Title	Authors	Abstract
State of the field and strategies for program directors	Frank Rühli will lead a discussion by directors of evolutionary medicine programs.	This meeting is for directors of evolutionary medicine programs and those who would like to create programs to share news and strategies for developing the field, but others are welcome.
Welcome reception	Hosting Committee	
Eco-evolutionary dynamics of Escherichia coli when it colonizes the intestinal tract	Nelson Frazão, Instituto Gulbenkian de Ciência, Oeiras; Anke Konrad, Instituto Gulbenkian de Ciência; Daniela Güleresi, Instituto Gulbenkian de Ciência, Oeiras; Michael Lässig, University of Cologne, Cologne; Isabel Gordo, Instituto Gulbenkian de Ciência, Oeiras;	Bacteria live in highly diverse ecosystems inside the intestines of many organisms. How and at what pace do they evolve in that ecosystem is not yet understood. Here we address these questions using the power of mouse models and the wealth of functional knowledge on a human gut commensal, Escherichia coli. We demonstrate that the colonization success of a new invader E. coli strain depends on the microbiota diversity. We follow invader strain populations over 7000 generations and map their adaptive evolution by genomic analysis combined with functional and fitness assays. Our main finding is that following colonization, two modes of evolution were observed: one in which diversifying selection leads to long-term coexistence of ecotypes and another in which directional selection propels selective sweeps. The directional selection mode is characterised by selective sweeps, while the ecotype formation mode is governed by negative-frequency dependent selection. We identify metabolic functional adaptations as the main drivers of the evolutionary dynamics in both modes, while adaptation to phages is specific to the directional selection mode. Our results are of broad impact to the understanding of bacterial evolution in species rich ecosystems, such as human guts.
Different predictors of intimate partner and natal family violence against women	Olympia L K Campbell, UCL, London; Ruth Mace, UCL, London.	Violence against women is often studied in the context of violence from intimate partners. However, women receive violence from a wider range of individuals - such as their natal kin - including their siblings, parents, uncles, and cousins. Applying insights from evolutionary theory we examine whether cousin marriage, which has been hypothesised to both reduce the risk of partner violence but increase the risk of natal family violence, associates differently with each type of violence. Secondly, we test whether common risk factors for intimate-partner violence, such as wealth, associate similarly with natal violence. Analysing over 16,000 Jordanian women from the Jordan Demographic Health Surveys we find that being married to a patrilateral cousin but not a matrilateral cousin is associated with a reduced risk of reporting intimate partner violence, in line with predictions from behavioural ecology. As expected, wealth is negatively associated with partner violence, but we find no association with natal family violence. Lastly, individuals with more children are more likely to report IPV, in line with violence having fitness relevant outcomes. Findings indicate the importance of distinguishing between types of cousin marriage and highlight substantial differences in risk factors for intimate partner compared to natal family violence.
Inequality has inconsistent effects on health in an agricultural society undergoing rapid market transition	Siobhán M. Mattison, University of New Mexico; Neil MacLaren, SUNY Buffalo; Chun-Yi Sum, Boston University; Mingjie Su, Fudan University; Peter M. Mattison, University of New Mexico; Mary K. Shenk, Pennsylvania State University; Tami Blumenfield, University of New Mexico; Hui Li, Fudan University; Katherine Wander, SUNY Binghamton	Although social and material inequality are now persistent and pervasive, they were typically more transient phenomena over human evolutionary history. This mismatch creates the potential for illness if human biologies have not evolved in response to sustained and significant inequality. In this talk, we investigate these issues by asking whether inequality predicts poor health outcomes. Specifically, we ask how the risk of diabetes and hypertension varies in relation to wealth (access to resources) and prevailing levels of material inequality among matrilineal and patrilineal Mosuo of Southwest China. The Mosuo are agriculturalists experiencing rapid market integration and levels of material inequality varying from low to high, depending on the extent of livelihood diversification (the “Bram Tucker effect”). We collected sociodemographic, anthropometric, and biometric data from 505 households in 2017 and 2018 and used generalized linear modeling in R to model predictors of diabetes and hypertension. We found that inequality negatively predicted diabetes but positively predicted hypertension in matrilineal communities, whereas inequality positively predicted diabetes and had no relationship with hypertension in patrilineal communities. These results suggest that pathways among wealth, inequality, and health are specific to social and ecological environments.

Title	Authors	Abstract
Toward an integration of Ecology and Evolution with One Health	Meredith Spence Beaulieu, Triangle Center for Evolutionary Medicine/Duke University, Durham, NC, USA; Tyler Barrett, Duke University, Durham, NC, USA; Casey Farmer, Northern Illinois University, DeKalb, IL, USA; Kayla Kauffman, University of California, Santa Barbara, CA, USA; Caroline Rush, Duke University, Durham, NC, USA; Emily Sandberg, Duke University, Durham, NC, USA; Alma Solis, Duke University, Durham, NC, USA; Rebecca Supple, Duke University, Durham, NC, USA; Courtney Werner, Duke University, Durham, NC, USA; Charles Nunn, Triangle Center for Evolutionary Medicine/Duke University, Durham, NC, USA	Earth's ecosystems have been transformed by human use, including through land-use change, extractive industries, climate change, and international travel and trade. These human-driven transformations are affecting human health, food security, and economic systems, including through the emergence of infectious diseases and the loss of essential ecosystem services. The field of One Health is assuming an increasingly vital role in addressing these challenges by recognizing the interconnections among humans, other organisms, and our shared environments. We believe the suite of principles, theories, and tools used in ecology and evolution are vital to advancing the goals of One Health, yet research in these fields have largely operated in separate spheres and with less collaboration than expected given overlapping goals and disciplinary needs, particularly when considering issues at the human-animal-environment interface. Here, we explore the ways that increasing overlap between research in ecology and evolution and One Health would advance both fields. We discuss major subfields within ecology and evolution and highlight how theoretical foundations in each subfield could inform One Health research. We include case examples of realized integration with One Health, as well as the potential for further integration in future evolutionarily-focused One Health research.
Genetic confounding in health disparities research	I. King Jordan, Georgia Institute of Technology, Atlanta, Georgia, USA; Shivam Sharma, Georgia Institute of Technology, Atlanta, Georgia, USA; Leonardo Mariño-Ramírez, National Institute on Minority Health and Health Disparities, Bethesda, Maryland, USA	We contend that unmeasured genetic factors are likely to be a major source of hidden confounding in observational studies of health disparities that focus exclusively on social and environmental disease risk factors. In support of this idea, we used population biobank data to illustrate (1) the extent to which socioenvironmental and genetic factors are correlated between Black and White ethnic groups in the United Kingdom, and (2) how genetic confounding can lead to spurious associations between social disadvantage and genetically influenced disease disparities. For example, sickle cell anemia appears to be significantly associated with socioeconomic deprivation if genetic risk factors are not considered in a multivariable logistic regression model of disease. This association disappears when genetic factors are included in the model, consistent with the known genetic architecture of the disease. Genetic factors also mediate associations of socioeconomic deprivation with complex disease health disparities that disproportionately impact individuals who self-identify as Black: hypertension, type 2 diabetes, and uterine leiomyomas (fibroids). Our results underscore the importance of an agnostic and integrated approach to health disparities research that considers the joint effects of genetics, the environment, and their interactions on the disease burden borne by socially disadvantaged ethnic groups.
Evolutionary and epidemiological consequences of damage-limiting therapies	Pedro Vale, University of Edinburgh, Edinburgh, Scotland.	Widespread antimicrobial resistance is driving an intense search for therapies that may compliment, enhance or even replace traditional antibiotics. 'Damage-limiting' therapies that do not kill pathogens directly, but that target pathogen virulence or instead reduce the severity of infection by enhancing host disease tolerance, have been presented as promising therapies because by not targeting pathogen viability directly, selection for resistance should be reduced. However, the evolutionary and epidemiological consequences of using these therapies remains underexplored, and recent work suggests there are a range of conditions under which these treatments may still lead to the evolution of more virulent and more prevalent infections. I will explore theoretical predictions under which employing these therapies may potentially be feasible and desirable. Building on a previously published model of pathogen evolution and transmission under tolerance boosting or anti-virulence therapies, I will explore how these treatments interact with variation in host clearance and transmission rates to impact the evolutionarily stable virulence and prevalence of infection. I will also explore how these outcomes are affected by the intrinsic severity of the infection, and by the extent that disease severity is linked to transmission.

Title	Authors	Abstract
Oral heat-killed fast growing mycobacteria increases tolerance to Mycobacterium marinum infection	Marta Arch. Institut Germans Trias i Pujol (IGTP). Badalona. Catalonia (Spain) *Maria Vidal. Institut Germans Trias i Pujol (IGTP). Badalona. Catalonia (Spain) *Esther Fuentes. Institut Germans Trias i Pujol (IGTP). Badalona. Catalonia (Spain) *Pere-Joan Cardona. Hospital Universitari Germans Trias i Pujol (HUGTIP). Badalona. Catalonia (Spain)	Nowadays, it is estimated that a third of the world population is infected with Mycobacterium tuberculosis (Mtb). However, just a reduced percentage will develop the active tuberculosis disease (TB). It has been shown that this progression is related to massive neutrophil infiltration of lesions infected with Mtb and subsequent induction of Th17 type immune response. Previous studies have shown that the induction of regulatory T cells (Tregs) by repeated oral administration of a low dose of heat-inactivated Mycolicibacterium manresensis (hkMm) has de ability to stop this process. The M. marinum infection in D. melanogaster has shown to be a good experimental model of TB. We have use it to evaluate the pathogen-host coevolution for 10 generations, and to evaluate the impact of oral administration of hkMm. Results have revealed a progressive loss of virulence of M. marinum together with an increased tolerance with the oral administration of hkMm. These results support the hypothesis of the benign character of Mtb infection, especially with the constant contact of environmental fast-growing mycobacteria, and the origin of TB as a consequence of the host loss of tolerance due to stressful living conditions linked to poverty, which has favoured the increase of antibiotic resistance.
Mycobacterium tuberculosis, a case of evolution towards antibiotic resistance selection	Pere-Joan Cardona. Hospital Universitari Germans Trias i Pujol (HUGTIP). Badalona. Catalonia (Spain)	Origin of mycobacteria thousand million years ago has to be understood as a way to avoid antibiotics generated by actinomycetes mediated by the construction of a heavy hydrophobic cell. Originally these mycobacteria were fast-growers and survive in the soil landscape both as a free form or as a parasite of amoebae. This condition allowed to not only infect fishes, amphibians or reptiles, but mammals at the end. This was possible thanks to its capacity to infect the amoebas implied in the innate immune response, i.e. macrophages in the case of mammals, to become progressively obligate human parasites 70 Kyears ago with the second “out of Africa”, as M. tuberculosis. Recent modelling data supports the benign character of this infection, able to persist subclinically, generating lesions with low density mycobacterial populations less able to generate spontaneous resistance against antibiotics (ATBR). Subsequent Neolithic revolution caused worse health conditions that favored the neutrophilic infiltration of the lesions, becoming larger and generating a mortal disease (tuberculosis), increasing mycobacterial concentrations in the tissues and thus the capacity for ATBR selection. Host-directed strategies to avoid this excessive inflammatory response are required to reduce the severity of M. tuberculosis infection and the progressive increase of ATBR.
The per-pathogen virulence of HIV-1 subtypes A, C and D	Judith Bouman, ETH Zurich, Zurich; Collin Venner, University of Western Ontario, London; Courtney Walker, University of Western Ontario, London; Eric Arts, University of Western Ontario, London; Roland Regoes, ETH Zurich, Zurich	HIV-1 subtypes differ, among other things, in their clinical manifestations and the speed in which they spread. In particular, the frequency of subtype C is increasing relative to subtype A and D. We aim to investigate whether HIV-1 subtype A, C and D differ in their per-pathogen virulence and to what extend this can explain the difference in spread between these subtypes. We use data from the Hormonal Contraception and HIV-1 Genital Shedding and Disease Progression among Women with Primary HIV Infection (GS) Study. For each study participant, we determine the set-point viral load value, CD4+ T cell level after primary infection and CD4+ T cell decline. Based on both the CD4+ T cell count after primary infection and CD4+ T cell decline, we estimate the time until AIDS for each individual. We then obtain our newly introduced measure of virulence as the inverse of the estimated time until AIDS. This new measure of virulence has an improved correlation with the set-point viral load compared to the decline of CD4+ T cells alone. After fitting a model to the measured virulence and set-point viral load values, we tested if this relation varies per subtype. We found that subtype C has a significantly higher per-pathogen virulence than subtype A. Based on an evolutionary model, we then hypothesize that differences in the primary length of infection period cause the observed variation in the speed of spread of the subtypes.

