us to detect the most dynamic parts in human immunity. These are the processes which are connected with adaptive immune response, autoimmune disorders, and nonspecific response to pathogens.

Our results showed that evolution changes in some pathways can influence other ones. For some of them, this connection is direct (for example, HLA-mediated processes), while for others there are more complex interactions involving a number of additional, both internal and environmental, factors. Understanding these relationships is crucial for supporting the balance in the human body during the treatment of immune diseases of different etiologies.

Overall, we believe that our results represent the important step to deciphering of human immune system mechanisms, which, in turn, can help to form the basis for development of new therapeutic treatment.

Keywords human immune system

Keywords human evolution

Keywords immune response

Presentation pref. Oral presentation (no poster)

Additional file

Extra information UMERIC

Presentation

Session Session 1A : Immune system

Time 10:00 - 10:15

Date 19/08/2017

Location Round Room

Abstract Registration No: 33

Conference	ISEMP	ISEMPH
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Abstract no. 33

Abstract code

Title of abstract **Natural selection, mismatch, and differences in female human true pelvis morphology with respect to age**

Author Auerbach,
The University of Tennessee; United States of America; Tel: 8659744408, auerbach@utk.edu

Co-Author(s)

Topic Call for abstracts : ISEMPH conference

Abstract text Recent studies call into question whether human pelvic morphology reflects evolutionary tradeoffs suggested in the obstetrical dilemma, in which responses to competing selection pressures for obstetrical sufficiency and locomotor efficiency shape the pelvis. Nevertheless, dimensions of the true pelvis likely evolved in response to selection pressures for parturition of large fetuses. Thus, females with narrow bony birth canals may have encountered difficulties in childbirth in the past, even though recent research shows that fetal size and maternal size covary, lessening the possible selection pressure that might result from mismatches in fetal and maternal size. Age-at-death in females recovered from archaeological contexts is correlated with dimensions of the true pelvis, with younger females exhibiting narrower dimensions, a pattern not observed in males. Here, I examine whether selection motivated the relationship between female age-at-death and true pelvis dimensions. The effects of age-at-death, sex, and morphological integration were observed against fourteen pelvic dimensions taken from 188 females and 139 males. Comparisons show no support for selection against narrow dimensions, though females dying at younger ages have narrower pelvic canals. Further analysis indicates that the pelvis continues to grow throughout early adulthood, but growth is not driven by any single region of the pelvis.

Keywords obstetrical dilemma

Keywords integration

Keywords variation

Keywords human evolution

Presentation pref. Oral presentation (no poster)

Additional file

Extra information UMERIC

Presentation

Session Session 2B : Culture, gender and sexual health

Time 12:30 - 12:45

Date 19/08/2017

Location Red Room

Abstract Registration No: 35

Conference	ISEMP	ISEMPH
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Abstract no.	35
Abstract code	
Title of abstract	Does early infection shape the rate of aging? An experimental test with pro- and anti-inflammatory parasites
Author	Sorci, CNRS; France; Tel: +33380399028, gabriele.sorci@u-bourgogne.fr
Co-Author(s)	Guivier, Lippens, Faivre,
Topic	Call for abstracts : ISEMPH conference
Abstract text	<p>While the antagonistic pleiotropy hypothesis has provided a fertile ground of investigation to explain the evolution of aging, the physiological functions underlying it remain poorly known. Early work, based on the analysis of age specific mortality rate of human cohorts, suggested that infection-induced inflammation at early age might have deleterious effect on late survival. Evidence based on historical human data is, however, correlative by nature and prone to the potential confounding effects. We experimentally tested the idea that the inflammatory response has antagonistic pleiotropic functions with benefits in early life in terms of protection towards infection and costs in late life in terms of accelerated senescence. To this purpose we ran two experiments. In one experiment, young mice were infected with <i>Plasmodium yoelii</i> which stimulates the pro-inflammatory response. In another experiment, young mice were infected with the gut nematode <i>Heligmosomoides polygyrus</i> which dampens the inflammatory response. Infected and control mice were subsequently monitored during their entire lifespan. We found little support to the hypothesis. Early infection with pro-inflammatory parasites did not accelerate aging, lifespan being similar across the different experimental groups. On the contrary, infection with anti-inflammatory parasites did accelerate age-specific mortality and resulted in reduced longevity.</p>
Keywords	aging
Keywords	infection
Keywords	inflammation
Keywords	antagonistic pleiotropy
Presentation pref.	Oral presentation (no poster)
Additional file	
Extra information	UMERIC

Presentation

Session	ISEMPH abstracts during ESEB
Time	09:00 - 17:00
Date	21/08/2017
Location	

Abstract Registration No: 37

Conference	ISEMP	ISEMPH
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Abstract no. 37

Abstract code

Title of abstract Infeering clonal mutations from in silico model of intratumour heterogeneity

Author Opasic,
Max Planck Institute for Evolutionary Biology; Germany; Tel: + 49 45227635, opasic@evolbio.mpg.de

Co-Author(s)

Topic Call for abstracts : ISEMPH conference

Abstract text The discovery of cancer heterogeneity and clonal evolution added a further layer of complexity upon biology of cancer and its treatment. Thus, ability to correctly distinct clonal from subclonal mutations became important for making the right therapeutic choice. We investigate the effect of biopsy size on the ability to identify truly clonal alteration from multi-region profiling of tumours. We simulated neoplastic growth and dynamics of tumour heterogeneity in structured and unstructured populations in order to generate mutational profiles. Different sampling strategies were then compared on generated data. We found that biopsy size affects the ability to correctly estimate the sizes of two populations after the first bifurcation in phylogenetic history of each tumour, which the crucial parameter for classification of clonal mutations. In all simulated scenarios accuracy of estimation decreased or stayed the same as the biopsy size increased. Our model suggests an optimal biopsy size in order to reduce the probability to misclassify truly clonal alterations.

Keywords Cancer

Keywords Intratumour heterogeneity

Keywords Clonal dynamics

Keywords Cancer evolution

Presentation pref. Oral presentation preferred (otherwise poster)

Additional file

Extra information

Presentation

Session Session 3B : Cognition and aging

Time 16:45 - 17:00

Date 19/08/2017

Location Red Room

Abstract Registration No: 39

Conference	ISEMP	ISEMPH
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Abstract no. 39

Abstract code

Title of abstract **What is the genetic basis of the variation in susceptibility to infection by parasitoid wasps in *Drosophila* species?**

Author Arunkumar,
University of Cambridge; United Kingdom; Tel: 447422372994, arunkumarramrsh@gmail.com

Co-Author(s) Leitao,
Jiggins,

Topic Call for abstracts : ISEMPH conference

Abstract text Within and between populations it is normal to find considerable genetic variation in susceptibility to infection. Despite the central role of resistance in evolutionary theory, we have little understanding of the genetic basis of susceptibility to infection. Insects are ideal to study the genetic architecture of resistance as both highly resistant and susceptible genotypes occur within populations. The fruit fly (*Drosophila*; *D. melanogaster*) and its sister species (*D. simulans*) are commonly attacked by the parasitoid wasp *Leptopilina boulardi*; that kills a substantial proportion of a population in a single generation. Nevertheless, there is considerable genetic variation in susceptibility to wasps within *Drosophila* populations possibly because it is costly to be resistant. We exposed large populations of *D. melanogaster* and *D. simulans* to *L. boulardi*, and replicate populations were artificially selected for resistance, resulting in increased resistance over six generations. Using whole genome resequencing on pooled individuals, we identified SNPs with higher frequency in resistance lines when compared to progenitors and a few were shared between the two *Drosophila* species. Understanding the causes for genetic variation in susceptibility to infection is necessary as it determines the burden of disease within populations, and is the raw material that allows populations to evolve resistance.

Keywords pooled GWAS

Keywords host-parasite coevolution

Keywords susceptibility to infection

Keywords genetic variation

Presentation pref. Oral presentation preferred (otherwise poster)

Additional file

Extra information

Presentation

Session Session 7A : Genetics

Time 16:15 - 16:30

Date 20/08/2017

Location Red Room

Abstract Registration No: 40

Conference	ISEMP	ISEMPH
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Abstract no. 40

Abstract code

Title of abstract **The potential of fast and random drug changes to constrain antibiotic resistance evolution**

Author Schulenburg,
University of Kiel; Germany; Tel: 00494318804141, hschulenburg@zoologie.uni-kiel.de

Co-Author(s) Roemhild,

Topic Call for abstracts : ISEMPH conference

Abstract text 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 extreme environments or periodic fluctuations. Adaptation may however be more difficult, if conditions change fast or randomly. We used evolution experiments to specifically test to what extent fluctuating antibiotic environments affect resistance evolution. Based on 190 replicate populations of the pathogen *Pseudomonas aeruginosa* challenged over 96 seasons with different antibiotic treatments, we found that the evolution of multidrug resistance was constrained when antibiotics were switched fast rather than slowly or not at all (single drug treatments). Additionally, unpredictable (i.e., random) fluctuations impeded adaptation compared to predictable regular changes. Within the treatment types, the precise order of antibiotics determined the extent of resistance increases. Using whole genome sequencing and comprehensive phenotyping, we demonstrate that the fast regular and random sequences favor specific genotypes with different mutational spectra and resistance characteristics than those found under slow changes and monotherapy. In sum, our study identifies selective conditions that constrain the emergence of drug resistance and may be of use for the further development of sustainable antibiotic therapy.

Keywords Antibiotic resistance

Keywords Collateral sensitivity

Keywords Sequential treatment

Keywords *Pseudomonas aeruginosa*

Presentation pref. Oral presentation preferred (otherwise poster)

Additional file

Extra information

Presentation

Session ISEMPH abstracts during ESEB

Time 09:00 - 17:00

Date 21/08/2017

Location

Abstract Registration No: 41

Conference	ISEMP	ISEMPH
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Abstract no. 41

Abstract code

Title of abstract **Patterns of genomic variation in the emerging fungal pathogen *Candida glabrata* reveals recombination within species and a secondary association to the human host.**

Author Carreté,
Centre for genomic regulation; Spain; Tel: 933160281, Laia.Carrete@crg.eu

Co-Author(s) Ksiezopolska, Bader,
Pegueroles, Fairhead,
Gómez-Molero, Gabaldón,
Saus,
Iraola-Guzmán,
Loska,
Bader,

Topic Call for abstracts : ISEMPH conference

Abstract text Infections caused by opportunistic pathogens (i.e. candidiasis) are becoming of increasing medical importance. *Candida glabrata* is one of the most common pathogenic fungi in humans, ranking as the second causative agent of candidiasis worldwide. Despite its name, *C. glabrata* is more closely related to the baker's yeast *Saccharomyces cerevisiae*, and distantly related to the model pathogen *Candida albicans*. Furthermore, both *C. glabrata* and *C. albicans* have closely related non-pathogenic relatives, indicating that the ability to infect humans in these two lineages has originated independently. As a result of that, both pathogens have different virulence mechanisms, for instance *C. glabrata* has resistance to antifungals (i.e. fluconazole). In order to understand the recent evolution of this important opportunistic pathogen we analyzed the genomes of 33 different clinical *C. glabrata* isolates sampled from different human body sites and different countries. Our results show 7 deeply divergent clades, which show recent geographical distribution and large within-clade genomic and phenotypic differences. We show compelling evidence of recent admixture and of purifying selection on mating genes. Altogether, these findings support the existence of a sexual cycle, and suggest that humans are only a secondary niche for this pathogenic yeast.

Keywords human fungal pathogens

Keywords *Candida glabrata*

Keywords population genomics

Keywords mating

Presentation pref. Oral presentation preferred (otherwise poster)

Additional file

Extra information

Presentation

Session ISEMPH abstracts during ESEB

Time 09:00 - 17:00

Date 21/08/2017

Location

Abstract Registration No: 43

Conference	ISEMP	ISEMPH
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Abstract no. 43

Abstract code

Title of abstract Ancient Mycobacterium tuberculosis complex genomes from the Americas

Author Stone,
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Co-Author(s) Honap, Krause,
Vågene,
Herbig,
Rosenberg,
Buikstra,
Bos,
Krause,

Topic Call for abstracts : ISEMPH conference

Abstract text Tuberculosis, caused by members of the *Mycobacterium tuberculosis* complex (MTBC), was prevalent in the pre-Columbian Americas as shown by skeletal and ancient DNA data; however, today European *M. tuberculosis* strains predominate, indicating replacement after contact. Our previous analyses of three ~1000-year old human MTBC strains from Peru showed that these were closely related to strains found in Southern Hemisphere pinnipeds (seals and sea lions). Whether these pinniped-derived MTBC strains caused the majority of pre-contact tuberculosis (TB) cases in the Americas, or if other strains were also present, is unknown. We screened ~70 individuals for the presence of MTBC DNA using quantitative PCR assays. Eleven samples showed adequate preservation of ancient pathogen DNA and were selected for MTBC genome enrichment and sequencing. These samples are from archaeological sites in North and South America and date to the pre- and post-contact eras. Average coverage of these ancient strains ranged from 5 -26.6 X, with 70 - 97% of the genome recovered. Preliminary phylogenetic analyses show evidence for the spread of the pinniped-derived MTBC strains to non-coastal areas of the Americas possibly due to human-to-human transmission. Our data also suggest that introduction of European Lineage 4 *M. tuberculosis* strains occurred rapidly post-contact.