Title	Authors	Abstract
How Inclusive Stakeholding (ISH) can help to further advance evolutionary medicine: A panel discussion	Joon Yun, Yun Family Foundation	Inclusive Stakeholding (ISH), adapted from Hamilton's theory of inclusive fitness, is a method of promoting cooperation to induce positive change. It updates the natural operating system of human sociality, which includes bioalgorithms of self-interest and kin altruism, with social algorithms of interdependent incentives among all stakeholders to envision a higher fitness world from a multidimensional selection perspective. Examples of recent successful applications of ISH include the advancements of the healthy longevity movement and food system policy innovation movement. After a brief introductory presentation, the discussants will explore the potential utility of inclusive stakeholding (ISH)—itself a theory adapted from evolutionary biology—as an intellectual framework that can accelerate the paradigmatic integration of evolutionary medicine into mainstream society. The panelists include: Helena Canhão Full Professor of Medicine, NOVA Medical School, Universidade NOVA de Lisboa. Coordinator Comprehensive Health Research Center (CHRC), Coordinator of REAL Associate Laboratory and Head of EpiDoC Unit, CEDOC, NMS. Head, Rheumatology Department CHULC and Rheumatology Unit, CUF Tejo. President, Portuguese Society of Rheumatology. Head of the Advisory Board of AICIB and of the Advisory Board Value for Health Collaborative Laboratory. Member of General Council Universidade NOVA de Lisboa. www.nms.unl.pt Barbara Natterson-Horowitz, M.D. Harvard Medical School – Harvard-MIT Health Sciences & Technology Harvard University Department of Human Evolutionary Biology Professor of Medicine, UCLA Division of Cardiology, David Geffen School of Medicine at UCLA https://bnatterson-horowitz.com Frank Rühli, MD, PhD. Director of Institute of Evolutionary Medicine, Medical Faculty, University of Zurich. Head Paleopathology and Mummy Studies Group Head Museum, Medical Collection and Human Remains Group https://www.iem.uzh.ch/en/people/dir/frankruehli.html Joon Yun, MD President and Managing Partner of Palo Alto Investors LP, a healthcare hedge fund founded in 1989. Board certified in radiology, Joon served on the clinical faculty at Stanford from 2000-2006. Joon has served on numerous boards, and he is currently a trustee of the Salk Institute. Joon is a member of the President's Circle of the National Academies of Sciences, Engineering, and Medicine. Joon has published dozens of patents and scientific articles. Joon and his wife Kimberly launched the $1 million Palo Alto Longevity Prize in 2013 to reverse the aging process and recently donated $2 million to launch the National Academy of Medicine Aging and Longevity Grand Challenge. http://www.drjoonyun.com/ Randolph M. Nesse, MD Founding Director of The Center for Evolution and Medicine, Arizona State University Professor Emeritus, Departments of Psychiatry and Psychology, and Institute for Social Research, The University of Michigan Founding President: The International Society for Evolution, Medicine, and Public Health https://www.randolphnesse.com

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Panel discussion	Frank Rühli, University of Zurich	Inclusive Stakeholding (ISH), adapted from Hamilton's theory of inclusive fitness, is a method of promoting cooperation to induce positive change. It updates the natural operating system of human sociality, which includes bioalgorithms of self-interest and kin altruism, with social algorithms of interdependent incentives among all stakeholders to envision a higher fitness world from a multidimensional selection perspective. Examples of recent successful applications of ISH include the advancements of the healthy longevity movement and food system policy innovation movement. After a brief introductory presentation, the discussants will explore the potential utility of inclusive stakeholding (ISH)—itself a theory adapted from evolutionary biology—as an intellectual framework that can accelerate the paradigmatic integration of evolutionary medicine into mainstream society. The panelists include: Helena Canhão Full Professor of Medicine, NOVA Medical School, Universidade NOVA de Lisboa. Coordinator Comprehensive Health Research Center (CHRC), Coordinator of REAL Associate Laboratory and Head of EpiDoC Unit, CEDOC, NMS. Head, Rheumatology Department CHULC and Rheumatology Unit, CUF Tejo. President, Portuguese Society of Rheumatology. Head of the Advisory Board of AICIB and of the Advisory Board Value for Health Collaborative Laboratory. Member of General Council Universidade NOVA de Lisboa. www.nms.unl.pt Barbara Natterson-Horowitz, M.D. Harvard Medical School – Harvard-MIT Health Sciences & Technology Harvard University Department of Human Evolutionary Biology Professor of Medicine, UCLA Division of Cardiology, David Geffen School of Medicine at UCLA https://bnatterson-horowitz.com Frank Rühli, MD, PhD. Director of Institute of Evolutionary Medicine, Medical Faculty, University of Zurich. Head Paleopathology and Mummy Studies Group Head Museum, Medical Collection and Human Remains Group https://www.iem.uzh.ch/en/people/dir/frankruehli.html Joon Yun, MD President and Managing Partner of Palo Alto Investors LP, a healthcare hedge fund founded in 1989. Board certified in radiology, Joon served on the clinical faculty at Stanford from 2000-2006. Joon has served on numerous boards, and he is currently a trustee of the Salk Institute. Joon is a member of the President's Circle of the National Academies of Sciences, Engineering, and Medicine. Joon has published dozens of patents and scientific articles. Joon and his wife Kimberly launched the $1 million Palo Alto Longevity Prize in 2013 to reverse the aging process and recently donated $2 million to launch the National Academy of Medicine Aging and Longevity Grand Challenge. http://www.drjoonyun.com/ Randolph M. Nesse, MD Founding Director of The Center for Evolution and Medicine, Arizona State University Professor Emeritus, Departments of Psychiatry and Psychology, and Institute for Social Research, The University of Michigan Founding President: The International Society for Evolution, Medicine, and Public Health https://www.randolphnesse.com

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Panel discussion	Helena Canhão, NOVA Medical School	Inclusive Stakeholding (ISH), adapted from Hamilton's theory of inclusive fitness, is a method of promoting cooperation to induce positive change. It updates the natural operating system of human sociality, which includes bioalgorithms of self-interest and kin altruism, with social algorithms of interdependent incentives among all stakeholders to envision a higher fitness world from a multidimensional selection perspective. Examples of recent successful applications of ISH include the advancements of the healthy longevity movement and food system policy innovation movement. After a brief introductory presentation, the discussants will explore the potential utility of inclusive stakeholding (ISH)—itself a theory adapted from evolutionary biology—as an intellectual framework that can accelerate the paradigmatic integration of evolutionary medicine into mainstream society. The panelists include: Helena Canhão Full Professor of Medicine, NOVA Medical School, Universidade NOVA de Lisboa. Coordinator Comprehensive Health Research Center (CHRC), Coordinator of REAL Associate Laboratory and Head of EpiDoC Unit, CEDOC, NMS. Head, Rheumatology Department CHULC and Rheumatology Unit, CUF Tejo. President, Portuguese Society of Rheumatology. Head of the Advisory Board of AICIB and of the Advisory Board Value for Health Collaborative Laboratory. Member of General Council Universidade NOVA de Lisboa. www.nms.unl.pt Barbara Natterson-Horowitz, M.D. Harvard Medical School – Harvard-MIT Health Sciences & Technology Harvard University Department of Human Evolutionary Biology Professor of Medicine, UCLA Division of Cardiology, David Geffen School of Medicine at UCLA https://bnatterson-horowitz.com Frank Rühli, MD, PhD. Director of Institute of Evolutionary Medicine, Medical Faculty, University of Zurich. Head Paleopathology and Mummy Studies Group Head Museum, Medical Collection and Human Remains Group https://www.iem.uzh.ch/en/people/dir/frankruehli.html Joon Yun, MD President and Managing Partner of Palo Alto Investors LP, a healthcare hedge fund founded in 1989. Board certified in radiology, Joon served on the clinical faculty at Stanford from 2000-2006. Joon has served on numerous boards, and he is currently a trustee of the Salk Institute. Joon is a member of the President's Circle of the National Academies of Sciences, Engineering, and Medicine. Joon has published dozens of patents and scientific articles. Joon and his wife Kimberly launched the $1 million Palo Alto Longevity Prize in 2013 to reverse the aging process and recently donated $2 million to launch the National Academy of Medicine Aging and Longevity Grand Challenge. http://www.drjoonyun.com/ Randolph M. Nesse, MD Founding Director of The Center for Evolution and Medicine, Arizona State University Professor Emeritus, Departments of Psychiatry and Psychology, and Institute for Social Research, The University of Michigan Founding President: The International Society for Evolution, Medicine, and Public Health https://www.randolphnesse.com

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Panel discussion	B. Natterson-Horowitz, Harvard Medical School	Inclusive Stakeholding (ISH), adapted from Hamilton's theory of inclusive fitness, is a method of promoting cooperation to induce positive change. It updates the natural operating system of human sociality, which includes bioalgorithms of self-interest and kin altruism, with social algorithms of interdependent incentives among all stakeholders to envision a higher fitness world from a multidimensional selection perspective. Examples of recent successful applications of ISH include the advancements of the healthy longevity movement and food system policy innovation movement. After a brief introductory presentation, the discussants will explore the potential utility of inclusive stakeholding (ISH)—itself a theory adapted from evolutionary biology—as an intellectual framework that can accelerate the paradigmatic integration of evolutionary medicine into mainstream society. The panelists include: Helena Canhão Full Professor of Medicine, NOVA Medical School, Universidade NOVA de Lisboa. Coordinator Comprehensive Health Research Center (CHRC), Coordinator of REAL Associate Laboratory and Head of EpiDoC Unit, CEDOC, NMS. Head, Rheumatology Department CHULC and Rheumatology Unit, CUF Tejo. President, Portuguese Society of Rheumatology. Head of the Advisory Board of AICIB and of the Advisory Board Value for Health Collaborative Laboratory. Member of General Council Universidade NOVA de Lisboa. www.nms.unl.pt Barbara Natterson-Horowitz, M.D. Harvard Medical School – Harvard-MIT Health Sciences & Technology Harvard University Department of Human Evolutionary Biology Professor of Medicine, UCLA Division of Cardiology, David Geffen School of Medicine at UCLA https://bnatterson-horowitz.com Frank Rühli, MD, PhD. Director of Institute of Evolutionary Medicine, Medical Faculty, University of Zurich. Head Paleopathology and Mummy Studies Group Head Museum, Medical Collection and Human Remains Group https://www.iem.uzh.ch/en/people/dir/frankruehli.html Joon Yun, MD President and Managing Partner of Palo Alto Investors LP, a healthcare hedge fund founded in 1989. Board certified in radiology, Joon served on the clinical faculty at Stanford from 2000-2006. Joon has served on numerous boards, and he is currently a trustee of the Salk Institute. Joon is a member of the President's Circle of the National Academies of Sciences, Engineering, and Medicine. Joon has published dozens of patents and scientific articles. Joon and his wife Kimberly launched the $1 million Palo Alto Longevity Prize in 2013 to reverse the aging process and recently donated $2 million to launch the National Academy of Medicine Aging and Longevity Grand Challenge. http://www.drjoonyun.com/ Randolph M. Nesse, MD Founding Director of The Center for Evolution and Medicine, Arizona State University Professor Emeritus, Departments of Psychiatry and Psychology, and Institute for Social Research, The University of Michigan Founding President: The International Society for Evolution, Medicine, and Public Health https://www.randolphnesse.com
Panel discussion	Randolph Nesse, Arizona State University	
Monastic celibacy, operational sex ratio, and gender inequality in workloads.	Yuan Chen, University College London, London; Erhao Ge, University College London, London; Liqiong Zhou, Lanzhou University, Lanzhou; Juan Du, Lanzhou University, Lanzhou; Ruth Mace*, University College London, London.	Here, we evaluate the role of monastic celibacy on the sexual division of labour. We exploit the cultural diversity of southwestern China, where some sex ratios are female-biased due in part to the practice of a proportion of males entering monastic celibacy. Monasticism in some, but not all cultures, provide a quasi-natural experiment by biasing the operational sex ratio in areas where the monastic tradition exists. We used a detachable activity tracker to quantify workload differentials between the sexes in 55 villages in six different areas. Our data revealed that a higher prevalence of monastic celibacy is associated with increases in women's workload and depresses men's workload. High operational sex ratios appear to increase women's bargaining power in the marriage market, thus reducing their work burden. We show that gender inequality was diminished as the operational sex ratio increased, suggesting a harmful effect of prevalent monastic celibacy in these populations on women's burden of work.
New strategies to reduce anaemia and	Maria Inês Varela-Silva, School of Sport, Exercise	Peru is experiencing rapid societal change with increasing economic development and internal migration towards urban centres. Significant reductions in stunting among infants and young children (IYC) have

Title	Authors	Abstract
risk of overweight and obesity in infants and young children in Peru: The PERUSANO Project	and Health Sciences, Loughborough University, Loughborough, UK Emily Rousham, School of Sport, Exercise and Health Sciences, Loughborough University, Loughborough, UK Rossina Pareja, Instituto de Investigacion Nutritional (IIN), Lima, Peru Rebecca Pradeilles, School of Sport, Exercise and Health Sciences, Loughborough University, Loughborough, UK Deysi Ortega Román, School of Computer Science and Informatics, Cardiff University, Cardiff, UK Nervo Verdozoto, School of Computer Science and Informatics, Cardiff University, Cardiff, UK Rosario Bartolini, Instituto de Investigacion Nutritional (IIN), Lima, Peru Paula Griffiths, School of Sport, Exercise and Health Sciences, Loughborough University, Loughborough, UK Emma Haycraft, School of Sport, Exercise and Health Sciences, Loughborough University, Loughborough, UK Michelle Holdsworth, IRD-French National Research Institute for Sustainable Development, Montpellier, France Edwige Landais, IRD-French National Research Institute for Sustainable Development, Montpellier, France	been recorded, but iron-deficiency anaemia prevalence is high, and risk of overweight/obesity is increasing. Multiple forms of malnutrition, therefore, coexist. PERUSANO addresses the double-burden of anaemia and excess energy intake among IYC in Lima and Huánuco. PERUSANO is developing culturally appropriate strategies to promote healthy diets during the complementary feeding period, among caregivers and health personnel. A mixed-methods approach is being used to: i) identify biocultural determinants of IYC nutritional status; ii) co-design and pilot new strategies to address anaemia and risk of overweight through participatory methods and prototyping interventions with families and communities; iii) inform the development of feeding guidelines; and iv) develop capacity among stakeholders to implement strategies, recommendations, and support participatory approaches to IYC interventions. Results show that 33% of mother-child pairs and 20% of mothers had concurrent overweight/obesity and anaemia, highlighting the need for double-duty actions tackling multiple forms of malnutrition at individual and dyad levels. Recommended actions to be implemented are being refined through policy-mapping exercises and the co-design of culturally appropriate interventions in partnership with Peruvian communities.