Keywords ancient DNA

Keywords phylogeny

Keywords tuberculosis

Presentation pref. Oral presentation preferred (otherwise poster)

Additional file

Extra information

Presentation

Session Session 3A : Pathogens

Time 16:45 - 17:00

Date 19/08/2017

Location Round Room

Abstract Registration No: 45

Conference	ISEMP	ISEMPH
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Abstract no. 45

Abstract code

Title of abstract **The Evolution of Cancer Suppression: Solutions to Peto's Paradox Revealed by Genomic Analyses of Elephants and Whales**

Author Tollis,
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Co-Author(s) Abegglen, Palsbøll,
Caulin, Schiffman,
Cabrerria, Maley,
Pourmand,
Green,
Robbins,
Palsbøll,

Topic Call for abstracts : ISEMPH conference

Abstract text Large body size has evolved at least 11 times during mammalian evolution, exemplified by the proboscidean (elephant) and cetacean (whale) lineages. These species should face a higher lifetime risk of cancer due to the greater probability of oncogenic mutations occurring during somatic evolution in an organism containing 100 to 1000X more cells than a human. However, zoo necropsy data reveals elephants have only a 1-3% probability of death from cancer compared to 11-25% for humans. We find elephant genomes harbor up to 40 alleles of the tumor suppressor gene TP53, and at least some TP53 retrogene copies are transcribed and translated. Functional assays demonstrate TP53 redundancy in elephants is related to an increased apoptotic response to DNA damage in elephant cells when compared to human cells. To investigate cancer suppression in gigantic baleen whales, we have sequenced and assembled the genome of the humpback whale (<i>Megaptera novaeangliae</i>). We find that cancer suppression in cetaceans is associated with positive selection on protein-coding genes involved in cell signaling, cell proliferation, apoptosis, as well as cancer. Our findings suggest independent evolution towards gigantism during the mammalian radiation was accompanied by divergent cancer suppression mechanisms, expanding our knowledge of nature's toolkit in fighting tumorigenesis.

Keywords cancer

Keywords mammals

Keywords Peto's Paradox

Presentation pref. Oral presentation preferred (otherwise poster)

Additional file

Extra information

Presentation

Session Session 4A : Cancer

Time 10:30 - 10:45

Date 20/08/2017

Location Room 4

Abstract Registration No: 46

Conference	ISEMP	ISEMPH
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Abstract no. 46

Abstract code

Title of abstract **Cumulative health risks of preeclampsia exposure in the womb are consistent with an evolutionary interpretation of the etiology of the disorder**

Author Hollegaard,
University of Copenhagen; Denmark; Tel: +45 26200027, hollegaard@gmail.com

Co-Author(s) Boomsma,
Lykke,
Poulsen,

Topic Call for abstracts : ISEMPH conference

Abstract text Preeclampsia negatively affects maternal health and has no cure except delivery. Using large Danish public health databases, we show that exposure to preeclampsia in the womb has consistent, albeit subtle negative effects on the future health prospects of children. The magnitude of these effects appears to be cumulative across the mild and severe preeclampsia diagnoses. This suggests that the clinical management of preeclampsia would benefit from conceptualizing these hypertension-related diagnoses as a continuum rather than as distinct diagnoses. Evolutionary explanations of why preeclampsia has not been removed by ancestral natural selection focus on antagonism between paternal and maternal genes, which may be expressed or silenced in the placenta depending on parent-of-origin imprints. Also such ultimate explanations offer little justification for considering severe preeclampsia as a condition requiring induced delivery as soon as premature birth is considered to no longer compromise child health, and mild preeclampsia as a diagnosis that should often allow pregnancies to be carried to term.

Keywords Reproductive health

Keywords Pregnancy induced hypertension

Keywords Parental conflict

Keywords Clinical management

Presentation pref. Oral presentation (no poster)

Additional file

Extra information

Presentation

Session Session 1B : Women's health

Time 10:30 - 10:45

Date 19/08/2017

Location Red Room

Abstract Registration No: 47

Conference	ISEMP	ISEMPH
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Abstract no. 47

Abstract code

Title of abstract **PISCA: a new phylogenetic method for the reconstruction of somatic evolution using somatic chromosomal alteration data**

Author Mallo,
Biodesign Center for Personalized Diagnostics; United States of America; Tel: +14802499074, dmalload@asu.edu

Co-Author(s) Kuhner, Graham,
Martinez, Maley,
Paulson,
Li,
Sanchez,
Reid,
Graham,

Topic Call for abstracts : ISEMPH conference

Abstract text

Despite the introduction of the evolutionary theory of cancer decades ago, only recently have we witnessed a rise in genomic studies reconstructing somatic evolution. Phylogenetic reconstruction of cell lineages is key to understanding how cancer evolves and could improve cancer detection, prevention and treatment. Phylogenetic methods have been developed for more than a century in for organisms. Unfortunately, it is difficult to use current methods for the reconstruction of somatic evolution due to important model misspecifications and/or assumptions that do not hold for cell-level evolution.

We developed a new phylogenetic method intended to reconstruct the evolution of homogeneous somatic samples (i.e., single cells, single crypts or de-convoluted clones) using somatic chromosomal data (in this case, generated from SNP arrays). We implemented our method as an open-source plugin for a well-known Bayesian phylogenetic reconstruction method (BEAST 1.8), available at <https://github.com/adamallo/PISCA>. Additionally, we used this method to estimate the acquisition rate of somatic chromosomal alterations in Barrett's Esophagus (BE) and discovered that the slow rate of evolution in this tumor is due to a low acquisition rate at the crypt level. This helps to explain the low rate of progression from BE to esophageal adenocarcinoma.

Keywords Phylogenetic method

Keywords Somatic evolution

Keywords Mutation rate

Keywords Somatic Chromosomal

Presentation pref. Oral presentation preferred (otherwise poster)

Additional file

Extra information

Presentation

Session Session 4A : Cancer

Time 10:45 - 11:00

Date 20/08/2017

Location Room 4

Abstract Registration No: 48

Conference	ISEMP	ISEMPH
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Abstract no. 48

Abstract code

Title of abstract Evolutionary perspectives on Hypertension in African Americans

Author KIM,
Pusan National University Yangsan Hospital; Korea; Tel: 82-10-8577-1469, kikim@pusan.ac.kr

Co-Author(s) Pollard,

Topic Call for abstracts : ISEMPH conference

Abstract text Characteristics of hypertension in African American can be argued by evolutionary perspectives. The review of the literature published from 1990 to 2016 identified two key evolutionary hypotheses on hypertension in African Americans. Human evolved for million years in a low salt environment where there was strong selection pressure for genes and mechanisms to preserve salt. This trait has been more prominent for those who have lived in tropical Africa. Among the genes that influence blood pressure, allele which increases salt avidity (i.e. <i>GNB3 825T</i> & <i>AGT A(-6)/M235</i>) was more frequent in African than non-African population. An alternative hypothesis focuses on the antagonistic pleiotropy of gene (<i>APOL1</i> & <i>risk alleles G1 and G2</i>), which may have been selected to protect against <i>Trypanosoma</i> infestation. This gene also predisposes to chronic renal disease (focal segmental glomerulosclerosis) and consequent hypertension. The prevalent area of trypanosomiasis roughly matches with the most enslaved areas in sub-Saharan Africa. 51% of African Americans carry at least one risk allele of <i>APOL1</i> compared to 0% of European Americans. The high prevalence of hypertension in African Americans may be partially explained by an evolutionary perspective. Hypertension in African American is more likely to foretell ongoing chronic kidney disease compared to European American.

Keywords Hypertension

Keywords African American

Keywords Salt avidity genes

Keywords antagonistic pleiotropy

Presentation pref. Poster presentation

Additional file

Extra information

Presentation

Session Session 2A : Metabolic and cardiovascular diseases

Time 12:30 - 12:45

Date 19/08/2017

Location Round Room

Abstract Registration No: 49

Conference	ISEMP	ISEMPH
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Abstract no. 49

Abstract code

Title of abstract Evolutionary Game Theory of Cancer: Harnessing Clonal Selection to Impair Intra-Tumor Cooperation

Author Archetti,
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Co-Author(s)

Topic Call for abstracts : ISEMPH conference

Abstract text Anti-cancer therapies generally fail because mutations that confer resistance spread by clonal selection within the tumor. We need evolution-proof therapies. I have been working for a few years on a new type of cell therapy based on concepts developed in evolutionary game theory. I will discuss how the theory of non-linear public goods applies to cancer, in particular to the analysis of the dynamics of growth factor production, how it helps explain intra-tumor heterogeneity and suggest a possible evolutionarily stable therapy. We can modify cancer cells derived from patients by knocking out genes coding for essential growth factors, and reinsert these modified cells into the tumor, where they spread by clonal selection and impair tumor growth. By harnessing clonal selection, instead of succumbing to it, this approach is both self-promoting and evolutionarily stable. I will discuss my initial approach, recent theoretical and experimental developments and future possible directions.

Keywords Cancer

Keywords Evolutionary Game Theory

Keywords Evolution of Cooperation

Keywords Cell Therapy

Presentation pref. Oral presentation (no poster)

Additional file

Extra information

Presentation

Session Session 4A : Cancer

Time 10:15 - 10:30

Date 20/08/2017

Location Room 4

Abstract Registration No: 50

Conference	ISEMP	ISEMPH
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Abstract no. 50

Abstract code

Title of abstract **To wean or not to wean? Extended breastfeeding and infant growth in a deprived and food- insecure agricultural setting.**

Author Núñez-de la Mora,
Universidad Veracruzana; Mexico; Tel: 228-812-77-05, anunezdlm@gmail.com

Co-Author(s) Molina-Castaneira,
Perroni-Marañón,
Negrete-Yankelevich,
Amescua-Villela,

Topic Call for abstracts : ISEMPH conference

Abstract text The WHO recommends exclusive breastfeeding for the first 6 months of an infants life, with continued breastfeeding up to 2 y of age or beyond, along with nutritionally adequate, safe, and appropriate complementary foods. Although there is nearly universal agreement that breast milk alone is the optimal first food, the age range in which solids should be introduced is less clear. The complementary feeding period accompanies a critical window of vulnerability. In many low-income countries, infants are small at birth, show catch-up growth in the first few months of life, and then enter a period of reduced growth velocity, which results in substantial growth faltering by the second year of life. Evidence as to how breastfeeding patters during the first months affect infant growth in settings of nutritionally inadequate complementary foods is limited. We use data on growth and infant feeding practices for 40 infants in Ocoteppec, a small subsistence agricultural community in Veracruz to investigate the impact of different weaning patterns on growth in a setting were food availability, food diversity, nutritional status and hygiene are poor. Findings are presented within the framework of human life history evolution and the implications for childs health are discussed.

Keywords Weaning dilemma

Keywords Breastfeeding

Keywords Food security

Keywords Child's health

Presentation pref. Oral presentation preferred (otherwise poster)

Additional file

Extra information

Presentation

Session Session 1B : Women's health

Time 10:00 - 10:15

Date 19/08/2017

Location Red Room

Abstract Registration No: 52

Conference	ISEMP	ISEMPH
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Abstract no. 52

Abstract code

Title of abstract **Network analysis of common disease identifies shared inherited risk pathways across independent datasets consistent with evolutionary mismatch and trade-offs and a mechanism for disease progression**

Author Buetow,
Arizona State University; United States of America; Tel: 480-727-9413, kenneth.buetow@asu.edu

Co-Author(s) Ferrell,
Lu,
Buetow,

Topic Call for abstracts : ISEMPH conference

Abstract text The common complex traits of obesity, type 2 diabetes, and cancer have been the subject of extensive genetic investigation. Motivated in part by the observed heritability of these traits, multiple genome-wide association studies have found dozens of associated SNPs. These SNPs explain a very small fraction of the heritability and are only rarely replicated across studies. In this study heritable components of the interconnected phenotypes of obesity, type 2 diabetes (TD2), and hepatocellular carcinoma (HCC) are identified using genome-wide SNP datasets publicly accessible through dbGaP. The study uses a novel analytic strategy that incorporates canonical biologic network information obtained from KEGG, Reactome, and Pathway Commons. Network-based analysis captures interlocus association information that is important in complex phenotypes and integrates differences in local population history. Unlike single locus analysis of the data sets, common biologic pathways are observed across multiple independent datasets within phenotypes (T2D, obesity). These pathways have larger odds ratios than individual SNP-based loci. The locus content of the pathways overlap, as do functional modules within pathways. Interestingly common networks were observed across obesity, TD2, and HCC studies suggesting a mechanism for disease progression. Provocatively, the pathways identified suggest both mismatch and tradeoffs underpinning risk for these common traits

Keywords biologic networks

Keywords complex traits

Keywords disease progression

Keywords trade-off mismatch

Presentation pref. Oral presentation (no poster)

Additional file

Extra information

Presentation

Session ISEMPH abstracts during ESEB

Time 09:00 - 17:00

Date 21/08/2017

Location

Abstract Registration No: 53

Conference	ISEMP	ISEMPH
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Abstract no. 53

Abstract code

Title of abstract Phage therapy can restrain antibiotic bloom of multiresistant gut bacteria

Author Mikonranta,
University of Exeter; United Kingdom; Tel: +447584960844, l.mikonranta@exeter.ac.uk

Co-Author(s) Buckling,
Raymond,

Topic Call for abstracts : ISEMPH conference

Abstract text Phage therapy is attracting growing interest among clinicians as antibiotic resistance continues becoming harder to control. *Enterobacter cloacae* is an opportunistic pathogen capable of overtaking normal gut flora during antibiotic treatment in humans. We use a gnotobiotic insect gut model system to demonstrate that while phage therapy cannot reduce the proportion of resistant *E. cloacae* in the population, it can potentially alleviate the antibiotic induced blooming by lowering the overall bacterial load.

Keywords Phage therapy

Keywords Antibiotic resistance

Keywords Insect model

Keywords Gut flora

Presentation pref. Oral presentation preferred (otherwise poster)

Additional file

Extra information UMERIC

Presentation

Session Session 4B : Antibiotic resistance

Time 10:45 - 11:00

Date 20/08/2017

Location Red Room

Abstract Registration No: 54

Conference	ISEMP	ISEMPH
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Abstract no. 54

Abstract code

Title of abstract Resistance selection on non-target bacterial populations

Author Kinnear,
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Co-Author(s) Hansen,
Patel,
Young,
Read,
Woods,

Topic Call for abstracts : ISEMPH conference

Abstract text Vancomycin-resistant enterococcus (VRE) is a leading cause of hospital acquired infection. Due to intrinsic multi-drug resistance, <i>Enterococcus faecium</i> blood stream infections have limited treatment options, with daptomycin often being the preferred treatment. Since 2010, the University of Michigan Health Service (UMHS) has seen an increase in daptomycin resistance within patients over the course of VRE infection, as well as an increase in the proportion of initial infection isolates being daptomycin non-susceptible. These observations suggest that while daptomycin use selects for resistance within an infection, this resistance is also transmitting around the hospital. In hospitalized patients, colonization of the gut with VRE is common, and often observed prior to patients developing a sterile site infection. The use of daptomycin and other drugs to treat sterile site infections will likely impact resistance not only at these sites, but also in the intestinal microbiota. To determine the impact of daptomycin use on resistance in the gut, we utilize perirectal swab samples collected for a VRE infection prevention programme and compare resistance profiles from patients with and without prior daptomycin exposure. Understanding the impact of daptomycin use on the non-target population in the gut may enable development of methods to reduce transmitted resistance.

Keywords antibiotic

Keywords resistance

Keywords enterococcus

Keywords microbiome

Presentation pref. Oral presentation preferred (otherwise poster)

Additional file

Extra information UMERIC

Presentation

Session Session 4B : Antibiotic resistance

Time 10:00 - 10:15

Date 20/08/2017

Location Red Room

Abstract Registration No: 55

Conference	ISEMP	ISEMPH
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Abstract no. 55

Abstract code

Title of abstract **Are seasonal and multiannual infectious disease dynamics determined by human aggregation? A long-term study in historical Finns**

Author Briga,
University of Turku; Finland; Tel: +31616081022, michbriga@gmail.com

Co-Author(s) Metcalf,
Lummaa,

Topic Call for abstracts : ISEMPH conference

Abstract text Many infectious diseases show seasonal and/or multiannual dynamics of incidence. For directly transmitted childhood infections, the mechanisms underlying these dynamics are not well understood. It is often believed that these dynamics are driven mostly indirectly by host aggregation patterns. However, these dynamics may also be determined directly by pathogen persistence. Here, we use an exceptional >100 year dataset of disease monitoring in 18th and 19th century Finns to investigate the association between human aggregation patterns and the incidence dynamics of three major infectious diseases: smallpox, measles and scarlet fever. We show that the seasonal incidence dynamics associate well with patterns of human aggregation, but that there are discrepancies for the multiannual dynamics. Thus while seasonal disease dynamics seem mostly driven by human aggregation, this is not the case for the multiannual dynamics. Hence the more complex multiannual dynamics are additionally determined by various other pathogen and host life history traits and we here discuss possible options.

Keywords epidemiology

Keywords disease transmission

Keywords human aggregation

Keywords life history

Presentation pref. Oral presentation preferred (otherwise poster)

Additional file

Extra information UMERIC

Presentation

Session Session 1A : Immune system

Time 10:45 - 11:00

Date 19/08/2017

Location Round Room

Abstract Registration No: 56

Conference	ISEMP	ISEMPH
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Abstract no. 56

Abstract code

Title of abstract A FORMAL MODEL OF CLONAL EXPANSION IN BACTERIAL POPULATION GENETICS

Author Ledda,
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Co-Author(s)

Topic Call for abstracts : ISEMPH conference

Abstract text Recent advances in sequencing techniques have dramatically increased the availability of bacterial whole genomes in the last few years. Given the relatively small cost of sequencing, it is now possible to sequence many closely related bacteria and thus to study exhaustively their evolution in great detail. One phenomenon that is particularly evident on a short timescale of bacterial evolution is the clonal expansion of certain lineages in a bacterial population that have a selective advantage and thus expand, creating clonal subpopulations. The concept of clonal expansion is widely used in the bacterial genetics literature, yet has not been formally conceptualised. In this talk we will present a formal stochastic model of clonal expansion. We will show how this model can be used to simulate patterns resembling those observed in natural bacterial populations. We will also present a method to perform Bayesian inference under the clonal expansion model, thus allowing to estimate key parameters of our model such as effective populations size, time scales and expansion rates. Finally we apply this model to identify and quantify a clonal expansion responsible for a recent multi-resistant *Staphylococcus aureus* epidemic in England.

Keywords clonal expansion

Keywords bayesian inference

Keywords genetics

Keywords staphylococcus aureus

Presentation pref. Oral presentation preferred (otherwise poster)

Additional file

Extra information UMERIC

Presentation

Session Session 7A : Genetics

Time 15:45 - 16:00

Date 20/08/2017

Location Red Room

Abstract Registration No: 57

Conference	ISEMP	ISEMPH
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Abstract no. 57

Abstract code

Title of abstract **Optimal virulence in a macroparasite, the cestode *Schistocephalus solidus* in its specific intermediate host, the three-spined stickleback *Gasterosteus aculeatus***

Author Scharsack,
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Co-Author(s) Kalbe,
Kurtz,

Topic Call for abstracts : ISEMPH conference

Abstract text Virulence of pathogens is defined by the damage they cause to their hosts. Evolutionary medicine seeks to understand the evolution of virulence. To this end macroparasites, such as helminths are interesting models since they are often long lived and grow substantially in their hosts. Their virulence coincides with alterations of immunity and nutrient drain from the host. Some helminth parasites even manipulate behaviors of their hosts to facilitate transmission to the next host. Given the complexity of their virulence traits macroparasites risk to overexploit their hosts and might be under selection to optimize their virulence, i.e. maximizing their fitness while avoiding host overexploitation. We used growth rates of *S. solidus* in their stickleback hosts as estimate for parasite virulence and compared different origins in experimental sympatric and allopatric host-parasite combinations. Allopatric combinations uncovered two extremes, parasites with high virulence from host populations with high resistance and parasites with low virulence from less resistant hosts. Interestingly, parasite growth rates were almost identical across sympatric *S. solidus*-stickleback combinations, suggesting that these parasites evolved optimal virulence towards their sympatric hosts. We discuss if variation in excretory/secretory products used by *S. solidus* for host manipulation might be drivers to maintain their optimal virulence.

Keywords virulence

Keywords macroparasite

Keywords immunity

Keywords fitness

Presentation pref. Oral presentation preferred (otherwise poster)

Additional file

Extra information UMERIC

Presentation

Session Session 3A : Pathogens

Time 17:30 - 17:45

Date 19/08/2017

Location Round Room

Abstract Registration No: 59

Conference	ISEMP	ISEMPH
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Abstract no. 59

Abstract code

Title of abstract Gender-specific Inequality in pre- and early historic Europe

Author Koepke,
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Co-Author(s)

Topic Call for abstracts : ISEMPH conference

Abstract text Associated with a micro-evolutionary perspective is a potential influence of gender-specific inequality on the long-run trend of a human population's well-being (with health and nutrition as fundamental dimensions). Net nutritional status depends, among other factors, on resources' allocation and provision of care; these aspects are closely interlinked with socio-cultural circumstances, and gender-effects need to be considered. Significant female-specific gender inequality jeopardises the outcome for the entire society due to a potential double burden: an immediate impact for the directly suffering cohort and an indirect one due to potential intergenerational effects (affecting foeti of any sex). This might even result in the risk of a long-term vicious cycle in the trajectory of health-related human capital and well-being in a population. Yet, alternatively, selection effects might occur. As European pre-modern societies have been mostly patriarchally structured, gender-related disproportionate allocation is expected to disadvantage females. However, to what extent did European females actually experience neglect in the long-run? Did regional differences result in diverging legacies of intergenerational effects? To face these questions, skeletal material was utilised to study two complementary proxies, relative height dimorphism and female deficit, to describe potential variation in different regions of Europe in ancient times, pre-historic and later centuries.

Keywords well-being

Keywords long-run

Keywords gender

Keywords health

Presentation pref. Oral presentation (no poster)

Additional file

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Presentation

Session Session 2B : Culture, gender and sexual health

Time 12:15 - 12:30

Date 19/08/2017

Location Red Room

Abstract Registration No: 62

Conference	ISEMP	ISEMPH
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Abstract no. 62

Abstract code

Title of abstract Evolution of iron resistance in *Escherichia coli*.

Author Graves Jr,
North Carolina A&T State University; United States of America; Tel: 3362852858, gravesjl@ncat.edu

Co-Author(s) Ewunkem,
Boyd,
Van Beveren,
Johnson,

Topic Call for abstracts : ISEMPH conference

Abstract text Multi-drug resistant (MDR) bacteria are a growing public health concern. Bacteria have rapidly evolved resistance to traditional antibiotics. This condition has led to a crucial need for new antimicrobial agents. While iron is an essential micronutrient, excess iron can be toxic. On the other hand, silver is not a nutrient and is highly toxic to bacteria as it impacts numerous physiological pathways. We have already demonstrated that bacteria can rapidly evolve resistance to both silver nanoparticles (AgNP) and ionic silver (Ag⁺). Here we examine whether a previous history of silver resistance aids or impairs the evolution of resistance to Fe²⁺ and Fe³⁺ sulfate in *E. coli* K12 MG1655. After 118 days of selection (~765 generations) we have shown conclusively that Ag resistant bacteria are strongly impaired in iron resistance and show no evidence of having acquired resistance to iron. On the other hand, non-Ag resistant bacteria show modest gains in Fe³⁺ resistance. Finally, non-Ag resistant bacteria selected for iron resistance have improved their resistance to silver. This suggests that these bacteria may have acquired a resistance mechanism (e.g. ROS resistance) that operates to ameliorate both the damages of toxic levels of iron and silver. Our studies are ongoing.

Keywords Antimicrobial resistance

Keywords *E. coli*

Keywords iron

Keywords silver

Presentation pref. Oral presentation (no poster)

Additional file

Extra information UMERIC

Presentation

Session Session 3A : Pathogens

Time 17:15 - 17:30

Date 19/08/2017

Location Round Room

Abstract Registration No: 63

Conference	ISEMP	ISEMPH
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Abstract no. 63

Abstract code

Title of abstract **Intercellular Competition and the Inevitability of Multicellular Aging**

Author Nelson,
University of Arizona; United States of America; Tel: 2177144232, pgnelson@email.arizona.edu

Co-Author(s) Masel,

Topic Call for abstracts : ISEMPH conference

Abstract text Intercellular competition in aging plays a principle role in the development of senescence and cancer. We lay out the first general model of the interplay between intercellular competition, cellular senescence, and cancer. Our model shows that shows that aging is a fundamental feature of multicellular life. Current understanding of the evolution aging is holds that aging is due to weak selection on alleles that increase mortality late in life allowing such allele to persist. Our model, while fully compatible with current theory, makes a stronger statement: multicellular organisms would age even if selection is perfect. These results inform how we think about evolution of aging and the role of intercellular competition in senescence and cancer.