Title	Authors	Abstract
	Oonagh Markey, School of Sport, Exercise and Health Sciences, Loughborough University, Loughborough, UK Doris Delgado-Perez, Universidad Nacional Mayor de San Marcos, Lima, Peru Teresita Vela Lopez, Universidad Nacional Hermilio Valdizan, Huanuco, Peru Luzvelia Alvarez Ortega, Universidad Nacional Hermilio Valdizan, Huanuco, Peru Violeta Magdalena Rojas Huayta, Universidad Nacional Mayor de San Marcos, Lima, Peru Hilary Creed-Kanashiro, Instituto de Investigacion Nutritional (IIN), Lima, Peru	
Age-specific and time-varying impacts of parent polygyny-status, parent presence, and parent death on child well-being, among Pimbwe in rural Tanzania	Riana Minocher, Max-Planck Institute for Evolutionary Anthropology, Germany; Monique Borgerhoff Mulder, Max-Planck Institute for Evolutionary Anthropology, Germany; Cody T. Ross, Max-Planck Institute for Evolutionary Anthropology, Germany	Parents are critical for the survival and well-being of children. The presence/absence and marital status of either parent may affect children---mother/father absence, polygynous marriage, divorce, and the presence of step-parents have all been claimed to negatively impact child growth and survival. However, there is substantial variation in the literature about the timing and impact of these variable parental states on child well-being. Much of the literature detailing the costs of parental absence/marital status is fraught with inferential issues, making it difficult to resolve the causes of this variation. These issues include confounding due to the use of nationally aggregated statistics (“ecological regression fallacy”), selection-bias, and failure to account for the time-varying and age-specific effects of parent-status. To address some of these limitations, we introduce a hierarchical Bayesian modelling approach to flexibly model the effects of time-varying and age-dependent parent-status on child well-being. To test our predictions, we draw on a detailed, longitudinal dataset on child survival, growth, and education, from a 20-year prospective study in rural Tanzania---which contains data on 2371 children born to 499 mothers and 416 fathers between 1931 and 2013. Our analysis demonstrates that in some contexts, such as where women are less constrained in marital choices and relatively autonomous in terms of economic production, the absence of fathers and the existence of stereotypically harmful institutions, such as polygyny, may have less impact on child well-being than is generally predicted.

Title	Authors	Abstract
Who gets contraceptive side-effects? Using principles of reproductive ecology to explain variation in side-effect experiences among hormonal contraceptive users in Central Oromia, Ethiopia	Rose Stevens, Oxford University; Eshetu Gurmu, Addis Ababa University; Christopher Smith, London School of Hygiene and Tropical Medicine; Tamrat Abebe, Addis Ababa University; Virginia Vitzthum, Indiana University; Sisay Teklu, Addis Ababa University; Rebecca Sear, London School of Hygiene and Tropical Medicine; Jenny Cresswell, London School of Hygiene and Tropical Medicine; Elizabeth Ewart, Oxford University; Alexandra Alvergne, CNRS Montpellier.	Background: A key barrier to reducing unmet need for contraception is the experience of contraceptive side-effects. Currently, little is known about drivers of side-effect variation. We aimed to test the hypothesis that women with lifestyles associated with having lower endogenous reproductive hormone levels experience more side-effects. Methods: We recruited 259 new injectable or implant users and 115 non-users across urban and rural locations in Adama, Ethiopia. Using a pre-tested locally specific side-effects measurement tool based on qualitative work, we measured participants' symptoms across three months. Sociodemographic data relevant to reproductive hormone levels, including economic status, diet, activity levels, and infection histories, were also collected. Results: Using predictions from reproductive ecology, we will use multivariable linear regression to investigate whether factors associated with lower reproductive hormone levels increase risk of side-effects. Directed acyclic graphs will be used to determine adjustment covariates to minimise confounding and obtain accurate effect estimates. Implications: This research will provide a novel understanding of side-effect prevalence and aetiology in different socioecological settings. Our findings may challenge existing clinical practice for designing contraceptive methods and dosing regimes, as well as contraceptive counselling policies, which currently ascribe to a one size fits all model.
The impact of direct challenges to student endorsement of teleological reasoning on understanding and acceptance of natural selection	Jason R. Wingert, University of North Carolina Asheville, Asheville; Gennie M. Bassett, University of North Carolina Asheville, Asheville; Caitlin E. Terry, University of North Carolina Asheville, Asheville; Jimin Lee, University of North Carolina Asheville, Asheville.	Teleological reasoning impacts students' abilities to understand, learn, and accept natural selection. In a convergent mixed methods study (N=83), we examined the influence of instructional activities that directly challenged student endorsement of teleological explanations for evolutionary adaptations on their learning of natural selection in an evolutionary medicine course. Additionally, we explored whether students with creationist views responded differently to education intended to directly challenge design teleological reasoning, compared to students with naturalist views. Results showed that students are mostly unaware of their tendency towards teleological thinking upon entrance to an evolution course. However, with anti-teleological instruction, students decreased teleological thinking and increased understanding of natural selection ($p<0.0001$). Furthermore, results indicated that students with creationist views had higher levels of design teleological reasoning and lower levels of acceptance and understanding of evolution ($p<0.05$) at the beginning of the semester, compared to students with naturalist views. Students with creationists views experienced significant improvements in teleological reasoning and acceptance and understanding of evolution ($p<0.05$), but they never reached the level of evolution understanding and acceptance as their counterparts with naturalist views. We will suggest anti-teleological pedagogical practices to strengthen student learning of evolution.
Biological Normalcy and its relevance to public health and medicine	Andrea S Wiley	In this paper I describe the concept of biological normalcy and its relevance to public health and clinical medicine. I first consider how the term "normal" is used in these fields. Normal reflects both a statistical distribution of a biological characteristic in the population as well as normative ideas or judgements about variations in the trait. Biological normalcy is concerned with the relationships between these two aspects of normal: how does the distribution of a trait (measures of central tendency and variance) influence normative ideas, and in turn, how do normative ideas shape the distribution in the population by generating differential survival and reproduction, thereby having evolutionary impacts. Terminology used in clinical medicine and public health reveals culturally-influenced normative beliefs about "normal" human biology, which often equates to "health." These terms derive, in part, from reference populations that established the "normal range;" however, these are frequently small samples or biased toward adult males of European descent, and thus do not adequately represent variation within our species. I provide examples to illustrate, including variation in age, skin pigmentation, and my research on variation in adult lactose digestion.

Title	Authors	Abstract
Evobiopsychosocial Medicine	Adam Hunt, University of Zürich, Zürich; Paul St-John Smith, Evolutionary Psychiatry Special Interest Group, Royal College of Psychiatrists, London; Riadh Abed, Evolutionary Psychiatry Special Interest Group, Royal College of Psychiatrists, London.	The biopsychosocial model is the overarching framework of current healthcare. We introduce a new schema for integrating evolutionary considerations into it, applying Tinbergen's four questions across the three biopsychosocial levels. This 'Evobiopsychosocial' schema provides a more complete framework for understanding causation of medical conditions, directing research programs and clinical solutions; the multiple levels of analysis encouraged by the biopsychosocial model gain greater depth referencing evolutionary causation. We exemplify the application of such a schema by tabulating depression, rheumatoid arthritis and COVID-19 within an evobiopsychosocial framework, and considering how evolutionary perspectives enhance medical responses to these conditions in different ways. Such tabulations highlight the implications of evolutionary medicine, recognising practical applications of an evolutionary analysis at biological, psychological and social levels, for example by constraining medical research to specific animal models, explaining psychological reactions to illness or directing public health measures. We propose that such tabulations, and the evobiopsychosocial concept more generally, could serve as a useful tool for smoothly introducing evolutionary concepts into mainstream medical education. Where the utility of evolutionary medicine is underappreciated but the biopsychosocial model widely recognised, the evobiopsychosocial provides a fuller model for understanding health and disease.
Biological normalcy and body size: What's "normal" about weight and height?	Jennifer Cullin, Indiana University, Bloomington	Biological normalcy provides a framework to examine biological variation by assessing tensions between clinical definitions of "normal," statistical norms, and normative beliefs around a particular trait. Body size is a highly visible aspect of human biological variation, and is often evaluated largely in a cultural context, where certain phenotypes may be viewed as either positive or negative, depending on place, time, and localized histories. Such cultural understandings are also likely influenced by measures of central tendency within a population. Body size, including weight, height and their ratios or correlates, is also widely evaluated within clinical and public health contexts through use of cut-off points or standards that denote which phenotypes are "healthy" or in the "normal" range and which are potentially "abnormal" or pathological. But what exactly is normal weight, height, BMI, or growth? How do these vary by population and how might conflation between statistical norms and normative understandings of body size contribute to differential health outcomes within a population? This paper uses the biological normalcy framework to assess the tensions between clinical definitions of "normal," statistical norms, and normative beliefs around body size and how such tensions may generate differential survival and reproduction.
Social determinants of health in a small-scale human society	Adrian Jaeggi, University of Zurich; Aaron Blackwell, Washington State University; Jordan Martin, University of Zurich; Bret Beheim, Max Planck Institute for Evolutionary Anthropology; Michael Gurven, UC Santa Barbara; Hillard Kaplan, Chapman University; Jonathan Stieglitz, Institute of Advanced Study Toulouse; Benjamin Trumble, Arizona State University	Why should the social environment affect health? Are phenomena like socio-economic health disparities a result of mismatch in modern societies or have they always haunted us? And if so, what factors might explain variation in health disparities and point towards possible public health interventions? In this talk I explore these questions in three steps and outline specific directions and open questions that should be addressed in future research. First, I summarize theoretical arguments for why and how much individuals should adjust health-related phenotypes to particular social environments. Future work should integrate recent theoretical developments on pace-of-life syndromes in behavioral ecology to better understand human life history variation. Second, I summarize empirical results on socio-economic health disparities (or lack thereof) among the Tsimane of Bolivia, showing mixed results that are partly consistent with effects of socio-economic position and inequality on health. Future field work should attempt to better understand the mechanisms underlying these results. Third, I present a new study showing how fertility variation, and therefore life history, among the Tsimane is influenced by social partners. Future work should apply this framework to other health-related phenotypes.
The myth of the 'traditional' nuclear family and its consequences for health	Rebecca Sear, London School of Hygiene and Tropical Medicine	The importance of social support for parental and child health is not yet sufficiently widely recognised. Parents and children benefit greatly from the transfer of resources, time, information and emotional support from other individuals, but the widespread myth in Western contexts that the male breadwinner-female homemaker nuclear family is the 'traditional' family leads to a focus on parents, particularly mothers, as the only individuals with responsibility for child (and parental) wellbeing. Inaccurate perceptions about the family have the potential to distort academic research and public perceptions, feed into problematic political narratives, and hamper attempts to improve parental and child health. This talk discusses the importance of taking a cross-cultural and historical approach to understanding the social determinants of health, given that it is evidence from such disciplines which clearly shows the importance of multiple individuals beyond the mother in raising children: in evolutionary anthropology, it's now widely accepted that we have evolved a strategy of cooperative reproduction. Expecting mothers to care for children with little support, while expecting fathers to provide for their families with little support, is likely to lead to adverse health consequences for mothers, fathers and children.

Title	Authors	Abstract
Neural basis of primate sociality	Camille Testard, University of Pennsylvania, Philadelphia, PA, USA, Department of Neuroscience, Blavatnik Family Fellow.	Social distancing measures implemented to slow the spread of COVID-19 have triggered a worldwide craving for social contact, leading to surges in anxiety and depression. This social desire is deeply rooted in our evolutionary history: most of our closest nonhuman primate relatives live in groups in which they form differentiated relationships with conspecifics. After a devastating hurricane destroyed over 60% of the vegetation on a small Caribbean island, instead of being more competitive, resident rhesus macaques became more tolerant of each other, less aggressive, and expanded their social networks. However, some monkeys increased their social connectedness by a lot –leading to better chances of survival almost 5 years after the storm– while others did not. What are the neurobiological underpinnings of macaques' ability to socially connect? In this same free-ranging rhesus macaque population before the storm, we found that the number of social connections individuals maintained predicted the volume of specific structures –the mid–superior temporal sulcus (mSTS) and ventral-dysgranular insula– implicated in social decision-making and empathy, respectively. Moreover, single-unit recordings in anatomically connected areas to the mSTS in freely-moving, socially-interacting rhesus macaques demonstrate that neural ensembles carry information about species-typical social stimuli, behavior, and contexts required for success in the wild.
Privileged Creatures: The Impact of Conferred Advantages and Protections on Individual Fitness	Barbara Natterson-Horowitz, UCLA and Harvard University	Wealth, health and social inequalities are widespread across human societies. Parallel inequalities are observed across a phylogenetically wide range of species. Inheritance of social rank, parental social networks, and nongenetic commodities (e.g., a nest, territory, tool) by some, but not other animal individuals, may play a far more significant role in shaping their future health and fitness than has been appreciated. The intergenerational transfer of wealth privileges some individuals over others through the transmission of resources external to an individual organism. Privileged access to household wealth (e.g., land, shelter, silver) positively influences the destinies of some (and their descendants) over others in human societies. Strikingly parallel phenomena exist in animal societies. Inheritance of nongenetic commodities (e.g., a nest, territory, tool) external to an individual also contributes greatly to direct fitness in animals. Here, we illustrate the evolutionary diversity of privilege and its disparity-generating effects on the evolutionary trajectories of lineages across the Tree of Life. We propose that integration of approaches used to study these patterns in humans may offer new insights into a core principle from behavioral ecology—differential access to inherited resources—and help to establish a broad, comparative framework for studying inequality in animals.
Using complete blood count tests to explore maintenance trade-offs in children experiencing food insecurity in a rural agricultural community in Veracruz, Mexico	Alejandra Núñez-de la Mora, Universidad Veracruzana, Mexico; René Rivera-Bonilla, Benemérita Universidad Autónoma de Puebla, México; Héctor A Cuevas-Méndez, Laboratorio Especializado de Análisis Clínicos Las Ánimas, México; Ana Gabriela Perroni-Marañón, Instituto de Salud Pública, México; Guadalupe Amescua-Villela, CESIGUE, México; Simoneta Negrete-Yankelevich, INECOL A.C., México.	Parasitic, gastrointestinal and respiratory infections are some of the leading causes of morbidity and mortality among children in low- and middle-income countries. In poor rural subsistence communities, undernutrition compounds the problem. Our previous work in a small rural subsistence community in Mexico with very high levels of food insecurity, poor housing and sanitation and limited access to health care, has documented a 90% prevalence of multi pathogenic parasitism, and 30% growth faltering among children under 5 years of age. Here we expand the analysis to document the prevalence of infection, inflammation, anemia and nutrient deficiency. Specifically, we use a battery of blood cell counts to explore not only the prevalence but to shed light on the potential etiology of the chosen health indicators. By capitalizing on the detailed information afforded by clinical tests of single fasting venous blood samples obtained from 112 children, we aim to provide a more nuanced analysis of the associations between nutritional and health biomarkers beyond those typically used in field settings. These results contribute to our understanding of the life history trade-offs incurred in a population living in a highly pathogenic, nutritionally poor but energetically sufficient environment, characteristic of populations undergoing nutritional and epidemiological transitions.