Keywords Aging

Keywords Senescence

Keywords Cancer

Keywords Intercellular competition

Presentation pref. Oral presentation (no poster)

Additional file

Extra information UMERIC

Presentation

Session Session 3B : Cognition and aging

Time 17:30 - 17:45

Date 19/08/2017

Location Red Room

Abstract Registration No: 64

Conference	ISEMP	ISEMPH
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Abstract no. 64

Abstract code

Title of abstract **An evolutionary perspective on back problems**

Author Haeusler,
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Co-Author(s) Frater,
Crawford,
Fornai,
Bonneau,

Topic Call for abstracts : ISEMPH conference

Abstract text Back problems are ubiquitous in modern people and affect nearly all of us at some point in life. Possible explanations include the sedentary lifestyle of Western populations, muscular disuse, other evolutionary mismatches with the environment, and trade-offs of bipedalism. Thus, a remarkably high prevalence of vertebral pathologies is observed in early hominins with >30% of all fossils being affected, including Scheuermann's disease, juvenile disc herniation and spondylolisthesis that all are associated with biomechanical stress during the vulnerable phase of adolescence. On the other hand, massive degenerative changes of the vertebral column have been observed in later hominins including Neanderthals. It is unclear whether these pathologies reflect a more physically demanding lifestyle or whether they result from a distinct un-economic posture and flat lumbar lordosis compared to modern humans as inferred from an analysis of lumbar articular process angles and pelvic incidence. Here, we discuss different aspects of Neanderthal vertebral pathologies including Baastrup's disease and facet joint osteoarthritis and their relevance for the evolution of a modern human-like posture and locomotion. We conclude that our spinal column has been shaped by natural selection to become less vulnerable than that of our ancestors, resulting in an optimized compromise between mobility and stability.

Keywords musculoskeletal disorders

Keywords spine

Keywords low back pain

Keywords human evolution

Presentation pref. Oral presentation (no poster)

Additional file

Extra information UMERIC

Presentation

Session Session 6A : Different topics

Time 15:00 - 15:15

Date 20/08/2017

Location Round Room

Abstract Registration No: 66

Conference	ISEMP	ISEMPH
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Abstract no. 66

Abstract code

Title of abstract **Are autoimmune diseases and the origin of the adaptive immune system linked?**

Author Catania,
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Co-Author(s) Bayersdorf,
Fruscalzo,

Topic Call for abstracts : ISEMPH conference

Abstract text The adaptive immune system (AIS) protects jawed vertebrates from infection by generating antibodies that target nonself-components. However, AIS-generated antibodies can also strike against healthy self-components, giving rise to autoimmune diseases (ADs). Why do ADs exist? Is self-reactivity the price we need to pay in return for a sophisticated defense system? We leverage concepts drawn from prominent theoretical arguments such as immune network theory and the hygiene hypothesis in synthesis with various experimental results on topics such as immunological changes that occur during normal pregnancy to shed light on these questions. We propose that ADs are a side effect of architectural and evolutionary constraints. We hypothesize that the AIS emerged gradually from a regulated system of self-recognition that remains to this day and produces natural autoantibodies via B-1a cells. A central idea that drives our hypothesis is that the production of AIS'antibodies was — and may still be — favored when the production/activity of B-1a cell-derived natural autoantibodies is low. These propositions might provide a complementary explanation for the elevated frequency of ADs throughout western societies.

Keywords Adaptive Immune System

Keywords Autoimmune diseases

Keywords Natural autoantibodies

Keywords Pregnancy

Presentation pref. Oral presentation preferred (otherwise poster)

Additional file

Extra information UMERIC

Presentation

Session Session 1A : Immune system

Time 10:30 - 10:45

Date 19/08/2017

Location Round Room

Abstract Registration No: 68

Conference	ISEMP	ISEMPH
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Abstract no. 68

Abstract code

Title of abstract Investigating Human Uniqueness in Relation to Health and Disease Using Phylogenetic Methods

Author Nunn,
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Co-Author(s) Miller,
Vining,
Barton,

Topic Call for abstracts : ISEMPH conference

Abstract text Understanding evolutionary history and the selective forces acting on humans increasingly informs medicine and public health. We are applying new phylogenetic methods to investigate phenotypic evolution along the human lineage, relative to evolution in primates more broadly. In this talk, we will present these methods and illustrate their application to several phenotypic traits of importance in human health and evolution. One method investigates phenotypic evolution comparatively to predict traits in humans using phylogenetic generalized least squares. The other approach estimates parameters associated with evolutionary regimes under an Ornstein-Uhlenbeck model of evolution, and then investigates whether those regimes have changed along the human lineage. We applied these methods to investigate the evolution of human brain size and physiology. As expected, analyses revealed that humans are exceptional for brain size, but not for all components of brain size. In addition, 10-20% of the 41 physiological traits we examined also showed evidence for exceptional evolution along the human lineage, with humans exhibiting more cases of distinct evolutionary change than other primates. We close by considering more generally the relevance of these and similar approaches for understanding human health and disease.

Keywords comparative methods

Keywords primates

Keywords brain size

Keywords physiology

Presentation pref. Oral presentation (no poster)

Additional file

Extra information UMERIC

Presentation

Session Session 6B : Theoretical considerations and methodology

Time 15:00 - 15:15

Date 20/08/2017

Location Red Room

Abstract Registration No: 70

Conference	ISEMP	ISEMPH
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Abstract no. 70

Abstract code

Title of abstract Immune priming decreases resistance to early-stage pathogenic infection

Author Armitage,
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Co-Author(s) Kurtz,
Kutzer,

Topic Call for abstracts : ISEMPH conference

Abstract text Invertebrate immune priming describes when an individual's initial exposure to a pathogen confers enhanced protection upon a second exposure. It can in some cases increase host survival, potentially through increased resistance, i.e., a lower host pathogen load after a second exposure. Theory predicts that priming could also enhance host tolerance, whereby tolerance-mediated priming decreases host mortality or improves pathology at a given pathogen burden, thereby a primed host might appear healthier than an unprimed host. We used four fly, *Drosophila melanogaster*, genotypes as model hosts and two opportunistic bacterial pathogens, *Lactococcus lactis* and *Pseudomonas entomophila*, to test whether priming is: 1. genetically variable, and 2. mediated by resistance or tolerance at a single early infection time point. Fecundity was genetically variable but not affected by bacterial infection. In contrast to our predictions, priming decreased resistance to *P. entomophila*. Fecundity tolerance showed genotypic variation but was not influenced by immune priming. We are currently analysing how priming affects both survival and gene expression after a second pathogen exposure. So far, our results suggest that priming may come with costs to resistance, at least during the early stages of infection, and highlights the complexities and context dependence of the phenomenon.

Presentation pref. Oral presentation (no poster)

Additional file

Extra information UMERIC

Presentation

Session Session 1A : Immune system

Time 10:15 - 10:30

Date 19/08/2017

Location Round Room

Abstract Registration No: 71

Conference	ISEMP	ISEMPH
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Abstract no. 71

Abstract code

Title of abstract **Can premenstrual symptoms be used as a cue to an undiagnosed infection? Insights from digital health**

Author Alvergne,
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Co-Author(s) Vlajic Wheeler,
Hogqvist Tabor,

Topic Call for abstracts : ISEMPH conference

Abstract text

Objective: The reasons why some women experience debilitating premenstrual symptoms and others do not are unknown. Here we test the evolutionary ecological hypothesis that severe premenstrual symptoms may be symptomatic of the presence of persistent sexually transmitted infections (STIs).

Methods: 30,000 women were recruited through a digital period-tracker app. Women were asked: (i) Have you ever been diagnosed with a STI? (ii) If yes, when was it, and were you given a treatment? Those data were combined with longitudinal data on menstrual bleeding patterns, cramps, emotions and hormonal contraceptives use.

Results: 946 women were eligible for analysis. We found that (i) women experiencing prolonged cramps before their menses are ca. 3 times more likely to be diagnosed with a sexually transmitted infection and (ii) among women diagnosed positive for an infection, treatment is associated with a reduction of premenstrual symptoms.

Conclusions: The results support the idea that PMS is an inflammatory disease and that it can be used as a cue to an undiagnosed infection, a leading cause of infertility worldwide. The study also demonstrates the potential of an evolutionary medicine approach for understanding why people are sick. The opportunities and limitations of data from digital health are discussed.

Keywords PMS

Keywords Menstrual cycle

Keywords Infections

Keywords Digital Health

Presentation pref. Oral presentation preferred (otherwise poster)

Additional file

Extra information UMERIC

Presentation

Session Session 1B : Women's health

Time 10:15 - 10:30

Date 19/08/2017

Location Red Room

Abstract Registration No: 72

Conference	ISEMP	ISEMPH
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Abstract no. 72

Abstract code

Title of abstract **Host genetic variation at B4galnt2 influences intestinal microbial ecology and susceptibility to enteric pathogens in house mice**

Author Baines,
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Co-Author(s) Rausch,
Vallier,
Suwandi,
Grassl,

Topic Call for abstracts : ISEMPH conference

Abstract text Glycans on mucosal surfaces play an important role in host-microbe interactions in the mammalian intestine. *B4galnt2* is a blood group-related glycosyltransferase whose two murine alleles (driving gastrointestinal- and vascular expression) are maintained by balancing selection and determine the presence/absence of *B4galnt2*-derived glycans in the intestinal tract. Analysis of *B4galnt2*-knockout mice reveals that the loss of *B4galnt2* expression in the intestine leads to widespread alterations in intestinal bacterial community structure. Given the signatures of selection present at *B4galnt2* and its influence on the intestinal microbiota, we hypothesize that *B4galnt2* expression may mediate susceptibility to intestinal pathogens. To test this, we challenged mice with a *Salmonella enterica* serovar Typhimurium (*S*. Typhimurium) infection model. We found that the loss of *B4galnt2* intestinal expression is associated with decreased susceptibility to *S*. Typhimurium. Further, fecal transfer experiments into previously germ-free mice confirm a role of the *B4galnt2*-dependent microbiota in conferring decreased susceptibility to *S*. Typhimurium. Interestingly, metagenomic analysis suggests that increased colonization resistance in *B4galnt2*-knockout mice might explain the decrease in susceptibility to *S*. Typhimurium. Finally, by employing a "pathometagenomic analysis" (metagenomics combined with histology and inflammation markers) to wild mouse populations, we identified several promising candidate pathogens that correlate with *B4galnt2* genotype and inflammation.

Keywords gut microbiota

Keywords host-pathogen interactions

Keywords balancing selection

Presentation pref. Oral presentation preferred (otherwise poster)

Additional file

Extra information UMERIC

Presentation

Session Session 5B : Microbiome

Time 12:30 - 12:45

Date 20/08/2017

Location Red Room

Abstract Registration No: 74

Conference	ISEMP	ISEMPH
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Abstract no. 74

Abstract code

Title of abstract **Improved detection of gene-microbe interactions in the mouse skin microbiota using high-resolution QTL mapping of 16S rRNA transcripts**

Author Belheouane,
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Co-Author(s) Gupta,
Ibrahim,
Baines,

Topic Call for abstracts : ISEMPH conference

Abstract text Understanding the role of host genetics in determining inter-individual variation in the microbiota is critical to understanding evolution at the level of the holobiont, and recent studies highlight the utility of quantitative trait locus (QTL) mapping for identifying host loci that influence microbial traits. In this study, we analyzed the skin microbiota of mice from the 15th generation of an advanced intercross line, using a novel approach of performing bacterial trait mapping at both the 16S rRNA gene copy (DNA)- and transcript (RNA) level. This allowed genomic intervals as small as 0.1 megabases containing single genes to be identified, and the inclusion of 16S rRNA transcript-level mapping dramatically increased the number of significant associations detected. The genomic intervals contain many genes involved in skin inflammation and cancer and are further supported by the bacterial traits they influence, which in some cases have known genotoxic or probiotic capabilities. Further, a significant enrichment of cancer-related pathways within genomic intervals suggests that similar to colon carcinogenesis, the resident microbiota may play a role in skin cancer susceptibility and its potential prevention and/or treatment. These results suggest that the skin microbiota may represent a yet underappreciated player influencing the fitness of the holobiont.