Title	Authors	Abstract
The impact of early life antibiotic use on atopic and metabolic disorders: meta-analyses of recent insights	Semeh Bejaoui, Section for Food Safety and Zoonoses, Department of Veterinary and Animal Sciences, University of Copenhagen, Denmark; Michael Poulsen, Section for Ecology and Evolution, Department of Biology, University of Copenhagen, Denmark.	The impact of antibiotics use early in life on later-in-life morbidities has received substantial attention as explanations for atopic and metabolic disorders with a surge as modern lifestyle diseases. The objective of this study was to perform meta-analyses to determine if antibiotics administration during the first two years of infant life is associated with increased risks of atopic or metabolic disorders later in life. We screened more than 100 English-language prospective and retrospective studies published between January 2002 and March 2020 and assessed study quality using the Newcastle–Ottawa scale. We performed overall and subgroup meta-analyses on 31 high-quality comparable studies on atopic and 23 on metabolic disorders, involving more than 3.5 million children. Antibiotic exposure prenatally and during the first two years of life significantly impacts the risk of developing atopic and metabolic disorders. Exposure during the first six months of life appears most critical, consistent with this being the time when the microbiome is most susceptible to irreversible perturbations. The presence of dose-response associations and stronger impacts of broad- than narrow-spectrum antibiotics further point to effects being mediated by microbiota-induced changes. Our findings support that antibiotics use is a mismatch to modernity that can negatively affect the symbiotic associations we rely on for proper immune function and metabolism. Improving our understanding of these associations, the underlying proximate mechanisms, and the impact of antibiotics use on future human-symbiont evolution will be important to improve human health
ACSL1, a gene under positive selection in Africans, may contribute to population-differential risks in prostate cancer and type 2 diabetes	Kaixiong Ye, University of Georgia, Athens, Georgia, US; Shuang Yang, University of Georgia, Athens, Georgia, US; Houjian Cai, University of Georgia, Athens, Georgia, US;	Prostate cancer is known to disproportionately affect individuals of African descent. Elevated frequencies of disease alleles in Africans, together with environmental and socioeconomic factors, are an important source of this health disparity. Large allele frequency differences across populations could be the results of random genetic drift or genetic adaptation to local environment. Our previous study in human cell lines and mice has shown that long-chain fatty acyl-CoA synthetase 1, encoded by ACSL1, promotes prostate cancer progression by elevating lipogenesis and fatty acid beta-oxidation. We aimed to examine if ACSL1 contributes to the health disparity of prostate cancer across human populations. We performed a series of statistical tests for positive selection based on population differentiation, haplotype homozygosity, and site frequency spectrum using whole-genome sequencing data from the 1000 Genomes Project. Positive selection signals were identified in the coding and regulatory regions of ACSL1, especially in Africans. Phenome-wide association analysis in GWAS Catalog and UK Biobank revealed that variants in ACSL1 are associated with HbA1c and glucose levels and risk of type 2 diabetes, but not with prostate cancer. In summary, positive selection on ACSL1 may contribute to population-differential risks in diabetes, but more studies are needed regarding prostate cancer.
A Case Series of Recurrent UTIs: Applying Evolutionary Medicine to a Common Clinical Quandary	Michelle Blyth	Recurrent urinary tract infections (UTIs) are a common issue faced in hospital medicine. They can be deadly, asymptomatic, or everything between. For patients who have frequent antibiotic courses during repeated attempts at treating their infections, their cultured organisms evolve increasing resistance over time, making treatment options fewer and often more risky. Complicating matters, many patients have bacteria in their urine that is not causing an infection, termed “asymptomatic bacteriuria”. Deciding when to treat these bacteriurias comes down to patients' symptoms - if they are asymptomatic, guidelines advise not to treat. However, evaluating symptoms in patient populations who are at increased risk of recurrent UTIs (and, not coincidentally, asymptomatic bacteriurias as well) - such as those with spinal cord injuries and dementia - can be difficult or seemingly impossible. Often these cases cannot be purely guideline driven, and further consideration of risks and benefits of treatment decisions are necessary. This case series presents examples of such difficult cases and how evolutionary thinking informed clinical decision making. Approaching treatment decisions with concepts of selection, competition, and environmental modification in hand can help clinicians make these choices with one more tool in their proverbial belt.

Title	Authors	Abstract
What Philosophy and Nutritional Ecology can teach one another	Paul E. Griffiths, University of Sydney, Sydney; David Raubenheimer, University of Sydney, Sydney	Some philosophers have suggested that evolutionary medicine is plagued by naive adaptationism leading to poor science through the proliferation of untestable 'just-so stories' and to poor medicine through not considering alternative explanations with different medical implications. Valles (2011) argues that evolutionary medicine is committed to 'empirical adaptationism' (Godfrey Smith 2001), the view that forces other than natural selection can be neglected in the explanation of organismic form. Instead, we show that the prominence of optimality analysis and related methods in nutritional ecology does not reflect on a commitment to strong empirical adaptationism. It reflects both 'methodological adaptationism', a powerful tool for revealing constraints on natural selection (Maynard-Smith 1978) and 'explanatory adaptationism' - an explanatory focus on the observed degree of adaptation. Understanding the actual ways in which nutritional ecology is 'adaptationist' will provide a safeguard against what we might call 'naive anti-adaptationism', the failure to appreciate the methodological sophistication with which researchers use optimality analysis and related methods. Our discussion is therefore an example of the idea at the heart of this symposium - that nutrition science is a rich and productive field for interaction between philosophy and science.
Nutritionism, nutritional ecology, and evolutionary medicine	Jonathan Sholl, Université de Bordeaux, Bordeaux.	One longstanding critique of nutrition research is that methodologically 'reducing' foods to nutrients ostensibly fosters adversarial debates about the health effects of isolated nutrients, obscures the complexity of food-organism interactions, and distorts how nutrients produce different outcomes in the context of foods or dietary patterns. While strongest in the social sciences, concerns over 'nutritionism' permeate nutrition research and are entering philosophy. In this presentation, I reevaluate this critique by engaging the field of nutritional ecology, a promising subfield within evolutionary medicine. For instance, nutritional ecologists propose that nutrient ratio variations, e.g., protein to carbohydrates, are the common threads among foods, meals, and diets that provide robust explanations of distinct outcomes in varying environments and across life stages—from metabolic regulation and biological fitness to obesity—including basic feeding behaviors: organisms select foods largely based on nutrient content. The challenge is to integrate the detailed nutritional requirements of the few well-studied species with the unifying generalizations across multiple species coming from evolutionary biology and ecology. By offering an epistemological evaluation of this nutrient-level research and its potentially integrative explanations of what in foods and dietary patterns affects health, I raise questions at the intersection of evolutionary biology and the health sciences.
Fitness and the Scales of Adaptation in Evolutionary Medicine	Peter Takacs, University of Sydney; Pierrick Bourrat, Macquarie University	Adaptation and its various cognates ('adaptedness', 'adaptiveness', 'aptness', etc.) are core concepts in evolutionary theorizing and, therefore, evolutionary medicine. Such concepts imply judgments concerning whether an organism is (mis)matched to its selective environment. As adaptations are presumably the product of natural selection, the notion of adaptation is inextricably linked to the concept and measurement of fitness. Only when a trait has a positive impact on fitness over time, in absence of constraints, does it become an adaptation. However, the concept of fitness is fraught with difficulties that still too often go unexamined in evolutionarily informed biomedicine. Recent developments in evolutionary theory (e.g., adaptive dynamics) show that particular trait variants have no definite fitness value when assessed independently of carefully specified selective environments. Determining which environments are selectively relevant and the criteria on the basis of which these are deemed so is thus a crucial step toward establishing whether a trait is an adaptation. We examine some of the implications of this reasoning in the context of contemporary evolutionary medicine.
Tacit creationism	Randolph M. Nesse	Tacit creationism is the pervasive tendency to view evolved bodies as if they are designed machines. The metaphor of body as machine has been invaluable for rejecting vitalism, but it inhibits recognition of fundamental differences between bodies and machines. Blueprints for machines describe parts with specific boundaries and functions that are connected in sensible ways. Genomes, by contrast, interact with environments to develop components whose multiple functions and connections are organically complex in ways no engineer could imagine, resulting in robustness unmatched by machines along with special vulnerabilities. For instance, studies of emotions tacitly assume that they are distinct modules with specific functions, resulting in endless debates that avoid the messy reality of overlapping states with multiple functions that increase gene transmission. Neuroscience similarly attempts to map specific functions to specific loci or neurotransmitters, inhibiting recognition that the components are neither distinct nor monofunctional. Biochemistry portrays molecules as if they have specific functions connected by simple clear pathways, avoiding the organic complexity of multiple molecules with multiple functions interacting with multiple receptors and enzymes with manifold cost-benefit tradeoffs. New ways to portray organic complexity are needed to transcend the tacit creationism that impairs our ability to understand disease.

Title	Authors	Abstract
The social and evolutionary dynamics of female genital mutilation/cutting (FGM/C) abandonment	Mhairi A Gibson, University of Bristol, U.K.	Why does female genital mutilation/ cutting (FGM/C) persist despite global efforts to end the practice? In this talk I review how evolutionary approaches are providing some answers. This includes developing new techniques to improve accuracy of data on FGM/C, identifying key sub-groups who support the practice, as well as explaining how and why FGM/C is socially transmitted and maintained within communities. By exploring the costs of FGM/C abandonment for those families who reject the practice in rural Ethiopia, I will also consider how alternative forms of investment in daughters can contribute more effective anti-FGM/C campaigns in the future.
Mutation rate of SARS-CoV-2 and emergence of mutators during experimental evolution.	Massimo Amicone, Instituto Gulbenkian de Ciência, Oeiras, Portugal; Vítor Borges, National Institute of Health Doutor Ricardo Jorge (INSA), Lisbon, Portugal; Maria João Alves, INSA, Lisbon, Portugal; Joana Isidro, INSA, Lisbon, Portugal; Líbia Zé-Zé, Faculty of Sciences, University of Lisbon, Portugal; Sílvia Duarte, INSA, Lisbon, Portugal; Luís Vieira, Universidade Nova de Lisboa, Lisbon, Portugal; Raquel Guiomar, INSA, Lisbon, Portugal; João Paulo Gomes, INSA, Lisbon, Portugal; Isabel Gordo, Instituto Gulbenkian de Ciência, Oeiras, Portugal.	To understand how organisms evolve, it is fundamental to study how mutations emerge and establish. Here, we estimated the mutation rate of the SARS-CoV-2 virus in vitro and investigated the repeatability of its evolution when facing a new cell type, but no immune or drug pressures. We performed experimental evolution with two strains of SARS-CoV-2: one carrying the originally described spike protein (CoV-2-D) and another carrying the D614G mutation that has spread worldwide (CoV-2-G). After 15 passages in Vero cells and whole genome sequencing, we characterized the spectrum and rate of the emerging mutations and looked for evidences of selection in both lineages. From the frequencies of the mutations accumulated, and excluding the genes with signals of selection, we estimate a spontaneous mutation rate of 1.3x10-6 ± 0.2x10-6 per-base per-infection cycle (mean across both lineages of SARS-CoV-2 ± 2SEM). We further show that mutation accumulation is larger in the CoV-2-D lineage and heterogeneous along the genome, consistent with the action of positive selection on the spike protein. We also observe the emergence of mutators in the CoV-2-G background, with a ten-fold increased mutation rate and an altered mutation bias. These results provide valuable information on how spontaneous mutations emerge in SARS-CoV-2 and on how selection can shape its genome towards adaptation to new environments.
Co-evolution of Homo sapiens and Mycobacterium tuberculosis on the Tibetan Plateau	Stephen Corbett Western Clinical School, The University of Sydney, Sydney, NSW, 2006, Australia Centre for Population Health, Western Sydney Local Health District, Sydney, NSW, 2151, Australi	Each year globally there are 10.4 million new cases of tuberculosis and 1.7 million deaths. One-quarter of humanity has latent TB infection. Phylogenetic analyses show that the causative organism, Mycobacterium tuberculosis is divided into 4 ancient and 3 modern bacterial lineages. The Beijing strain, lineage 2.3 is more virulent and is the most common isolate in East Asia. The Tibetan plateau has been stubbornly resistant to the incursion of this strain where a more ancient lineage 2.2 prevails. Co-evolution of Mycobacterium tuberculosis and Homo sapiens has been inferred from the observation that phylogenetically ancient lineages of TB cause less severe disease in the sympatric population, that is the population who originate in the region where the ancient lineage dominates. Over 95% of Tibetans have high altitude adaptations involving EPAS1 and EGLN1 genes in the Hypoxia inducible Factor pathway. Recently it has been shown that in addition to their effects on erythropoiesis, these mutations blunten inflammatory responses to hypoxia. The high prevalence of these mutations among Tibetans, and hypobaric hypoxia may be the driving forces of the co-evolution of M tuberculosis and H sapiens in this population.
Towards a mathematical understanding of colonization resistance in multispecies communities	Erida Gjini, Instituto Superior Tecnico, University of Lisbon, Lisbon, Portugal Sten Madec, Institut Denis Poisson, University of Tours, Tours, France	Microbial community composition and dynamics are key to health and disease. Explaining the evolutionary and ecological forces generating and shaping diversity in the microbial consortia making up our body's defenses is a major challenge in applied microbiology and biomedicine. For this, tractable models are needed, that bridge the gap between observations of patterns and underlying mechanisms. While most microbial dynamics models are based on the Lotka-Volterra framework, we still lack an analytic quantity for colonization resistance, by which a microbial system's fitness as a whole can be understood. In this work, inspired by an epidemiological perspective, we propose a rather general modeling approach whereby colonization resistance can be clearly mathematically defined and studied. In addition, we illustrate several key links between our proposed measure of colonization resistance and invader success in a multispecies consortium, including sensitivity to timing, and to the intrinsic pairwise invasion architecture of the resident community. This approach can provide new theoretical insights on system collective properties, mean trait evolution, invasibility, as well as new links with data on system's response to perturbations and critical shifts along environmental gradients.