Keywords skin microbiota

Keywords cancer

Keywords house mouse

Presentation pref. Oral presentation preferred (otherwise poster)

Additional file

Extra information UMERIC

Presentation

Session Session 5B : Microbiome

Time 12:45 - 13:00

Date 20/08/2017

Location Red Room

Abstract Registration No: 79

Conference	ISEMP	ISEMPH
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Abstract no.	79
Abstract code	
Title of abstract	Commensal and pathogenic microbiota and viruses from the oral cavity of deceased Gombe chimpanzees
Author	Ozga, Arizona State University; United States of America; Tel: 7089177313, aozga@asu.edu
Co-Author(s)	Nockerts, Wilson, Gilby, Pusey, Stone,
Topic	Call for abstracts : ISEMPH conference
Abstract text	<p>In order to understand the origins of microorganisms within the human oral cavity, it is imperative to examine the oral ecosystem of closely related primate species. Dental calculus (fossilized plaque) allows for the extraction of long term microbial and viral genetic information but has yet to be fully explored within non-human primates. Here we present results from shotgun prepared, Illumina sequenced dental calculus DNA libraries in order to understand the microbial and viral diversity over time compared to humans. Dental calculus from 12 deceased chimpanzees belonging to the Kasekela community are being examined, spanning 50 years of occupation at Gombe National Park. Preliminary results from two samples show the presence of DNA bacteriophages belonging to the Myoviridae, Siphoviridae, Herpesviridae, and Mimiviridae families. Dominant microbial phyla include Spirochaetes, TM7, and Euryarchaeota, all of which have been implicated, in some degree, to oral disease states within humans. Additionally, sequences belonging to all three members of the Red Complex, microbiota thought to be associated with periodontal disease in humans, were detected in both chimpanzee samples. Here will discuss how these results fit into our current knowledge of primate oral ecosystems and the implications of these findings for human health and evolution.</p>
Keywords	Non-human primates
Keywords	Microbiome
Keywords	Virome
Presentation pref.	Oral presentation preferred (otherwise poster)
Additional file	
Extra information	UMERIC

Presentation

Session	Session 5B : Microbiome
Time	12:15 - 12:30
Date	20/08/2017
Location	Red Room

Abstract Registration No: 80

Conference	ISEMP	ISEMPH
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Abstract no. 80

Abstract code

Title of abstract Adding Evolution to Comparative Pathology: Investigating the Unanswered Questions

Author Uhl,
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Co-Author(s)

Topic Call for abstracts : ISEMPH conference

Abstract text Veterinary medicine is comparative, but, as in human medicine, evolutionary origins of disease susceptibility are not fully considered. Thus while there are good descriptive studies, many 'why' questions concerning disease remain unanswered, and are not even asked. Consideration of the shared evolutionary heritage across species provides deeper insights into disease than comparisons based only on molecular mechanisms and morphology. Understanding the evolutionary basis for why there are both species similarities and differences in disease induced by defects in the same conserved gene (e.g.: dystrophin), can also inform treatment options. Questions of why disease occurs in specific locations can be investigated through consideration of organ evolution: for example why vascular tumors arise on the right side of the heart in both dogs and people. Diseases induced through environmental mismatches, (e.g.: hemochromatosis), reveal common shared susceptibility and pathology across species. Similarly, while specific pathogens vary in their molecular mechanisms of infection, they often exploit the same vulnerabilities as to cell type infected and the features of diseases induced across species. Adding an evolutionary perspective to comparative studies of disease allows critical questions, unable to be answered through descriptive studies, to be investigated and opens up important new avenues of research.

Keywords Veterinary

Keywords Pathology

Keywords Comparative

Keywords Disease Susceptibility

Presentation pref. Oral presentation preferred (otherwise poster)

Additional file

Extra information UMERIC

Presentation

Session Session 5A : Theoretical considerations and animal models

Time 12:30 - 12:45

Date 20/08/2017

Location Room 4

Abstract Registration No: 81

Conference	ISEMP	ISEMPH
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Abstract no. 81

Abstract code

Title of abstract **Cliff-edge fitness functions and disease vulnerability**

Author Randolph,
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Co-Author(s)

Topic Call for abstracts : ISEMPH conference

Abstract text Vulnerability to disease results when the level of a trait that maximizes fitness is pushed close to a cliff edge in a fitness landscape. This is well recognized in examples such as selection for speed in horses shaping a long thin cannon bone that is prone to catastrophic failure. This presentation describes strategies for expanding the search for such phenomena to metabolic and genetic systems. In particular, it may have relevance for understanding why only tiny effects are observed for all common alleles influencing vulnerability to highly heritable devastating disorders such as schizophrenia. Cliff edge effects may also help to explain why some systems, such as those that stabilized single carbon metabolism, remain stable in the face of mutations that have individually substantial effects, and why minor additional changes may nonetheless result in severe disease. Strong selection in short time frames may be especially prone to create fitness cliffs that, over evolutionary time, weather into flatter fitness surfaces because of the costs to individuals whose phenotypes go over the cliff. Coevolution with pathogens is also likely to shape fitness peaks with steep slopes because the high marginal costs of additional defenses are likely to be balanced by high marginal benefits.

Keywords Fitness landscapes

Keywords Missing heritability

Keywords Cliff Edge effects

Presentation pref. Oral presentation preferred (otherwise poster)

Additional file

Extra information UMERIC

Presentation

Session Session 6B : Theoretical considerations and methodology

Time 15:15 - 15:30

Date 20/08/2017

Location Red Room

Abstract Registration No: 82

Conference	ISEMP	ISEMPH
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Abstract no. 82

Abstract code

Title of abstract **Meta-analyses of variation: applications in evolutionary medicine and beyond**

Author Nakagawa,
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Co-Author(s) Senior,
O'Dea,
Lagisz,

Topic Call for abstracts : ISEMPH conference

Abstract text Most meta-analytical studies focus on differences between mean values, when comparing groups. However, differences in variation can also provide important insights. Disparities in phenotypic variation can hint at the mechanisms underlying the intrinsic differences between compared groups or treatments. Phenotypic variation is the evolutionary currency providing substrate for selection and, thus, it is valuable to know which factors can increase variation among individuals. For example, stressful events are predicted to change both the trait means and their variances; body sizes of females and males may vary differently within species due to the differences in the sexes' chromosomal make-ups. We provide an overview of existing methods for meta-analysis of variation, including the most recent advancements. We then demonstrate applications of these methods in meta-analytic studies spanning evolutionary research, social sciences, and medicine. Our examples include maternal diet effects on offspring phenotypes, differences in school grades between boys and girls, and placebo effects in medical research.

Keywords meta-analysis

Keywords variation

Keywords phenotype

Keywords methodology

Presentation pref. Oral presentation preferred (otherwise poster)

Additional file

Extra information UMERIC

Presentation

Session Session 6B : Theoretical considerations and methodology

Time 15:30 - 15:45

Date 20/08/2017

Location Red Room

Abstract Registration No: 83

Conference	ISEMP	ISEMPH
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Abstract no. 83

Abstract code

Title of abstract Sex, age, and reproduction: tooth loss among the Tsimané in lowland Bolivia.

Author Schwartz,
University of New Mexico; United States of America; Tel: 5059335170, mschwar1128@gmail.com

Co-Author(s) Trumble,
Gurven,
Kaplan,

Topic Call for abstracts : ISEMPH conference

Abstract text In modern populations the use of contraceptives, tooth brushing, and access to modern dentistry likely mask the true extent of the relationship between biological sex, parity, and oral health. We hypothesize that in a natural fertility setting, differences in missing teeth between men and women will be significant and become more pronounced over time. To test this hypothesis we surveyed the oral health and parity of the Tsimane (N=1753, 938 females, 815 males, ages 15+), an Amerindian population native to the Amazon River Basin of Bolivia The Tsimane have a high fertility (TFR= 9) and no access to modern dentistry. Multiple regression analysis of missing teeth on age, sex, and their interaction showed that females lose significantly more teeth per year than males ($p < .0001$) at a rate of about .17 more teeth per year than males ($b = -.17, p < .0001$). A second regression, restricted to women (N=565, ages 15+) of tooth loss on parity, controlling for age, revealed women lose about 0.44 teeth for each additional birth ($p < .01$), possibly implying that parity accounts for the sex difference. These results suggest that high fertility increases sex differences in oral health.

Keywords Oral Health

Keywords Cost of Reproduction

Keywords Maternal Depletion

Keywords Tooth loss

Presentation pref. Oral presentation preferred (otherwise poster)

Additional file

Extra information UMERIC

Presentation

Session Session 2B : Culture, gender and sexual health

Time 12:45 - 13:00

Date 19/08/2017

Location Red Room

Abstract Registration No: 84

Conference	ISEMP	ISEMPH
Abstract no.	84	
Abstract code		
Title of abstract	Identifying Evolutionary Medicine Core Principles	
Author	Grunspan, Arizona State University; United States of America; Tel: 2104885828, dgrunspan@asu.edu	
Co-Author(s)	Nesse, Barnes, Brownell,	
Topic	Call for abstracts : ISEMPH conference	
Abstract text	<p>National panels of science education experts (AAAS, AAMC-HHMI) advocate for education focused around disciplinary core principles. Constructing student-learning objectives based on core principles can help align instruction with higher level learning goals such as application and synthesis, while avoiding rote memorization. To help enable instructors of Evolution and Medicine to develop discipline specific learning objectives that align with these national recommendations, we identified and refined a list of core principles in Evolutionary Medicine. To create this list, we performed iterative surveys with a panel of diverse experts in Evolutionary Medicine. In the process, we identified 15 core principles with minimal disagreement among the panelists. We report on these disciplinary core principles, areas where consensus lacked among panelists, and ways to implement these principles for curriculum development.</p>	
Presentation pref.	Oral presentation preferred (otherwise poster)	
Additional file		
Extra information	UMERIC	

Presentation

Session	Session 5A : Theoretical considerations and animal models
Time	12:15 - 12:30
Date	20/08/2017
Location	Room 4

Abstract Registration No: 86

Conference	ISEMP	ISEMPH
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Abstract no. 86

Abstract code

Title of abstract **Mouse models of human disease: An evolutionary perspective**

Author Perlman,
University of Chicago; United States of America; Tel: +1 312-246-9830, r-perlman@uchicago.edu

Co-Author(s)

Topic Call for abstracts : ISEMPH conference

Abstract text The use of mice as model organisms to study human biology is predicated on the genetic and physiological similarities between the species. Nonetheless, mice and humans have evolved in and become adapted to different environments and so, despite their phylogenetic relatedness, they have become very different organisms. Mice often respond to experimental interventions in ways that differ strikingly from humans. Mice are invaluable for studying biological processes that have been conserved during the evolution of the rodent and primate lineages and for investigating the developmental mechanisms by which the conserved mammalian genome gives rise to a variety of different species. Mice are less reliable as models of human disease, however, because the networks linking genes to disease are likely to differ between the two species. The use of mice in biomedical research needs to take account of the evolved differences as well as the similarities between mice and humans.

Keywords Model organisms

Keywords Mice

Keywords Cancer

Presentation pref. Oral presentation (no poster)

Additional file

Extra information UMERIC

Presentation

Session Session 5A : Theoretical considerations and animal models

Time 12:45 - 13:00

Date 20/08/2017

Location Room 4

Abstract Registration No: 87

Conference	ISEMP	ISEMPH
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Abstract no. 87

Abstract code

Title of abstract Applications of Evolutionary Biology in Nutrition & Dietetics

Author Landolin,
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Co-Author(s) Suarez,

Topic Call for abstracts : ISEMPH conference

Abstract text

Background: Little is known about how health care disciplines other than medicine and public health use evolutionary biology concepts in their literature. Previously, Landolin and Suarez (2016) demonstrated a progressive increase in the utilization of evolutionary biology key terms in the nutrition literature between 1980 and 2016, outpacing other disciplines. Herein, the nutrition literature applying evolutionary biology concepts is characterized to further understand how those concepts are being used and why.

Objective: To characterize citations containing references to evolutionary biology in the nutrition literature, spanning from 1980 to the first half of 2016.

Method: Citations were classified according to population, age/gender, disease states, clinical focus, depth and nature of use of evolutionary biology concepts, and whether evolutionary concepts served as a principal theme.

Results: A total of 896 citations were reviewed. Evolutionary concepts were a principal theme in 71% of included publications in 1980, which declined to 31% by 2015. Publication subjects were wide-ranging. Interest in the concept of "thrifty genes" had a peak in 1995.

Discussion: Researchers in the field of nutrition have made substantial contributions to the study of evolutionary health science. Targeted outreach to these researchers to link this growing field with evolutionary medicine would be warranted.

Keywords Nutrition

Keywords Evolutionary Biology

Keywords Health Science

Presentation pref. Oral presentation preferred (otherwise poster)

Additional file

Extra information UMERIC

Presentation

Session Session 2A : Metabolic and cardiovascular diseases

Time 11:45 - 12:00

Date 19/08/2017

Location Round Room

Abstract Registration No: 90

Conference	ISEMP	ISEMPH
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Abstract no. 90

Abstract code

Title of abstract **The microbiome and host resilience**

Author Alcock,
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Co-Author(s)

Topic Call for abstracts : ISEMPH conference

Abstract text The gut microbiota is made up of 30 trillion cells, as many as the human cells in the body. We are host to microbial genes -the microbiome - that outnumber human genes by 10 to 1. The combined set of mammalian and microbial genomes has been termed the hologenome, and the combined organism is the holobiont. Some researchers argue that the microbial contribution to the hologenome permits adaptation to new environments, thereby increasing the fitness of the combined organism, the holobiont. One prominent example is the dramatic transformation of the microbiome that accompanies changes in diet, e.g. from a plant-based to animal-based diet. Similar observations prompt the hypothesis that the microbiome increases the resilience of the holobiont to variable environments. Here I systematically review the effects of the microbiome on host resilience. Evidence from three domains -nutrition, high altitude medicine, and thermal stress -challenge the resilient holobiont hypothesis. Malnutrition, overnutrition, altitude sickness, and heat stroke impair host fitness as a direct consequence of resident bacteria. These examples provide evidence that microbial contribution to host resilience - when it occurs - comes at a cost of decreased resilience in other areas.

Keywords microbiome

Keywords fitness

Keywords resilience

Keywords holobiont

Presentation pref. Oral presentation preferred (otherwise poster)

Additional file

Extra information UMERIC

Presentation

Session Session 5B : Microbiome

Time 11:45 - 12:00

Date 20/08/2017

Location Red Room

Abstract Registration No: 92

Conference	ISEMP	ISEMPH
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Abstract no. 92

Abstract code

Title of abstract **Negative selection in humans and fruit flies involves synergistic epistasis**

Author Sohail,
Harvard Medical School; United States of America; Tel: 8573898585, mashaal33@gmail.com

Co-Author(s) Vakhrusheva, De Bakker,
Sul, Bazykin,
Pulit, Kondrashov,
Francioli, Sunyaev,
Van den Berg,
Veldink,
De Bakker,

Topic Call for abstracts : ISEMPH conference

Abstract text A long-standing puzzle in evolutionary genetics is the population survival under strong pressure of incessant deleterious mutations. Recent direct estimates of human and *D.melanogaster* genomic mutation rates suggest that these rates are high and likely incompatible with population survival under simple multiplicative models of negative selection. A proposed theoretical solution involves negative selection with synergistic epistasis. We developed a statistical approach to test this conjecture directly in large sequencing datasets. Negative selection with synergistic epistasis must produce negative linkage disequilibrium (LD) between deleterious alleles, and therefore, an under-dispersed distribution of the number of deleterious alleles in the genome. Indeed, we detected under-dispersion of the genomic number of rare Loss-of-Function (LoF) alleles in eight independent datasets from human and *D.melanogaster* populations of European and non-European ancestry. We also detected under-dispersion of the number of missense mutations in highly constrained genes in both organisms. Further, by conducting regression analyses and forward simulations, we ruled out other potential sources of negative LD such as random genetic drift and population structure. Thus, empirical data suggests that ongoing selection against rare protein disrupting alleles is characterized by synergistic epistasis, which can explain how human and fly populations persist despite very high genomic deleterious mutation rates.

Keywords mutation

Keywords epistasis

Keywords sexual recombination

Keywords networks

Presentation pref. Oral presentation preferred (otherwise poster)

Additional file

Extra information

Presentation

Session

Time -

Date / /

Location

Abstract Registration No: 94

Conference	ISEMP	ISEMPH
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Abstract no. 94

Abstract code

Title of abstract How similar are women's hormone profiles from one pregnancy to the next?

Author Fox,
UCLA; United States of America; Tel: 310 206-4589, mollyfox@ucla.edu

Co-Author(s) Sandman,
Davis,
Glynn,

Topic Call for abstracts : ISEMPH conference

Abstract text It is unknown how similar a woman's hormone levels during one pregnancy are to the same woman's hormone levels during a subsequent pregnancy. Circulating hormone concentrations during pregnancy are of major interest for understanding how reproductive life-history endocrinology affects health and development of both mother and child. Knowing whether women experience similar concentrations of hormones in each of their pregnancies can improve our estimation of lifetime (cumulative) exposures to the endocrine conditions of pregnancy. For understanding child development, many studies compare monozygotic twins, dizygotic twins, and sibling pairs to determine the contributions of genetics, intrauterine environment, and postnatal environment to phenotype. These comparisons assume highly variable intrauterine conditions in different pregnancies of the same mother, and yet the degree of similarity between siblings' prenatal environments remains unknown. Our study aimed to investigate how consistent women's hormone profiles are across two successive pregnancies. This longitudinal, prospective study followed a cohort of 28 women across two pregnancies, measuring at multiple timepoints women's circulating adrenocorticotropic hormone (ACTH), placental corticotropin-releasing hormone (pCRH), cortisol, estradiol, and progesterone. Results reveal substantial consistency from one pregnancy to another, and substantial predictability from one pregnancy to another. This is the first study to describe maternal and placental hormone levels across successive pregnancies.

Presentation pref. Oral presentation (no poster)

Additional file

Extra information

Presentation

Session Session 2B : Culture, gender and sexual health

Time 11:45 - 12:00

Date 19/08/2017

Location Red Room

Abstract Registration No: 95

Conference	ISEMP	ISEMPH
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Abstract no. 95

Abstract code

Title of abstract **Analysis of Thousand Genomes data reveals unique genetic architectures, considerations for personalized medicine**

Author Niedbalski,
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Co-Author(s)

Topic Call for abstracts : ISEMPH conference

Abstract text If distinct genetic architectures can explain a portion of disparity in disease prevalence, manifestation, and/or pharmacological response, there must then exist genetic loci specific to populations experiencing disease disparity. Here we use both theoretical and empirical techniques to identify population-specific genetic architectures and potentials for personalized medicine. We performed coalescent simulations to model the global distribution of unique variation as predicted by human evolutionary history. Our simulations predict two instances of evolutionary opportunity for this type of variation: the Out of Africa migration and the Peopling of the Americas. We tested this result empirically using the Thousand Genomes sample, which provides whole genome sequences for N=2,577 from 26 global populations. Here our predictions, based in evolutionary theory, were upheld, we identified 43,625 SNPs unique to Africans, 2,253 unique to Non Africans, and 15,241 unique to Native Americans. Notably, there were no high frequency variants unique to any other biogeographic regions. Furthermore, we performed tests for natural selection and phenotypic (disease) association on all alleles generated from the Thousand Genomes query, identifying candidate loci for further investigation of health disparity in these populations. Our data provides a novel evolutionary framework for studying the complex biologies of common diseases.

Keywords Genomics

Keywords Evolution

Keywords Personalized Medicine

Keywords Thousand Genomes

Presentation pref. Oral presentation preferred (otherwise poster)

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Presentation

Session Session 7A : Genetics

Time 16:00 - 16:15

Date 20/08/2017

Location Red Room

Abstract Registration No: 96

Conference	ISEMP	ISEMPH
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Abstract no. 96

Abstract code

Title of abstract **Decreasing unnecessary antibiotic use and associated harms by incorporating evolutionary perspectives into the diagnostic criteria for sepsis**

Author Blyth,
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Co-Author(s) McNary,
Schubert,
Decano,
Kim,
Carey,

Topic Call for abstracts : ISEMPH conference

Abstract text The need for responsible antibiotic stewardship can be difficult to reconcile with the clinicians task of preventing septic patients from progressing to severe sepsis and septic shock, which are respectively associated with mortality rates of 25-30% and 40-70%. Empiric antibiotics are often administered before culture results can be acquired, yet administration of an antibiotic has significant risk, including nosocomial infections, drug reactions, antibiotic-resistant bacteria, and alterations of natural microbiota. SIRS are the most common clinical criteria used to recognize sepsis. From an evolutionary perspective most if not all of the findings used in SIRS likely constitute a predictable and adaptive host response to infection rather than a deteriorating patient in need of immediate antibiotics, and indeed SIRS has a notably low specificity. This prospective chart review aims to determine the frequency with which antibiotics are unnecessarily administered in the emergency department and the harms from antibiotic exposure. Without more accurate criteria, however, it is not clinically feasible to decrease emergent antibiotic use. To that end, several sets of criteria are being examined in terms of accurately identifying severe bacterial infection, including criteria that based on evolutionary thinking would be more likely represent a dysregulated and/or decompensated response to infection.

Keywords Sepsis

Keywords Antibiotic Stewardship

Keywords Nosocomial infections

Keywords Microbiome disruption

Presentation pref. Oral presentation preferred (otherwise poster)

Additional file

Extra information

Presentation

Session Session 3A : Pathogens

Time 17:00 - 17:15

Date 19/08/2017

Location Round Room

Abstract Registration No: 97

Conference	ISEMP	ISEMPH
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Abstract no. 97

Abstract code

Title of abstract **A Re-Conceptualization of Bacterial Virulence Emphasizing Interactions Among Pathogens of the Same or Different Species**

Author Greenspan,
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Co-Author(s)

Topic Call for abstracts : ISEMPH conference

Abstract text A major focus of microbiologists is "molecular pathogenesis," i.e. accounting for the details of infection by a given microbe through exploration of the functions of gene products, that are typically referred to as virulence factors, associated with that pathogen. This approach to explaining bacterial virulence can foster the views that: 1) there are pathogens and non-pathogens and 2) that virulence is an attribute of individual bacterial cells. Recent studies have demonstrated that optimal virulence can require cooperation between cells of a bacterial population that do and do not produce putative virulence factors. Other investigations have revealed that nominally non-pathogenic bacterial species can increase, or decrease, the virulence of a pathogenic species or that a pathogen can alter the host microenvironment so as to confer pathogenicity on a non-pathogen. Numerous studies have also established that the virulence manifest by a given strain of a microbial pathogen in any given host of a single species can vary with host genetics or body site. I will place virulence in evolutionary perspective in the context of challenging the notions that there is a clear dividing line between pathogens and non-pathogens or that virulence is an attribute primarily attributable to individual bacterial cells.

Keywords bacteria

Keywords virulence

Keywords pathogenesis

Keywords interactions

Presentation pref. Oral presentation (no poster)

Additional file

Extra information UMERIC

Presentation

Session Session 5A : Theoretical considerations and animal models

Time 11:45 - 12:00

Date 20/08/2017

Location Room 4

Abstract Registration No: 11

Conference	ISEMP	ISEMPH
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Abstract no. 11

Abstract code P01

Title of abstract **Developmental conditions are important for health: facial fluctuating asymmetry and risk of cardiovascular diseases**

Author Klimek,
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Co-Author(s) Galbarczyk,
Nenko,
Jasienska,

Topic Call for abstracts : ISEMPH conference

Abstract text Low degree of fluctuating asymmetry (FA) is proposed as a signal of developmental stability and good genetic quality, thus individuals with low FA should 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 relationship between facial FA and risk factors of cardiovascular diseases (cholesterol levels and hypertension). Data come from Mogielica Human Ecology Study Site in Poland. The participants were 263 women aged 45-92, and 81 men aged 47-87. Fasting blood sample and facial images were collected. Age, body mass, smoking, diabetes, alcohol consumption and taking drugs lowering cholesterol were included as covariates. 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 ($R^2=0.12$; $p=0.04$) and LDL-cholesterol ($R^2=0.05$; $p=0.02$). Facial FA was not related to levels of HDL-cholesterol ($p=0.19$). No significant results were observed for men. Our results indicate 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 early-developmental conditions are important for later health.

Keywords facial fluctuating asymmetry

Keywords developmental environment

Keywords cholesterol levels

Keywords hypertension

Presentation pref. Poster presentation

Additional file

Extra information

Presentation

Session Coffee break & Posters

Time 15:45 - 16:30

Date 19/08/2017

Location Fountain patio

Abstract Registration No: 6

Conference	ISEMP	ISEMPH
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Abstract no. 6
Abstract code P02
Title of abstract **Environmental influences on the Malagasy skin microbiome**

Author Manus,
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Co-Author(s) Yu,
Park,
Mueller,
Council,
Horvath,
Nunn,

Topic Call for abstracts : ISEMPH conference

Abstract text The skin is continuously exposed to the outside environment, resulting in microbial transfer between the humans, animals, and environment with which an individual comes into contact. Most research on the skin microbiome has focused on Western human populations living in largely hygienic conditions, yet these populations have vastly different patterns of environmental contact than the majority of people on the planet who live in low- and middle-income countries or rural settings. We studied the skin microbial communities of humans and domesticated cattle (zebu) living in rural Madagascar to investigate how zebu ownership affects microbial community composition, and to characterize non-Western human skin communities and zebu skin communities more generally. Analysis of 16S rRNA gene sequencing data suggests that humans have a skin microbial community that is not influenced significantly by zebu ownership. However, there were clear differences in microbial communities among human body sites, likely explained by variation in the level of contact between different body sites and the outside environment. In contrast to Western populations, we failed to find evidence for similarities between individual humans and their domesticated animals, likely due to profound lifestyle differences between rural Malagasy and Western human populations.