Title	Authors	Abstract
Parasite sharing between human and non-human primates: Using phylogeny and geography to identify future zoonotic disease risks	Courtney S. Werner, Duke University Koray Kasan, Bezmialem Vakif University Julie K. Geyer, University of North Carolina Mohamad Elmasri, University of Toronto Maxwell J. Farrell, University of Toronto Charles L. Nunn, Duke University	The SARS-CoV-2 pandemic has renewed calls for understanding the origins of zoonotic diseases. Given their close phylogenetic relatedness and geographic overlap with humans, non-human primates (NHPs) have been the source of many novel infectious diseases throughout human evolution. We applied a novel link-prediction model to predict undocumented instances of parasite sharing between humans and NHPs. Our model makes predictions based on phylogenetic distances and geographic overlap among NHPs and humans in six countries with high NHP diversity. Of 899 human parasites documented in the Global Infectious Diseases and Epidemiology Network (GIDEON) database for these countries, 12% were shared with at least one other NHP species. The link prediction model identified an additional 54 parasites that are likely to infect humans but were not reported in GIDEON. These parasites were mostly host generalists, yet their phylogenetic host specificities varied substantially. Our study points to specific infectious organisms to monitor in countries with high NHP diversity, while the comparative analysis of host specificity, parasite taxonomy, and transmission mode provides insights to types of parasites that represent high zoonotic risk more generally.
Antagonistic pleiotropy and tumor suppressor genes. What is the evidence?	Konstantinos Voskarides	Mutations in Tumor Suppressor Genes (TSGs) can cause several types of cancer. However, evidence is increasing that these mutations can be adaptive as well. “Mutators” microorganisms are well known. These have increased mutagenesis rate because of mutations in DNA mismatch repair genes, surviving in highly adverse environments, like antibiotics. Reduced apoptosis potential in some mammals help them to survive in cold and high-altitude environments. This is explained by certain p53 amino-acid residues, that have been associated with multiple primary cancers in humans. TP53 mutations may have positive effects in living organisms like increased longevity in mouse, drosophila, C. elegans and humans, and higher fertilization rates in mice. Carcinogenic TP53 mutations were found to increase survival of zebrafish larvae under extreme starvation conditions. Additionally, mutations under selection in NOTCH1 and TP53 genes were found in a large percentage of somatic cells in healthy humans. People living in extreme environments have mutations in or close to TSGs, assisting survival and probably predisposing them to higher rates of cancer. Utah women with BRCA1/2 mutations had more children and shorter inter-birth intervals, a less clear pattern for women with modern contraception. These data need further investigation. However, it seems that evidence will continue increasing.
How and Why Do Testosterone Levels Predict Male Mortality?	Michael Muehlenbein, Baylor University, Waco; Jeffrey Gassen, Baylor University, Waco; Tomasz Nowak, Baylor University, Waco; Alexandria Henderson, Baylor University, Waco; Brooke Morris, Baylor University, Waco; Edward Thum, Baylor University, Waco; Eric Shattuck, University of Texas at San Antonio, San Antonio; Corey Sparks, University of Texas at San Antonio, San Antonio; Sally Weaver, Waco Family Medicine, Waco; Erich Baker, Baylor University, Waco.	Because testosterone is central to male mammalian life history trajectories and trade-offs, changing levels during the lifespan may be associated with diminished physiological functioning and elevated mortality risk. Testosterone could directly contribute to mortality risk by influencing oxidative stress, energy balance, and immune function. Testosterone levels also decrease in the context of many infectious and chronic diseases. Accordingly, relationships between testosterone levels and mortality may be largely indirect; men in poor health are expected to have both lower testosterone levels and experience a greater risk for mortality. The results of two studies supported this hypothesis. Results from the Waco COVID Survey (n = 138) showed that younger men (< 50 years old) with more chronic health conditions (i.e., pre-existing conditions for severe COVID-19) had lower testosterone levels than men with fewer conditions. Moreover, data from the National Health and Nutrition Examination Survey (NHANES; n = 2,561) revealed that lower serum testosterone levels were associated with higher all-cause mortality risk in men across age groups, as well as greater risk for mortality from infectious diseases after age 80. This research may lay the groundwork for future studies to further untangle intricate relationships among androgens and male health across the lifespan.
(Symposium) Antagonistic pleiotropy expanded: from human disease to antibiotic resistance	Paul Turke, Turke and Thomashow Pediatrics, Dexter	“Williams’ caveat, which is that antagonistic pleiotropic effects emerge from changes in somatic environments, can help explain our increased vulnerability to dementia” In his seminal article on the evolution of senescence, Williams assumed the existence of “genes that have opposite effects on fitness at different ages, or, more accurately, in different somatic environments." Here, I give some examples of antagonistic pleiotropic effects emerging from changes in somatic environments, which adds breadth to the concept of antagonistic pleiotropy. I conclude with a discussion of how the neotenic phenotype that evolved in hominins as they diverged from other apes produced a somatic environment that can be expected to have changed the expression of previously fixed antagonistic pleiotropic genes, leading to delayed senescence in many organ systems, with the exception of the nervous system (particularly cognitive function). This asynchrony in the timing of senescence can account in part for why we now increasingly outlive our cognitive abilities. Key concepts discussed along the way are the coevolution of physical altriciality and cognitive precociality, and the selective pressures that drove this coevolution.

Title	Authors	Abstract
Antagonistic pleiotropy of antibiotic resistance and its potential to improve therapy	Hinrich Schulenburg, Kiel University & Max-Planck Institute for Evolutionary Biology Ploen, Germany	The current spread of antibiotic resistance is a major threat to global health. Evolutionary principles may help to optimize antibiotic therapy and thereby reduce selection for resistance. One promising evolutionary principle is collateral sensitivity. Collateral sensitivity describes the phenomenon that evolution of resistance to one antibiotic causes an increase in sensitivity to another antibiotic. It is based on changes in genes (or pathways) with antagonistic pleiotropy, where the mutation enhancing resistance also leads to higher sensitivity to another drug. Collateral sensitivities have now been characterized for a variety of bacteria and antibiotics. The underlying genetic changes are still only poorly characterized. In my talk, I will present our current understanding of the distribution of collateral sensitivity and its genetic basis. I will further summarize current studies that explore how collateral sensitivity can be used to improve antibiotic therapy and where it fails when bacteria are able to overcome such genetic constraints. I will conclude by highlighting future avenues of research that will help to establish collateral sensitivity as a principle for effective therapy that achieves both, the eradication of the infecting bacterial pathogen and the reduction of antibiotic resistance evolution.
Early life adversity predicts behavioral and physiological aging in wild female baboons	Chelsea J Weibel, University of Notre Dame, Notre Dame, IN; Mauna Dasari, University of Pittsburgh, Pittsburgh, PA; David A Jansen, University of Notre Dame, Notre Dame, IN; Laurence R Gesquiere, Duke University, Durham, NC; Jenny Tung, Duke University, Durham, NC; Susan C Alberts, Duke University, Durham, NC; Elizabeth A Archie, University of Notre Dame, Notre Dame, IN	Biological aging is a fact of life; across species, individuals exhibit predictable patterns of physical decline with age, and these patterns underlie mortality and disease risk. However, our understanding of the factors that influence biological aging are limited. Here, we test the hypothesis that early-life adversity leads to accelerated aging, which in turn leads to short lifespans. To do so, we leverage 50 years of continuous, individual-based data from wild female baboons in Kenya to identify 49 behavioral and physiological traits that have an association with age. We use these data to construct a biological aging index via supervised machine learning and calculate individuals' relative biological age (the difference between their predicted biological age and true chronological age). We find that individuals who have more adverse social and nutritional experiences in early life (before age 4) appear biologically older than those who do not experience early life hardships. Further, we find that individuals who appear biologically old for their age live shorter lives. Together, these results provide valuable insight into the long-term effects of early life adversity and offer a new, non-invasive tool for measuring biological aging in a long-lived non-human primate.
Evolution of Non-Allometric Longevity in a Clade of Long-Lived Bats Resolved Using Chromosome-Length Genome Assemblies	Juan M Vazquez, University of California, Berkeley; Elise Lauterbur, University of Arizona, Tucson; Devaughn Fraser, Connecticut Department of Wildlife, Hartford; Michael Buchalski, California Department of Fish and Wildlife, Sacramento; David Enard, University of Arizona, Tucson; Peter H Sudmant, University of California, Berkeley	Lifespan is one of the most variable traits across the entire tree of life, and especially in mammals. Differences in lifespans between closely-related species provides a promising avenue for discovering novel pro-longevity pathways using evolutionary techniques. Previous studies looking at the genetics underpinning aging in long-lived mammals have suffered from a combination of low-quality genomes, low-phylogenetic coverage, or long evolutionary times, all of which can negatively affect their power to detect genes associated with longevity. In order to comprehensively study the evolution of aging and aging-associated traits in bats, we generated chromosome-level reference genomes and primary cell line libraries from a 14.2-million-year-old clade of 9 Californian Myotis species, which span a wide range of lifespans. Leveraging these genomes, we have identified several pathways associated with aging, both independent of and specific to other longevity-associated traits such as body size. These pathways represent new targets for exploration using primary cell cultures, and contribute to our understanding of how both agonistic and antagonistic pleiotropy play a role in the evolution of longevity.

Title	Authors	Abstract
Intergenerational conflict may help explain why parents delay their children's ages at first birth	Cristina Moya, University of California, Davis; Monique Borgerhoff Mulder, University of California, Davis; Heidi Colleran, MPI Evolutionary Anthropology, Leipzig; Drew Gerkey, Oregon State University, Corvallis; Mhairi Gibson, Bristol University; Michael Gurven, University of California, Santa Barbara; Joseph Henrich, Harvard University, Cambridge; Paul Hooper, Chapman University, Irvine; Hillard Kaplan, Chapman University, Irvine; Michelle Kline, Brunel University; Jeremy Koster, University of Cincinnati; Karen Kramer, University of Utah, Salt Lake City; Donna Leonetti, University of Washington, Seattle; Siobhan Mattison, University of New Mexico, Albuquerque; Dilip Nath, Gauhati University; Catherinie Sanders, Unity College, Maine; Brooke Scelza, University of California, Los Angeles; Mary Shenk, Pennsylvania State University, College Station; Kristin Snopkowski, Boise State University, Jonathan Stieglitz, Institute for Advanced Studies, Toulouse; Mary Towner, Oklahoma State University, Stillwater; Christopher von Rueden,University of Richmond, John Ziker, Boise State University; Rebecca Sear, London School of Hygiene & Tropical Medicine	Public health professionals and governmental organizations often promote delayed reproduction and pathologize teenage pregnancy. The fact that parental presence is often associated with delayed first births in high income, low fertility human societies may reflect these norms. However, parental delays to first births have been less consistently documented in higher fertility societies and counters a straightforward evolutionary prediction that parental investment should enable offspring to reproduce earlier. Here we present the most extensive systematic cross-cultural comparison of parental effects on first births to date. We (1) test whether parental presence is consistently associated with offspring's age at first birth using data from 20 populations, predominantly representing small-scale and higher fertility societies; and (2) test hypotheses about cross-cultural variation in these associations derived from several theoretical accounts. We find that on average parental presence is associated with later reproductive onset for daughters, but not sons. Yet these effects are cross-culturally variable and patterned in ways that suggest intergenerational conflict may help account for parental delays to reproduction.