Keywords Microbiome

Keywords Evolutionary mismatch

Keywords Environment

Keywords Madagascar

Presentation pref. Poster presentation

Additional file

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Presentation

Session Coffee break & Posters

Time 15:45 - 16:30

Date 19/08/2017

Location Fountain patio

Abstract Registration No: 12

Conference	ISEMP	ISEMPH
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Abstract no. 12
Abstract code P03
Title of abstract **Importance of conditional selection in somatic evolution of cancer**
Author B.,
IISER; India; Tel: 9840570894, vibishan.b@students.iiserpune.ac.in
Co-Author(s) Watve,

Topic Call for abstracts : ISEMPH conference

Abstract text Cancer occurs through somatic accumulation of mutations, but the precise dynamics of this process remain unclear. It is now recognized that the possibility of all oncogenic mutations passively co-occurring in one cell is highly remote, and mutations are instead thought to spread through clonal expansion. However, this involves the implicit assumption that each mutation provides an all-time advantage. This stands in contrast to cell competition experiments that have revealed a high degree of tissue-context dependence of this advantage. We test, using a model of somatic cellular evolution, the relative importance of the basal mutation rate, clonal expansion, and micro-environmental variations in explaining cancer incidence. The model reveals that the mutation rate and default clonal expansion are, by themselves, insufficient to replicate epidemiological trends in cancer incidence. The model also shows that individual variations in microenvironmental and physiological factors impose strong selective constraints on mutation accumulation, and this differential conditional selection is both necessary and sufficient to reproduce population-level and age-wise incidence of cancer as observed epidemiologically. We therefore argue that the selective landscape imposed by the micro-environment is the crucial missing link in understanding cancer progression in the soma.

Keywords Somatic evolution
Keywords Selection
Keywords Cancer
Presentation pref. Poster presentation

Additional file
Extra information

Presentation

Session Coffee break & Posters
Time 15:45 - 16:30
Date 19/08/2017
Location Fountain patio

Abstract Registration No: 23

Conference	ISEMP	ISEMPH
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Abstract no. 23
Abstract code P04
Title of abstract **The Project SALUTOGENETICS: Bridging Evolution and Health**

Author Kitsiri,
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Co-Author(s)

Topic Call for abstracts : ISEMPH conference

Abstract text Our pathologies including psychopathology are not only deeply embedded in our personal biology but in our collective biology of the species or even the whole biosphere. A result of the evolutionary forces, dynamics and phenomena that the species and the biosphere were subjected to. Therefore any attempt to find treatment and preventive measures cannot ignore the evolutionary history of all living things in general and mankind in particular. Evolutionary genetics could be considered as the starting point of the search for healing that the Humanity and the planet on which it has evolved seem to desperately long. The Project Salutogenetics aims to bridge our evolutionary history with this search for healing and lasting health and a sustainable planet before we embark upon spreading life across the universe. Salutogenetics is both a new word and a concept. It aims to combine the salutogenic model of health promotion introduced by Aaron Antonovsky in 1979 and the emerging fields of personal and evolutionary genetics to develop a framework that encompasses personal health, public health as well as a sustainable planet. The aim of this abstract is to introduce this new concept in order to gather momentum to consolidate the ideas presented in it.

Keywords Evolution

Keywords Genetics

Keywords Health

Keywords Salutogenetics

Presentation pref. Poster presentation

Additional file

Extra information

Presentation

Session Coffee break & Posters

Time 15:45 - 16:30

Date 19/08/2017

Location Fountain patio

Abstract Registration No: 27

Conference	ISEMP	ISEMPH
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Abstract no. 27
Abstract code P05
Title of abstract **Rapid adaptation of clinical *Pseudomonas aeruginosa* populations to antibiotic therapy**

Author Tüffers,
Kiel University; Germany; Tel: +494318804146, ltueffers@zoologie.uni-kiel.de

Co-Author(s) Bobis, Schreiber,
Schubert, Schulenburg,
Heinsen, Friedrichs,
Fickenscher, Bewig,
Schreiber,

Topic Call for abstracts : ISEMPH conference

Abstract text *Pseudomonas aeruginosa* is one of the most problematic multidrug-resistant bacteria and the major airway pathogen in adult cystic fibrosis. Antibiotics are used extensively to maintain lung function in these patients, but empirical support for therapy success is scarce. While the long-term adaptation of *Pseudomonas* to the cystic fibrosis lung was shown to lead to diversification and antibiotic resistance, there is little data on fast adaptation to newly applied antibiotic pressures. Meanwhile, designing therapies along evolutionary principles to minimize resistance evolution is a promising concept. Using sputum metagenomics and deep sampling of *Pseudomonas* isolates from a cohort of cystic fibrosis patients taking intravenous antibiotics, we could show that this therapy has a limited effect on bacterial load, but can lead to rapid population-wide shifts towards resistance. This shows that individual therapy courses can contribute to the overall antibiotic resistance within cystic fibrosis patients. In order to test alternative antibiotic regimens, which have been shown to reduce adaptation of laboratory strains, we performed experimental evolution of clinical isolates. The results could improve the management of *Pseudomonas* lung infections by modeling future therapy regimens to exploit bacterial evolutionary constraints, resulting in higher rates of successful clearance while reducing antibiotic resistance.

Keywords antibiotic resistance

Keywords *Pseudomonas aeruginosa*

Keywords experimental evolution

Presentation pref. Poster presentation

Additional file

Extra information UMERIC

Presentation

Session Coffee break & Posters

Time 15:45 - 16:30

Date 19/08/2017

Location Fountain patio

Abstract Registration No: 34

Conference	ISEMP	ISEMPH
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Abstract no. 34
Abstract code P06
Title of abstract **An evolutionary model of function and pathology of the human hallux:**
Author Tamer,
Student; Case Western Reserve University; United States of America; Tel: 661-706-1619,
Co-Author(s) Simpson,

Topic Call for abstracts : ISEMPH conference

Abstract text Between humans and primates, morphological differences in hallucial shape and orientation reflect fundamental differences in function and pathology. Our statistical comparisons of metatarsal heads across species using the Hamann-Todd Human Osteological Collection at the Cleveland Museum of Natural History confirm previous studies's affirmations of dorsal extension of the articular surface in humans consistent with the function of propulsive toe-off, which is in contrast to the grasping function of the plantar-oriented extension of the articular surface in primates.
Hallucial morphological differences also play a key role in human foot pathology. Hallux valgus, commonly known as a bunion, is the most common forefoot problem in adults. This acquired deformity, which is often correlated with pain and impaired gait, is rooted not only in external factors such as narrowed footwear, but also in the intrinsic structure of the hallucial orientation. Primarily as a consequence of hallucial torsion, measured using the same collection of specimens, when the hallucial phalangeal flexors contract during propulsion, their course shears obliquely across the inferior aspect of the metatarsal head. Under increasing stress, the oblique orientation of the phalangeal flexors can laterally displace the hallucial sesamoids and intervening Flexor Hallucis Longus tendon, thereby deflecting the hallucial phalanges laterally.

Keywords Hallux valgus
Keywords bunions
Keywords human metatarsal
Keywords MTP1
Presentation pref. Poster presentation
Additional file
Extra information UMERIC

Presentation

Session Coffee break & Posters
Time 15:45 - 16:30
Date 19/08/2017
Location Fountain patio

Abstract Registration No: 38

Conference	ISEMP	ISEMPH
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Abstract no. 38

Abstract code P07

Title of abstract **Evolutionary emergence of bacteriophages in heterogeneous bacterial populations**

Author Chabas,
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Co-Author(s) Nicot,
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Tremblay,
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Van Houte,
Westra,
Westra,
Gandon,

Topic Call for abstracts : ISEMPH conference

Abstract text Different public-health strategies are used to prevent or limit the emergence of infectious diseases. Several control strategies rely on the increase in the frequency of resistant hosts in the host population (e.g. resistant cultivars in plants, vaccination in vertebrate hosts). The evolutionary emergence of pathogens able to infect resistant hosts, however, may erode the benefit of these control strategies. In the present work, using a bacteria/phages model, we monitor the probability of parasite evolutionary emergence as a function of the heterogeneity of the host population. In addition, we discuss the variability of the speed at which different types of resistance can be overcome by pathogens. This work has strong implications in evolutionary epidemiology as the phage/bacteria model can help us understand the evolutionary emergence of other pathogens. This work has also practical applications in the dairy industry as manipulating the heterogeneity of these bacteria may be a way to limit the emergence of potentially devastating bacteriophage epidemics.

Keywords Evolutionary epidemiology

Keywords parasite evolution

Keywords heterogeneous population

Keywords Evolutionary emergence

Presentation pref. Poster presentation

Additional file

Extra information

Presentation

Session Coffee break & Posters

Time 15:45 - 16:30

Date 19/08/2017

Location Fountain patio

Abstract Registration No: 42

Conference	ISEMP	ISEMPH
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Abstract no. 42
Abstract code P08
Title of abstract Early life effects on C-reactive protein levels among Bangladeshi migrants to the UK

Author Bentley,
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Co-Author(s) Begum,
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Akhter,
Nahar,
Kasim,

Topic Call for abstracts : ISEMPH conference

Abstract text Exposure to pathogens during early life educates the immune system, informs adult immunological phenotypes, and establishes anti-inflammatory regulatory pathways. Lack of immunological stimuli during childhood in excessively hygienic conditions typical of many contemporary environments may have increased human vulnerability to autoimmune diseases. Studies from developing countries show that greater childhood exposure to pathogens results in lower adult levels of C-reactive protein (CRP) (a general marker of inflammation) compared to those with less exposure. Using ELISA kits (Salimetrics), we compared salivary levels of CRP between first-generation (adult migrants, n=174; child migrants, n=148) and second-generation (n=130) Bangladeshi migrants living in England. We hypothesized that first-generation Bangladeshis, exposed during childhood to a greater number of infectious and parasitic diseases, would have lower levels of CRP as adults compared to second-generation British-Bangladeshis. Our hypothesis is supported. Results from multiple linear regression showed that CRP levels were significantly lower between generations [estimates = -0.101, 95% CI = -0.198, -0.004, and -0.108, 95% CI = -0.209, -0.007] for second generation vs. adult and child migrants, respectively] after adjusting for gender, age, childhood disease score, the body mass index, and waist circumference. Inflammatory changes may explain some aspects of metabolic disorders among South Asian migrants.

Keywords early life development

Keywords inflammation

Keywords C-reactive protein

Keywords migrants

Presentation pref. Poster presentation

Additional file

Extra information

Presentation

Session Coffee break & Posters

Time 15:45 - 16:30

Date 19/08/2017

Location Fountain patio

Abstract Registration No: 51

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Abstract no. 51

Abstract code P09

Title of abstract **Evolutionary Medicine: Carpal Tunnel Syndrome**

Author Perez,
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Co-Author(s) Simpson,

Topic Call for abstracts : ISEMPH conference

Abstract text Carpal tunnel syndrome (CTS) can occur during median nerve entrapment because of high intra-tunnel pressure notably due to repetitive movements of the hand and wrist. Individuals with CTS may feel pain, tingling, numbness and weakness in the palmar surface of the first three digits and on the lateral side of the fourth digit, greatly reducing fine motor skills and mobility of the affected fingers – those with CTS experience greatly reduced quality of life. Interestingly, *Homo sapiens* is the only species of primates known to suffer from CTS, despite having similar physical anatomy in the carpal tunnel and wrist to that of other monkeys and apes. The absence of CTS pathologies in other primates can be attributed to 1) osteological and muscular adaptations commonly found in suspensory or vertical climbers and 2) the development and orientation of the pisiform bone, both of which contribute to a decreased *carpal tunnel index*, a ratio that can accurately predict incidence of CTS.

Keywords carpal tunnel syndrome

Keywords wrist

Keywords nerve entrapment

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Location Fountain patio

Abstract Registration No: 65

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Abstract no. 65
Abstract code P10
Title of abstract **A call to use cultural competence when teaching evolution to religious undergraduate students: Introducing Religious Cultural Competence in Evolution Education (ReCCEE)**
Author Brownell,
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Co-Author(s) Barnes,

Topic Call for abstracts : ISEMPH conference

Abstract text While evolution is a core component of biology, many students in undergraduate biology classes do not accept evolution due to a perceived conflict with their religious beliefs. However, college evolution instructors may struggle with addressing the perceived conflict between religion and evolution in an effective way due to a disconnect between their own religious beliefs and that of their students; although the majority of students learning evolution are religious, most instructors teaching evolution at the college level are not. In an interview study with instructors from secular institutions, we found that instructors avoided discussions about religion in the classroom, largely due to their own beliefs. We also conducted an interview study of religious students in biology classes at a secular institution and showed that religious students did not feel included in the classroom when learning evolution and highlighted that instructors did not acknowledge their religious beliefs. To compensate for this disconnect between the secular culture of evolution instructors and the religious cultures of many of their students, we propose using a lens of cultural competence to form Religious Cultural Competence in Evolution Education (ReCCEE) to help decrease students' perceived conflict between evolution and religion.