Title	Authors	Abstract
An evolutionary perspective on microchimerism and human health	Amy Boddy, UC Santa Barbara Tiffany Pan, UC Santa Barbara Henderson Cleaves, Earth-Life Science Institute, Tokyo Michael Eikmans, Leiden University Medical Center Frank Schildberg, University Hospital Bonn Thomas Kroneis, Medical University of Graz	Microchimerism is the harboring of a small number of cells between two distinct individuals. This transfer of cells is well known to occur between mothers and offspring during gestation. The current understanding of microchimerism is puzzling and little is known about the role microchimeric cells play in host physiology, including health and disease states. Evolutionary biology and maternal-fetal conflict theory can provide a framework to understand the persistence of microchimeric cells, and how this may lead to disease vulnerability. Further, little is known about the variation in the presence and quantity of microchimerism across different stages of pregnancy. First, we will provide an overview on what is known about microchimerism in the context of maternal-fetal conflict theory. Next, we will provide a summary of current data from pregnant women (n=105) who have received prenatal care at Santa Barbara Cottage Hospital. We report 11.4% of the women (n=15) had detectable levels of Y-chromosome in this cross-sectional dataset. The earliest detected of microchimerism was a gestational age of 26 days. Lastly, we will end the talk on how to re-launch the field of microchimerism research to evaluate the impact on human health and disease.
Challenges in the analysis of rare cells – preparing for microchimerism analysis	Michael Gruber, Medical University of Graz, Austria; Lilli Bonstingl, Medical University of Graz, CBmed GmbH, Austria; Katja Sallinger, Medical University of Graz, CBmed Gmbh, Austria; Karin Pankratz, Medical University of Graz, Austria; Amin El-Heliebi, Medical University of Graz, CBmed GmbH, Austria; Thomas Kroneis, Medical University of Graz, CBmed GMBH Austria;	Microchimerism (MC) research always performs at the borderline of analytical noise as the incidences of microchimeric cells reported in literature range from parts per million to a few per mill. In addition microchimeric cells cannot be easily discriminated from host cells based on predefined markers, with the Y-chromosome being an exception, because differences between microchimeric and host cells are rather to be found in individual SNPs, insertions/deletions (InDels) or different HLA alleles. Thus, research mainly focused on the presence of microchimerism linking levels of mismatch signatures to health data. Despite these quantitative and qualitative (e.g., HLA-specific) importance for interpreting MC related effects, future research targeting the meaning of microchimerism needs to go beyond these techniques. In our talk will discuss pitfalls of rare cell analysis, the use of in situ padlock and sequencing technology for identifying cell types and biological processes in rare cell and cancer tissue samples, and how in situ techniques can be used to help unraveling the nature of microchimerism.
Is maternal-origin microchimerism protective against early life infection symptoms in Filipino women?	Tiffany D. Pan, University of California, Santa Barbara; J. Lee Nelson, Fred Hutchinson Cancer Research Center and University of Washington, Seattle; Nanette R. Lee, USC-Office of Population Studies Foundation, Inc., Cebu City; Dan T.A. Eisenberg, University of Washington, Seattle	Mothers augment an infant's inexperienced immune system by passing antibodies across the placenta during pregnancy and via breastmilk. Maternal cells and DNA can also transfer to offspring by similar routes. Retention of small quantities of these maternal cells or DNA by the offspring is called maternal-origin microchimerism (MMc). Previous research suggests that, where malaria is endemic, MMc may protect infected young children from severe symptoms. Whether MMc has protective effects against the severity of other common infections is unknown. We tested whether women in the Philippines with greater MMc had decreased diarrheal or respiratory morbidity during their first two years of life (n=89). We found no relationship between MMc in young adulthood and early life diarrheal or respiratory morbidity (ps>0.38). However, most (16 of 22) of our assays for MMc rely on distinguishing mismatched HLA between mother and offspring. Individuals who were compatible with their mothers at HLA-DRB1, -DQA1, and -DQB1 had non-significantly lower rates of diarrheal (p=0.11) and respiratory morbidity (p=0.17). It is possible that the mother-child HLA relationship could influence MMc, and if so, maternal HLA-compatibility may have obscured our ability to detect a relationship between MMc and early life infections.

Title	Authors	Abstract
Cooperation or competition of fetal and maternal microchimerism in primigravid women?	Marina El Haddad*, INSERM UMRs 1097 AA, Aix Marseille University, Marseille, France; Karlin R. KARLMARK*, INSERM UMRs 1097 AA, Aix Marseille University, Marseille, France; Xavier-Côme DONATO, St Joseph Hospital, Marseille, France; Gabriel V. MARTIN, INSERM UMRs 1097 AA, Aix Marseille University, Marseille, France; Florence BRETELLE, AP-HM, Aix Marseille University, Marseille France; Nathalie LESAVRE, CIC1409, Aix Marseille University, AP-HM, Marseille, France; Jean-François COCALLEMEN, AP-HM, Aix Marseille University, Marseille France; Marielle MARTIN, INSERM UMRs 1097 AA, Aix Marseille University, Marseille, France; Christophe PICARD, UMR7268 (ADES), EFS, Marseille, France; Jean ROUDIER, INSERM UMRs 1097 AA, Aix Marseille University, Marseille, France ; Raoul DESBRIERE St Joseph Hospital, Marseille, France and Nathalie C. LAMBERT**, INSERM UMRs 1097 AA, Aix Marseille University, Marseille, France * Authors have equally contributed to this work ** Corresponding author	Fetal cells enter the maternal circulation from the first weeks of pregnancy and persist in the mother for decades, creating a natural phenomenom called fetal microchimerism (FMc). Conversely, maternal cells enter the fetal circulation and persist in the growing child and adult as maternal Mc (MMc). Fetal and maternal cells influence the immune system of their host and have been implicated in benefic roles, such as tissue repair after injury, as well as in detrimental mechanisms leading for example to autoimmunity. Pregnancy is a crucial moment where maternal Mc, from the mother of pregnant women, and fetal Mc can cohabit and, on this cohabitation, the health of their host will depend. Do pregnant women carry maternal and fetal Mc simultaneously? How do the two chimerisms evolve during pregnancy and childbirth? We present the first most complete monitoring of both natural microchimeric sources during, and two months after, pregnancy in whole blood, T cells, B cells and granulocytes in 37 healthy primigravid women. Interestingly, reversed patterns to those observed for FMc are often observed for MMc, highlighting a genetically and immunologically controlled homeostasis of the two Mc sources.
Teaching Evolutionary Medicine Using Active Pedagogies: A Two-Part Workshop	Jay Labov, U.S. National Academies of Sciences, Engineering, and Medicine (Retired); David Coall, Edith Cowan University; Barbara Horowitz, University of California, Los Angeles; Jason Mussel, University of North Carolina, Asheville	Evidence from the learning sciences over the past three decades has demonstrated that students at all levels and from all demographics learn more deeply when they participate actively in their learning. However, many faculty are either unfamiliar with this evidence or have had no experience implementing such approaches in courses, grand rounds, and other activities. These sessions will provide both background and hands-on experience for participants to learn how to teach topics in evolutionary medicine. The topics will be proposed by the ISEMPH community from suggestions submitted before and during the first workshop session.

Title	Authors	Abstract
Challenges to detecting differential reproductive success among post-reproductive Tibetan women	S Ye, George Mason University, Fairfax; J Sun, George Mason University, Fairfax; B Basnyat, Oxford Tropical Research Unit, Kathmandu; SR Craig, Dartmouth College, Hanover; TS Simonson, University of California, San Diego; JJ Yu, University of California, San Diego; EA Moya, University of California, San Diego; FL Powell, University of California, San Diego; D.Witonsky, University of Chicago, Chicago; A Di Rienzo, University of Chicago, Chicago; CM Beall, Case Western Reserve University, Cleveland.	Variation in reproductive success related to variation in heritable traits is central to evolution by natural selection. Biological variation reflects sociocultural factors, adaptation to the environment, aging, and reproduction costs. Testing hypotheses about human evolution, adaptation, and vulnerability to disease requires considering this complex set of inputs. We present a case study based on a sample of 430 ethnic Tibetan women living at 3500m-4100m in Nepal with an average age of 59 who had completed their childbearing years. They provided biosamples for DNA extraction, reproductive histories, social information, and physiological measurements. Comprehensive modeling using tree-based methods and regression analyses revealed traits associated with higher reproductive success. Demographic factors including earlier first birth, longer first marriage, and a miscarriage predicted more pregnancies. Physiologic factors including lower hypoxic heart rate response and higher resting percent of oxygen saturation predicted more pregnancies. An intermediate body mass index (BMI) and a higher Forced Expiratory Volume at six seconds (FEV6) predicted fewer children dying before 15. GWAS analyses detected SNPs associated at genome-wide level of significance with higher BMI and FEV6.Aging complicates interpretations of genotype – phenotype – reproductive success links, yet women who have completed their child-bearing provide comprehensive measures relevant to studies of natural selection.
The ApoE Gene Cluster in Aging and Reproduction.	Caleb E. Finch, U Southern clifornia; Ben C Trumble, Arizona State U; Tsimane Life History Project.	Human Apolipoprotein E (ApoE4) has allelic variants not found in other mammals. The ancestral ApoE4 isoform increases risk of elevated blood cholesterol, cardiovascular disease, and Alzheimer disease relative to ApoE3, which is more prevalent and human-specific. Nonetheless, ApoE4 increases survival of adults and neonates for indigenous populations with high levels of pathogenic infection in rural Ghana and Bolivia. In the Bolivian Tsimane, ApoE4 carriers had decreased fetal loss and greater total fertility (unpublished). Several neighboring genes on Chromosome 19 modify the impact of ApoE alleles on neurodegenerative processes. The co-expression of ApoE cluster genes responds to environmental toxins and is altered in the aging human brain. The ApoE gene cluster is highly conserved in mammals and includes genes associated with metabolism (ApoC1, -C2, -C4), pathogen resistance to herpes and polio virus (nectin1, -2), and reproduction (CBG, chorionic gonadotrophin; LBH, luteinizing hormone peptide). Several genes are co-regulated by shared transcription factors. The range of these associated functions and their mammal-wide presence suggests the ApoE gene cluster evolved as a life history gene complex. Trumble B.C., Finch C.E. Q. Rev. Biol 2019. Haghani A., Thorwald M., Finch C.E. Alzheimer Dement, 2021.
Sex Differences in Health among Chimpanzees	Melissa Emery Thompson, University of New Mexico, Albuquerque, NM	Across human populations, women exhibit a pronounced survival advantage over men, yet studies often report higher rates of disease in women. Because many factors contribute to sex differences in health, it has been difficult to determine whether the health-survival paradox is truly a paradox and whether female health disadvantages are evolutionarily ancient or the product of particular, novel environments. Our close primate relatives also exhibit higher rates of female survival, thus can be valuable comparative models to examine the origins of sex differences in health. Here, I review evidence on sex differences in health and aging across multiple systems in chimpanzees. As previously reported for wild baboons (Alberts et al. 2014), there is no consistent female (or male) health disadvantage among wild chimpanzees, despite significant social disadvantages and prolonged reproductive effort for females. However, there is intriguing evidence that male and female age in different ways, which may result from very different patterns of reproduction, social stress, and social support across the lifespan. Both menopause and degenerative disease are rare in chimpanzees, limiting some pathways that figure disproportionately in gendered health disparities in humans.

Title	Authors	Abstract
Women with higher number of daughters experience more rapid cognitive decline	Grazyna Jasienska, Jagiellonian University, Krakow; Mateusz Blukacz, Jagiellonian University, Krakow; Andrzej Galbarczyk, Jagiellonian University, Krakow; Magdalena Klimek, Jagiellonian University, Krakow; Magdalena Mijas, Jagiellonian University, Krakow; Ilona Nenko, Jagiellonian University, Krakow	Reproduction in women is costly, thus trade-offs between reproduction and other physiological functions are expected. Increased risk of many diseases and shorter lifespan in women with high parity suggest that insufficient allocation to non-reproductive physiology has long-lasting detrimental effects. However, it is not clear if women with high parity should experience faster cognitive aging, because children, while physiologically costly, also provide psychological stimulation and social support to their mothers. We tested the rate of cognitive decline in 174 older rural Polish women in relation to their total number of children, number of sons and number of daughters. Cognitive functioning was assessed twice over the period of 7 years by Mini Mental State Examination (MMSE). Number of children and number of sons did not have a significant effect on the MMSE score. In contrast, number of daughters was related to a significant cognitive decline (b=-0.37, p=0.009). Women's reproductive investment does not end with their own reproduction but often extends to helping their adult children and grandchildren. In the studied population, older women more often provided help to their adult daughters than to adult sons, and associated physiological costs of this help were likely to contribute to poorer health.
Integrating evolutionary and clinical perspectives on human menopause and womens' postreproductive health.	Donna Holmes, Biological Sciences | WWAMI Medical Education Program University of Idaho, Caleb Finch, University of Southern California, Los Angeles (symposium chair)	In women and other female mammals, the reproductive life span is constrained by basic developmental and physiological mechanisms. Menopause around age 50 is the ultimate step in a process of gradual fertility loss over decades; and the physiological result of a finite, declining pool of ovarian follicles. In industrialized cultures, life expectancy at birth has risen by more than 40 years since 1900, and the women's average postmenopausal life span by 30 years or more. Many otherwise healthy women over 50 present with symptoms and disorders related to low estrogen levels that affect function or quality of life. Evolutionary biologists have repeatedly suggested that menopause, followed by an extended postreproductive life, is an exceptional life-history pattern among vertebrates, or even represents an adaptive developmental shift promoting reproductive success among older women's close relatives. But aging-related fertility declines in both women and men are strikingly correlated with increasing prevalence of multiple, non-adaptive diseases and disabilities. There has been little integration of clinical and physiological perspectives with rigorous comparative analysis or evolutionary hypothesis-testing. I argue for a more holistic, interdisciplinary synthesis of perspectives on human reproductive aging combining clinical and epidemiological viewpoints with those from comparative reproductive physiology and evolutionary medicine.
A mammalian pattern of egg production and loss plus a lengthened lifespan results in menopause and post-reproductive life	Lynnette Leidy Sievert, UMass Amherst, MA	Menopause and post-reproductive life developed in a number of mammalian species, including humans, due to a conserved pattern of egg production and rapid oocyte/follicle loss coupled with a longer lifespan. Two questions are central to the how and the why of human menopause. First, why did female mammals adopt a new strategy, ending mitosis in primordial germ cells at the very beginning of the lifespan? This strategy of abbreviated mammalian (and avian) egg production will be contrasted with the continuing production of viable gametes by fish, amphibians, and male mammals. The benefit of the mammalian pattern will be considered in relation to maternal investment and other characteristics that differ across taxonomic groups. Second, why did some mammals evolve a lifespan that exceeded the cache of ovarian oocytes/follicles? This question will be addressed across a variety of species, with a focus on allometric relationships, e.g., brain size, body size, and lifespan. Ultimately, this investigation shows that menopause and post-reproductive life are not necessarily unique to humans. Menopause is possible for the females of any species that cease mitotic production of oogonia, follow the mammalian pattern of follicle loss, and evolved a lifespan that exceeds the supply of eggs.
Hearing acuity in later life improves social integration, an avenue for increasing inclusive fitness	Molly Fox, UCLA, Los Angeles, CA; Poshan Dahal, Case Western Reserve University, Cleveland, OH ; Cynthia Beall, Case Western Reserve University, Cleveland, OH; Jessica Moore, Case Western Reserve University, Cleveland, OH; Jelena O'Carroll, University College Dublin, Dublin; Noel Boaz, ICSM, Martinsville, VA	Hominin evolution is characterized by accelerated selection for hearing-related genes. The Grandmother Hypothesis posits that post-menopausal women can increase their inclusive fitness by assisting adult children in ways that allow shorter inter-birth intervals. Post-menopausal women with hearing decline may be severely limited in their ability to provide this kind of assistance, undermining the contribution of their post-menopausal longevity to inclusive fitness. We test the hypothesis that, among post-reproductive individuals, maintaining hearing acuity is crucial for social integration, which in turn increases inclusive fitness. We reason that hearing decline could undermine a grandparent's (particularly grandmother's) ability to provide social support to her progeny. Using a large, public dataset from the National Social Life, Health, and Aging Project, a longitudinal US population-based study of adults aged 57-85, we evaluate whether hearing loss is associated with lower measures of social connectivity and impaired relationships with children and grandchildren. Significant correlations were found between impaired self-reported hearing and more frustrations and problems when talking to family, limitations in personal/social life, and loneliness. These observations are consistent with the possibility that hearing decline undermines older individuals' ability to provide kin with assistance, such as childcare, that is the core mechanism of the "grandmother hypothesis."

Title	Authors	Abstract
Discussion and Q&A: Experiences of an evolutionary biologist in the pharmaceutical industry	Gunther Jansen, Personalized Healthcare Centre of Excellence, Roche/Genentech, Basel, Switzerland	As a former EMPH editor and academic working in evolutionary biology, I will provide insights on my current life and work in a large, R&D-driven pharmaceutical company. I will explain the drug discovery process, advances in tech and personalized healthcare, and highlight where evolution can and should be playing a role. The subsequent Q&A will provide ample opportunity to engage in a hopefully stimulating dialogue.
Experimental epidemiology with viruses: toward assessing phylodynamics	Roland Regöes, Department of Environmental Systems Science, ETH Zürich, Switzerland	Genetic sequences of organisms are imprints of their evolutionary and population history. To recover the evolutionary and population history, the complex inference scheme of phylodynamics has been developed that combines phylogenetics with population biological models, such as the coalescent, the birth-death models, or even the SIR model. Although these phylogenetic inference methods are being applied to a wide array of evolutionary, ecological, epidemiological and clinical systems, they have not yet been empirically validated. In this talk, I will introduce two long-term evolution experiments, with HIV-1 and the bacteriophage phiX174, that we conceived to validate phylodynamic methods. In the experiments with HIV-1, we have been passaging the virus in cell culture for over 3 years and have been seeing a continued accumulation of new mutations. We have also observed parallel evolution across different passaging lines, which confound phylogenetic and phylodynamic analyses. I am also going to introduce new experiments with the bacteriophage phiX174, in which we passaged for 426 generation with a pipetting robot. The resulting whole-genome, whole-population data again reveal extreme levels of parallel evolution, not just on the level of individual sites, but also for combinations of mutations. I will conclude by outlining the next steps to validate phylodynamic inference methods.
Adaptation to starvation and resilience in cavefish	Nicolas Rohner, Stowers Institute for Medical Research, Kansas City, MO, USA	Adapting to extreme environments requires drastic changes to an animal's metabolism. Adaptation to the total darkness and food limitation of caves can be particular challenging. The cavefish Astyanax mexicanus is a promising research organism to unravel the genetic basis of starvation resilience, as surface and cave morphs of the same species remain interfertile and can be bred outside their natural environments. We have previously shown that cavefish evolved impressive adaptations such as increased appetite, starvation resistance, and altered feeding due to mutations in mc4r. In addition, we found that cavefish display elevated blood sugar levels and insulin resistance caused by a mutation in the insulin receptor. In contrast to human patients, carrying the same mutations, cavefish do not display common markers of metabolic diseases or high blood sugar. Furthermore, cavefish develop hypertrophic visceral adipocytes without obvious signs of inflammation due to reduced amounts of pro-inflammatory cytokines. Taken together, our work suggests that cavefish develop these phenotypes as part of their starvation resistance and have evolved resilience phenotypes that allow them to tolerate stark deviations from what would be considered normal physiology in other vertebrates, including humans. This positions cavefish as a promising model to study disease phenotypes from an evolutionary and adaptive perspective.
Anatomical Characterization and Evolutionary Medicine of the Transcellular Fluid Compartment	Noel T. Boaz, Integrative Centers for Science and Medicine and Virginia Museum of Natural History, Martinsville, VA	Only some 2.5% of the total body water is contained in the "transcellular compartment," a physiological abstraction traditionally termed the "third space," defined as the aggregate of extracellular fluid spaces separated from the plasma and interstitial fluid by an epithelial barrier. Without anatomical detail such a diffuse concept is of limited utility. In this study over 50 examples of anatomical loci meeting the criteria of transcellular compartments are identified on the basis of 1) cells of origin producing the fluid, 2) the epithelial membrane or tube containing the fluid, 3) the anatomical exit point or boundary of the fluid compartment, and 4) the identity of the fluid. Every system and region of the body was found to have examples of transcellular compartments, suggesting that this morphophysiological entity is evolutionarily ancient. Shared characteristics include origination of the transcellular fluid from cells (intracellular fluid) and the presence of a "barrier" epithelium, relatively impermeable as in the "blood-brain barrier" or of varying permeabilities as in the nephron loop. Transcellular fluid transport is primarily by osmotic pressure, suggesting an adaptive origin pre-dating the cardiovascular system. "Third spacing" as used clinically affects only a small portion of the anatomically defined transcellular compartment.

Title	Authors	Abstract
Grandmothers buffer the relationship of discrimination and psychological distress	Delaney Knorr, UCLA; Molly Fox, UCLA	Maternal psychological distress is thought to be a major source of minority health disparities in birth outcomes. Harsh environmental stressors, including psychosocial stressors such as discrimination, can be embodied in ways that create an intergenerational cascade of disease risk. An evolutionary perspective reframes this morbidity risk as a decrease in offspring quality. Thus, related individuals may be evolutionarily motivated to buffer these psychosocial stressors. We ask if grandmothers buffer maternal psychological distress from discrimination. Through multiple linear regression models with self-report questionnaire data collected from 216 pregnant Latina women, we find that discrimination is significantly and positively associated with all measures of psychological distress (depression, anxiety, and stress) and that maternal grandmother communication moderated all three associations. This moderating effect was over and above the influence of her baby's father. Paternal grandmothers did not appear to have any significant moderation effects. Geographic proximity was not a significant stress-buffer for either grandmother nor the offspring's father. This suggests the important role maternal grandmothers play during pregnancy, and that these benefits exist uncoupled from geographic proximity. These findings have positive implications for perinatal mental health. We recommend phone and internet credits as critical prenatal care components for first-time mothers and immigrating women.

Title	Authors	Abstract
Research on the origin of vision and vision loss in naturally “blind” animal species can reveal the tasks that vision fulfills and the brain's role in visual experience. Models that incorporate evolutionary history, natural variation in visual ability, and experimental manipulations can help disentangle visual ability at a superficial level from behaviors linked to vision but not solely reliant upon it, and could assist the translation of ophthalmological research in animal models to human treatments. To unravel the similarities between blind individuals and blind species, we review concepts of 'blindness' and its behavioral correlates across a range of species. We explore the ancestral emergence of vision in vertebrates, and the loss of vision in blind species with reference to an evolution-based classification scheme. We applied phylogenetic comparative methods to a mammalian tree to explore the evolution of visual acuity using ancestral state estimations. Future research into the natural history of vision loss could help elucidate the function of vision and inspire innovations in how to address vision loss in humans.	Alexandra A. de Sousa Centre for Health and Cognition, Bath Spa University, Bath, United Kingdom,UKRI Centre for Accessible, Responsible & Transparent Artificial Intelligence, (ART:AI), University of Bath, United Kingdom; Michael J. Proulx UKRI Centre for Accessible, Responsible & Transparent Artificial Intelligence, (ART:AI), University of Bath, United Kingdom, Department of Psychology, REVEAL Research Centre, University of Bath, Bath, United Kingdom; Orlin S. Todorov, School of Biological Sciences, The University of Queensland, St Lucia, Queensland, Australia	Research on the origin of vision and vision loss in naturally “blind” animal species can reveal the tasks that vision fulfills and the brain's role in visual experience. Models that incorporate evolutionary history, natural variation in visual ability, and experimental manipulations can help disentangle visual ability at a superficial level from behaviors linked to vision but not solely reliant upon it, and could assist the translation of ophthalmological research in animal models to human treatments. To unravel the similarities between blind individuals and blind species, we review concepts of 'blindness' and its behavioral correlates across a range of species. We explore the ancestral emergence of vision in vertebrates, and the loss of vision in blind species with reference to an evolution-based classification scheme. We applied phylogenetic comparative methods to a mammalian tree to explore the evolution of visual acuity using ancestral state estimations. Future research into the natural history of vision loss could help elucidate the function of vision and inspire innovations in how to address vision loss in humans.

Title	Authors	Abstract
Horizontal gene transfer increases microbiome stability	K. Z. Coyte, University of Manchester, UK; C. Stevenson, University of Sheffield, UK; C. G. Knight, University of Manchester, UK; E. Harrison, University of Sheffield, UK; J. P. J. Hall, University of Liverpool, UK; M. A. Brockhurst, University of Manchester, UK.	Genes encoding resistance to stressors such as antibiotics are widespread across microbiomes, often encoded on mobile genetic elements. Yet despite their prevalence, the impact of resistance genes and their mobility upon the dynamics of microbial communities remains largely unknown. Here we develop eco-evolutionary theory to explore how resistance genes alter the stability of diverse microbiomes. We show that adding resistance genes to microbiomes typically increases overall community stability, particularly for mobile resistance genes with high transfer rates. However, the impact of resistance genes upon the stability of individual taxa varies depending upon the mobility of the resistance gene and the network of ecological interactions within the community. Non-mobile resistance genes can benefit susceptible taxa in cooperative communities, yet damage those in competitive communities. Moreover, whilst the transfer of mobile resistance genes generally increases the stability of previously susceptible recipient taxa to perturbation, it can, counterintuitively, decrease the stability of the originally resistant donor species. Crucially, we recapitulate each of these predictions within experimental microcosms. Together these findings highlight the importance of horizontal gene transfer in driving the eco-evolutionary dynamics of diverse microbiomes.
Adaptive dynamics of the adult human small intestinal microbiota	Dr. Bahtiyar Yilmaz, Department for Biomedical Research, University of Bern, Switzerland	Small intestinal microbes have been shown to substantially impact host metabolism and immunity in experimental animals. However, human studies have been limited by the inaccessibility of the small intestine without purging. In our current study, we used stoma samples from cured healthy colorectal cancer patients as a feasible non-invasive access route to the otherwise inaccessible small and large intestines. We investigated the inherent instability and temporal dynamics in the human small intestinal microbiota within individuals, and the contribution of fed and fasted states in microbial diversity and metabolism Two types of instability in ileal host-microbial relationships were observed: inter-digestive purging followed by the postprandial rapid blooming of bacterial biomass, and sub-strain appearance and disappearance within individual taxa after feeding. In contrast to the colonic microbiota, the human small intestinal microbiota biomass and its sub-strain composition can be highly dynamic.
Bacteriophages as drivers of bacterial genetic and phenotypic diversity in the human gut microbiome	Pauline Scanlan, APC Microbiome Ireland and School of Microbiology, University College Cork, Ireland.	Coevolution with bacteriophages is recognised as a key driver in the evolution and ecology of bacterial populations. However, our understanding of how this process shapes the genetic and phenotypic diversity of microbes in the human gut microbiome is limited. Here I discuss data generated from time-shift analysis and in vitro modelling of Enterobacteriaceae bacterial populations and associated phages sampled from the adult and infant gut microbiome. Our results indicate that Enterobacteriaceae-associated bacteriophages are predominantly lysogenic/temperate and resistance to phage infection is high. Several naturally occurring bacterial isolates were lysogens capable of spontaneous phage production in vitro. In vitro modelling of bacteria-phage interactions over time provided little evidence of arms race dynamics that are typically observed for lytic phages and associated bacterial hosts. However, resistance to lysogenic phages did emerge in bacterial populations via receptor modification and/or lysogenic conversion. Consistent with observations of naturally occurring bacterial isolates we noted that coevolution with lysogenic phages in vitro selects for bacterial hosts that spontaneously produce phages without induction. These findings have important implications for our understanding of bacteria-phage coexistence, bacterial competition and the evolution of genetic and phenotypic diversity within microbial communities that inhabit clinically relevant ecosystems such as the human gut microbiome.
Tell me what you eat, and I tell you how your bacteria evolve	Tanja Dapa, Instituto Gulbenkian de Ciência, 2780-156 Oeiras, Portugal Ricardo S Ramiro, InnovPlantProtect, 7350-999 Elvas, Portugal Miguel F Pedro, LEAF – Linking Landscape, Environment, Agriculture and Food, Instituto Superior de Agronomia, 1349-017 Lisbon, Portugal Isabel Gordo, Instituto Gulbenkian de Ciência, 2780-156 Oeiras, Portugal Karina B Xavier, Instituto Gulbenkian de Ciência, 2780-156 Oeiras, Portugal	Misbalances in the taxonomic composition of the gut microbiota (dysbiosis) have strong consequences for the health of the host. In Western societies, a common cause of gut dysbiosis is the switch from a diet low in fat and rich in fibres and plant polysaccharides to a diet rich in saturated fat and simple sugars, so-called Western-style diet. This switch affects the microbiota composition, causing an increase in Firmicutes and a decrease in Bacteroidetes, and prompts a prevalent Bacteroidetes, Bacteroides thetaiotaomicron, to consume host mucus glycans. This causes a reduction of the thickness of the mucosal layer, increasing dysbiosis and sensitivity to colonization by pathogens. Although the effects of such dietary changes on microbiota composition are well documented, their putative impact in gut bacterial evolution remained unexplored. Here we followed the emergence of mutations in Bacteroides thetaiotaomicron, a prevalent fiber-degrading microbiota member, upon colonization of the murine gut under different dietary regimens. We show that different nutritional diets do not only affect gut microbiota at ecological level, but as well affect single species, at the gene level. Bacteroides thetaiotaomicron evolved rapidly to the gut and Western-style diet selected for mutations that promote the degradation of mucin-derived glycans. Periodic changes in diet led to fluctuations in the frequency of such mutations and were associated with metabolic shifts, resulting in the maintenance of higher intra-species genetic diversity compared to constant dietary regimens. These results show that dietary changes leave a genetic signature in microbiome members and suggest that B. thetaiotaomicron genetic diversity could be a biomarker for dietary differences among individuals.