Keywords evolution education
Keywords religion
Keywords evolution
Keywords conflict
Presentation pref. Oral presentation preferred (otherwise poster)
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Location Fountain patio

Abstract Registration No: 69

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Abstract no. 69

Abstract code P11

Title of abstract **Phylogenetic Contrast Of Paralogous Genes And Toxin Resistance Genotypes In *Escherichia coli* and *Klebsiella pneumoniae***

Author Sharpe,
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Co-Author(s) Graves,
Harrison,

Topic Call for abstracts : ISEMPH conference

Abstract text We are investigating how bacteria evolve resistance to antimicrobial metals. The genetic basis for this survival can be due to specific resistance pathways encoded in the bacterial genome, many of which have been attributed to horizontal transferred genes, known as xenologs, across independently evolving lineages. We hypothesize that genomic duplications, resulting in paralogs, also contribute to toxin resistance. We investigated strains of *Escherichia coli* and *Klebsiella pneumoniae* having fully sequenced genomes. We used data from the Department of Energy Joint Genome Institute Integrated Microbial Genomes resource (IMG) curated set of 908 cellular pathways. Our workflow began with identifying phylogenetically paired groups of strains of *Escherichia coli* and *Klebsiella pneumoniae* with contrasting genotypes of silver and copper resistance and sensitivity based on the presence/absence of the *silE* and *cusS* genes. The next step for the comparison evaluated each pathway for being over-represented or under-represented in resistance groups compared to the sensitive groups. This evaluation was implemented through bootstrap resampling, where we measured phylogenetic contrasts of paralogous genes and toxin resistance genotypes. Literature comparison is validating many of the predictions from our bootstrapping method for how variable levels of paralogy drive some of the likely adaptive changes.

Keywords Bacterial Resistance

Keywords Bacterial Genomics

Keywords Bioinformatics

Keywords Phylogenetic Contrast

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Abstract Registration No: 73

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Abstract no. 73

Abstract code P12

Title of abstract Evolution of Copper resistance in Escherichia coli

Author Boyd,
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Co-Author(s) Ewunkem,
Graves Jr.,

Topic Call for abstracts : ISEMPH conference

Abstract text Multi-drug resistant (MDR) bacteria are a growing worldwide public health concern. Bacteria have rapidly evolved resistance to traditional antibiotics increasing the threat posed by antibiotic resistant “superbugs.” This condition has led to a crucial need for new antimicrobial agents. Metals such as copper and silver have been used as antimicrobial agents in clinical and non-clinical settings for centuries due to their effectiveness in limiting the growth of a broad range of microorganisms. Silver is highly toxic to bacteria as it impacts numerous physiological pathways. Unlike silver, copper is both an essential micronutrient and potent antibacterial agent. Due to copper’s antimicrobial properties it has been claimed that copper could be ideal to prevent the spread of MDR bacteria. Here we test the evolvability of resistance to excess ionic copper (Cu₂SO₄) by means of laboratory experimental evolution in <i>E.coli</i> strain K-12MG1655. Initial results suggest that copper resistance evolves much more slowly than silver resistance. Our studies are ongoing.

Keywords Anti-microbial resistance

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Abstract Registration No: 76

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Abstract no. 76
Abstract code P13
Title of abstract Invasion effects on native species: positive or negative?

Author Ashghali Farahani,
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Co-Author(s) Jan,

Topic Call for abstracts : ISEMPH conference

Abstract text Ecologists neglect about parasite spillback or resource competition as a potential threat to native species in relation with energy flow during invasion. Invasions could have effect on ecological tolerance and geographic distribution of native species, predators and their parasites. But on the other hand, economists discuss about positive effects like Biological control or increasing catch per unit area during some invasions. Taxonomical relation between native species and invaders are very important in invasive host & parasite coevolution. For example, population of native amphipods in central European rivers are progressively displaced by highly adaptive invasive species of amphipods with different salinity, temperature or drought tolerance. We hypothesized that deviations from normal behavior due to infection are more distinct in native species compared to the invasive one. According to our results invader amphipods (*Echinogammarus berilloni*) are less active and save energy to be used for survival in areas with high pollution and salinity. They also avoid predator odor more than native species. We discuss to what extent these results may explain the distribution patterns and invasion processes in relation to parasitism found in nature.

Keywords Invasion

Keywords Echinogammarus berilloni

Keywords parasitism

Keywords predation

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Location Fountain patio

Abstract Registration No: 77

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Abstract no. 77
Abstract code P14
Title of abstract **The role of ecological factors in parasite distribution and non-host predator niche**

Author Ashghali Farahani,
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Co-Author(s) Jan,

Topic Call for abstracts : ISEMPH conference

Abstract text Some factors like salinity, water velocity and anti-predator behavior have effects on adjusting main predator's effectiveness like aquatic birds in consuming gammarids as an intermediate host of acanthocephalan parasite , *Polymorphus minutus*. Our results suggest that changes in parasite prevalence during invasion of intermediate host, *Echinogammarus berilloni*, due to red queen dynamics could affect the trophic niche of host population. As a general finding, non-host predator like three spine stickleback was able to occupy its realized niche in middle and upper stream and it affect to parasite-invader's host coevolution.

Keywords parasite

Keywords Polymorphus minutus

Keywords trophic niche

Keywords non-host predator

Presentation pref. Oral presentation preferred (otherwise poster)

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Session Coffee break & Posters

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Location Fountain patio

Abstract Registration No: 78

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Abstract no. 78

Abstract code P15

Title of abstract **Phases of the menstrual cycle and women's perception of tattooed men**

Author Milkowska,
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Co-Author(s) Ziomkiewicz-Wichary,
Galbarczyk,

Topic Call for abstracts : ISEMPH conference

Abstract text

Objective: Traditionally evolutionary psychology studies underlie the importance of woman fertility and menstrual cycle phase for the assessment of men's certain characteristics. It is suggested that women's preferences toward tattooed men mate should increase during the fertile periods.

Methods: The data from 2437 heterosexual women were analyzed. Nine pairs of digitally modified men's pictures (without and with tattoo) were presented to women during the internet-based surveillance. Women assessed presented men in seven categories. Regularly menstruating women (N=1632) were assigned to fertile and non-fertile group.

Results: Men with tattoo were assessed as worst potential partners than men without tattoo only by women during non-fertile period ($F(1,1361)=4.41, p=0.04$). Women in fertile period did not find tattooed men as more or less suitable potential partner. Presence of tattoo did not influence the assessments between phases of cycle. Furthermore women, regardless cycle phase, rated tattooed men as healthier, more masculine, dominant, aggressive, but as worse potential partners and parents than non-tattooed men.

Conclusions: Our results demonstrate very limited influence of woman's fertility status on their perception of tattooed men. Moreover, results indicate that women ignore tattoo presence during assessment of suitability as a potential partner in fertile period.

Keywords mate choice

Keywords tattoo

Keywords handicap hypothesis

Keywords hormones

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Location Fountain patio

Abstract Registration No: 85

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Abstract no. 85

Abstract code P16

Title of abstract **Eliciting Common Student Misconceptions in Evolution and Medicine**

Author Grunspan,
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Co-Author(s) Nesse,
Brownell,

Topic Call for abstracts : ISEMPH conference

Abstract text Students often struggle with common misconceptions when learning. These misconceptions can represent critical roadblocks preventing mastery of curricular goals. Eliciting and documenting these common misconceptions enables the development of curriculum and assessment tools specified to these common pitfalls, and is an important step in improving pedagogy. While previous work has identified student misconceptions in evolution, no work has systematically elicited misconceptions specific to Evolution and Medicine. We present early research results from efforts to identify student misconceptions about disciplinary core principles in Evolutionary Medicine. These misconceptions will be the basis of a validated assessment tool to measure student mastery of evolutionary medicine concepts.

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Abstract Registration No: 101

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Abstract no. 101

Abstract code P17

Title of abstract **Absence of Long-Distance Dispersal in Ebola: A Phylogenetic Examination**

Author Downie,
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Co-Author(s)

Topic Call for abstracts : ISEMPH conference

Abstract text A common assumption underlying Ebola virus public health strategies is that the virus is spread in Sub-Saharan Africa by long-distance dispersal. The main evidence for this assertion is in the current phylogeny of Ebola virus. However, this phylogeny clashes with our understanding of the virus's ecology and prior spread. Here, we use a simulation approach to demonstrate how features of Ebola molecular evolution are producing underestimates of divergence dates in the phylogeny of the virus. In particular, we investigate evidence for multiple, geographically-partitioned substitution rates in Ebola that are affecting Bayesian inference. Our results suggest that the virus's spread fits better with a previously published wave-spread model, implying a slower, more constant rate of spread. Furthermore, our results also have significant implications for public health strategies for the prevention and containment of Ebola outbreaks.

Keywords EBOLA

Keywords PHYLOGENETICS

Keywords DISEASE ECOLOGY

Keywords PHYLODYNAMICS

Keywords MOLECULAR EVOLUTION

Keywords BAYESIAN PHYLOGENETICS

Keywords HOST ECOLOGY

Keywords VIROLOGY

Abstract Registration No: 101

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Session Coffee break & Posters

Time 15:45 - 16:30

Date 19/08/2017

Location Fountain patio

Abstract no. 99

Abstract code P18

Title of abstract **Mouth breathing effects on craniofacial development**

Author Glanville,
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Co-Author(s)

Topic Call for abstracts : ISEMPH conference

Abstract text Mouth breathing effects the growth and development of the craniofacial structures. Anthropologists have confirmed that mouth breathing didnt begin to around the 18th century. Mouth breathing alters the growth & development of the face and sets the individual up for common health problems like sleep apnea & snoring. I think its fair to say that if our ancestors did snore, that would of provided an easy meal for prehistoric predators and I doubt we would be here now if it was the norm. We have to remember that the maxilla makes up 85% of the nasal airway, if it continues to shrink is it the sepcies is suffocating itself? Is this mother natures way of wiping us out as we are no longer vital?

Keywords mouth breathing

Keywords snoring

Keywords craniofacial development

Keywords maxilla

Abstract Registration No: 99

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Time 15:45 - 16:30

Date 19/08/2017

Location Fountain patio

Abstract no. 100

Abstract code P19

Title of abstract **Iron-driven host-microbiota coadaptation: an influence factor in *Mycobacterium tuberculosis* infection?**

Author Ojong,
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Co-Author(s) Hauptmann,
Schaible,

Topic Call for abstracts : ISEMPH conference

Abstract text Iron is an indispensable micronutrient for growth, differentiation and survival of both, the eukaryotic host and bacteria, including commensal ones. We hypothesize that iron availability can shape host-microbiota coevolution, which in turn, can modulate susceptibility to tuberculosis as caused by *Mycobacterium tuberculosis* (Mtb). The iron regulatory proteins, IRP1 and IRP2 determine cellular iron availability through post transcriptional modulation of iron transport and iron storage protein expression. To investigate the influence of iron availability on commensal communities, we perform 16S rRNA sequencing from lung-, trachea-, and gut tissue of *Irp1*^{-/-} and *Irp2*^{-/-} mice, as well as their respective wildtype (wt) littermates. Changes in these mice's microbiota compositions are monitored upon iron depletion and supplementation. Innate defense responses to Mtb will be studied *in vivo* in these mice as well as in primary cells such as bone marrow-derived macrophages (BMM) from wt, *Irp1*^{-/-} and *Irp2*^{-/-} mice with or w/o, either iron supplementation or sequestration. Our studies will provide insight into the influence of iron availability on commensal populations *in vivo* and the downstream effects on Mtb infection. In summary, we investigate host-microbiota coadaptation, with iron availability constituting the driving force. Following the concept of evolutionary medicine, we aim to understand the susceptibility of the host microbiota superorganism to Mtb infection.

Keywords Evolution

Keywords Microbiota

Keywords Iron regulatory proteins

Keywords *Mycobacterium tuberculosis*

Abstract Registration No: 100

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Abstract no. 89

Abstract code P20

Title of abstract **Daf-2 lifespan extension in *Caenorhabditis elegans* : what are the fitness costs?**

Author Ravindran,
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Co-Author(s) Lind,
Maklakov,

Topic Call for abstracts : ISEMPH conference

Abstract text Genetic studies of the nematode *Caenorhabditis elegans* have shown that the evolutionarily-conserved insulin/IGF-1 signalling (IIS) pathway regulates longevity and reproduction. While evolutionary theories of ageing predicts that genes increasing lifespan should come with a fitness cost, RNA interference (RNAi) studies in *C. elegans* have found that decreased adult activity of the *daf-2* gene in the IIS pathway can double the lifespan of self-fertilized *C. elegans* hermaphrodites without a cost in reproduction. Therefore, we attempt to investigate whether there exist any fitness costs associated with increased lifespan in *daf-2* RNAi *C. elegans* beyond self-fertilized fecundity, since self-fertilizing hermaphrodites are sperm-limited. We predict that these fitness costs are observed in mated *C. elegans* hermaphrodites, since they can express their full reproductive potential. Using a 2X2 factorial design, we will evaluate the effect of RNAi *daf-2* knockdown versus empty vector control on longevity and age-specific fecundity of mated and unmated *C. elegans*. As *daf-2* largely increases post-self-reproductive lifespan, potential fitness costs when the adults are mated late in life will also be evaluated. Initial results will be presented and discussed to help understand the evolutionary context of ageing at the molecular level.

Keywords Ageing

Keywords *daf-2*

Keywords RNA interference

Keywords Evolution

Abstract Registration No: 89

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