Title	Authors	Abstract
A prenatal grandmother effect on cortisol trajectories across pregnancy	Kyle Wiley, University of California, Los Angeles Delaney Knorr, University of California, Los Angeles Dayoon Kim, University of California, Los Angeles Molly Fox, University of California, Los Angeles	The human reproductive strategy exhibits many features associated with cooperative breeding systems, in that mothers receive childcare assistance from other kin. These allomothers are adaptively incentivized to provide assistance due to inclusive fitness benefits. Previous studies across a broad range of populations identify grandmothers as particularly consistent allomothers, whose presence (survivorship and proximity) is associated with child survivorship and growth. Here, we examine how grandmother social support, communication frequency, and geographic proximity may exert beneficial effects on pregnant mothers, before the birth of their grandchildren. Data derive from the Mothers' Cultural Experiences study, a longitudinal cohort of pregnant Latina women in Southern California. We observe benefits conferred by maternal grandmother's social support and relationship quality for the mother's prenatal mental health and lower cortisol levels during early and mid-pregnancy. This work extends the traditional cooperative breeding model and grandmother hypothesis by identifying a prenatal grandmother effect, and, by examining a maternal biomarker. Our results suggest that grandmothers are able to improve their inclusive fitness by caring for pregnant daughters and daughters-in-law, and allomother support may positively impact prenatal health.
Title of Symposium: Adaptations and Tradeoffs in Female Reproductive Health and Disease Title of my presentation for Symposium: Testosterone Mediates Major Trade-offs in Female Reproduction and Disease	Bernard Crespi, Simon Fraser University, Burnaby	Hormones mediate trade-offs that impact reproduction and fitness. In human females, studies of hormonal trade-offs focus almost exclusively on progesterone, estrogen, and prolactin. Testosterone is usually considered as a 'male' hormone. However, testosterone is also central to female sexual development and reproduction, with strong impacts on sexual differentiation, ovarian and endometrial functions, and risks for endometriosis, polycystic ovary syndrome, premature ovarian insufficiency, and implantation failure. We describe and evaluate the first comprehensive theory for the mediation of female reproductive life histories and reproductive disease risks by levels of testosterone. From the available evidence, lower prenatal and postnatal testosterone are associated with earlier menarche and menopause, higher early fertility, more 'female-biased' sexually dimorphic and female-limited traits, higher risks of premature ovarian insufficiency and endometriosis and, overall, a faster life history. Higher prenatal and postnatal testosterone are, by contrast, associated with later menarche and menopause, lower early fertility, higher muscular strength, bone mineral density, and social dominance, higher risk of polycystic ovary syndrome, and a 'slower' life history. Extremes of the trade-off components manifest in disease. Testosterone-mediated trade-offs have direct implications for the evolutionary bases of female health and disease, and for prevention and treatment of female reproductive disorders.
Covid-19 infection and changes in menstrual cycles: health or disease?	Alexandra Alvergne, Gabriella Kountourides, Austin Argentieri, Jackie Maybin, Zuzanna Olszewska.	Background Reproductive ecology models posit that ovarian function is responsive to ecological conditions in a way that optimizes the timing of energy allocation to reproduction. While the importance of energetic factors for menstrual cycles is well understood, the impact of infection is largely unknown. We test the hypothesis that COVID-19 infection impacts menstrual characteristics, without necessarily leading to pathological outcomes. Methods We used (1) a retrospective survey conducted in the UK on >26 000 individuals and (2) longitudinal cycle data from a period tracker app paired with information on the timing of COVID-19 infection on > 13 000 individuals. We used directed acyclic graphs to establish adjustment variables for testing causal relationships between COVID-19 infection and cycle frequency, period duration, period flow and cycle regularity. Results We found that having been infected with COVID-19 increases the risk of reporting period "stopping" and longer periods, while long-COVID increases the risk of reporting irregular cycles (> 9 days) after adjusting for pandemic stress. We will also compare cycle and period length before and after COVID-19 infection using longitudinal cycle data. Implications The findings will increase our understanding of normal and pathological variation in menstrual cycles during the c19 pandemic.

Title	Authors	Abstract
Effects of extreme seasonality in ambient light on women's reproductive and immune function.	Virginia J. Vitzthum, Indiana University, Bloomington; Bryndis Eva Birgisdottir, University of Iceland, Reykjavik; Emily M. Chester, Indiana University, Bloomington; Geir Gunnlaugsson, University of Iceland, Reykjavik; Jonathan Thornburg, Indiana University, Bloomington.	In many mammals, seasonal shifts in day length modify the daily pattern and quantity of melatonin production which, in turn, affects the production of ovarian steroids and thus coordinates seasonal shifts in reproduction and immune functioning. The duration and intensity of daylight is thus an ecomarker of environmental conditions and a modulator of physiological responses to seasonal variation in environmental conditions as well as the driver of daily sleep/wake cycles. It has been hypothesized that in humans, disruptions (as a consequence of contemporary industrialized life) of these evolved responses to light may contribute to the relatively higher rates of hormone-sensitive cancers and other disorders observed in, for example, some shift workers and higher latitude populations. To investigate this hypothesis, the Cycles Iceland study measured reproductive and immune biomarkers in winter versus summer seasons (4 hours versus 21 hours of daily natural daylight) in a sample of women living in Reykjavik, Iceland
Seeking for autoimmunity risk variants with a strong functional effect by pinpointing targets of natural selection	Vasili Pankratov, Institute of Genomics University of Tartu, Tartu; Milyausha Yunusbaeva ITMO University, Saint-Petersburg; Sergei Ryakhovsky, ITMO University, Saint-Petersburg; Maksym Zarodniuk, University of Tartu, Tartu; Bayazit Yunusbayev, Institute of Genomics University of Tartu, Tartu & ITMO University, Saint-Petersburg	Causal variants for inflammatory diseases might have been under pathogen-driven natural selection. Such variants are promising for functional experiments since they likely strongly affect the immune response. While this hypothesis has important implications for biomedicine, its application in practice has been hindered by challenges with pinpointing the targets of selection (mutations). We attempted to approach this challenge using Biobank-scale sequence data and a new class of methods based on local tree inference. We focused on 593 risk loci associated with 21 autoimmune disorders. Altogether, 4838 candidate SNPs were analyzed across these loci using Relate-inferred local trees and likelihood-based selection tests using CLUES. We found that 204 out of 593 risk loci contain at least one candidate SNP with evidence for natural selection (logLR>1.59). Inferred selection coefficients suggest that these SNPs were likely under weak and moderate selective sweep. Such sweeps can leave some flanking variation, making it possible to fine-map the target of selection. We were able to fine-map likely targets of natural selection among candidate risk SNPs (57 loci out of 204), distinguish neutral hitchhikers and identify more complex scenarios. Risk SNPs with adaptive history are promising targets for functional analyses since natural selection picks mutations with a tangible effect on the phenotype.
Helminth infection is associated with dampened cytokine responses to viral and bacterial stimulations in Tsimane hunter-horticulturalists.	India A. Schneider-Crease, Arizona State University, Tempe, USA; Aaron D. Blackwell, Washington State University, Spokane, USA; Thomas S. Kraft, University of California Santa Barbara, Santa Barbara, USA; Melissa Emery Thompson, University of New Mexico, Albuquerque, USA; Ivan Maldonado Suarez, Tsimane Health and Life History Project, San Borja, Bolivia; Daniel K. Cummings, Chapman University, Orange, USA; Jonathan Stieglitz, Institute for Advanced Study, Toulouse, France; Noah Snyder-Mackler, Arizona State University, Tempe, USA; Michael Gurven, University of California Santa Barbara, Santa Barbara, USA; Hillard Kaplan, Chapman University, Orange, USA; Benjamin C. Trumble, Arizona State University, Tempe, USA	Soil-transmitted helminth (STH) infections catalyze immunological changes that shape the immune response to subsequent infections. Understanding these interactions is integral to public health in high-pathogen environments in the context of global pandemics. We worked with Tsimane forager-horticulturalists in the Bolivian Amazon, where STHs are prevalent, to test whether STHs and eosinophil levels— likely indicating infection in this population—are associated with dampened immune responses to in vitro stimulation with H1N1 and lipopolysaccharide (LPS) antigens. We assessed the effect of STHs and eosinophils on the expression of 13 cytokines in treated whole blood samples and found that Ascaris lumbricoides infection was significantly ($p \leq 0.05$) associated with lower response of certain cytokines—including those with primarily pro-inflammatory functions—to H1N1 and LPS in women. Eosinophils were significantly negatively associated with cytokine responses to H1N1 and LPS, with the strongest effects in women, and associated with dampened overall responses to H1N1 and LPS across the population. Our results demonstrate that STHs inhibit the inflammatory response to viral and bacterial infections in the Tsimane, which may underlie the low levels of inflammatory disease reported for this population and may contribute to lower incidence of cytokine storms in populations with high STH prevalence.

Title	Authors	Abstract
The durability of SARS-CoV-2 vaccine-mediated immunity and the optimal timing of booster vaccination	Hayley B. Hassler, Yale University, New Haven; Alex Dornburg PhD, University of North Carolina at Charlotte, Charlotte; Pratha Sah PhD, Yale University, New Haven; Alison P. Galvani PhD, Yale University, New Haven; and Jeffrey P. Townsend, Yale University, New Haven.	The durability of vaccine-mediated immunity to SARS-CoV-2 and the optimal timings of booster vaccination remain two of the most important unknowns in the global fight against SARS-CoV-2. Using comparative evolutionary analyses, we estimate the durability of immunity over time following vaccination by BNT162b2 (Pfizer-BioNTech), mRNA-1273 (Moderna), ChAdOx1 (Oxford-AstraZeneca), and Ad26.COV2.S (Johnson & Johnson/Janssen) and the statistical likelihood of breakthrough infections over time following different boosting schedules for BNT162b2. Peak antibody levels elicited by mRNA vaccines mRNA-1273 and BNT1262b2 exceeded that of natural infection and are expected to typically yield more durable protection against breakthrough infections (median 29.6 months) than natural infection (median 21.5 months). In contrast, viral vector vaccines ChAdOx1 and Ad26.COV2.S exhibit similar peak anti-S IgG antibody responses to that from natural infection, and are projected to yield lower, shorter-term protection against breakthrough infection than mRNA vaccines (median 22.4 and 20.5 months; respectively). Projecting antibody levels over time given BNT162b2 boosting every 6 months, 1 year, 1.5 years, 2 years, or 3 years yielded respective probabilities of no infection over a 6-year span of >99%, 76%, 37%, 25%, 17%, and 12%. These results provide a quantitative basis for public health policy.
COVID-19 and changes in experience of premenstrual syndrome: A United Kingdom (UK) retrospective case-control study.	Gabriella Kountourides, University of Oxford, Oxford; Zuzanna Olszeska, University of Oxford, Oxford; Alexandra Alvergne, Montpellier University, Montpellier, France.	Background: Premenstrual syndrome (PMS) is a condition which affects more than half of menstruating people over their life. Ewald's cyclical immunity defence paradigm suggests that PMS is part of a larger set of inflammatory symptoms that worsen in the premenstrual stage. This hypothesis of cyclical immunity suggests that infectious illnesses, such as COVID-19, are exacerbated by cyclic changes in immunosuppression, leading to increased inflammation, and worsening PMS. Methods: We test this hypothesis by investigating whether COVID-19 infection is associated with more severe PMS. We perform a secondary analysis of data from a large retrospective online survey conducted in March 2021 in the UK (n= 26,710). The survey included questions on PMS, menstrual cycle characteristics, COVID-19, as well sociodemographic data and standard proxies for health. Results: We use Bayesian models to investigate whether COVID-19 status can predict worsening PMS scores. Exposure variables are covid status, long covid status, and vaccination status. Adjustment variables were established through directed acyclic graphs, to test the causal links between COVID-19 infection and PMS score. Implications: This study is the largest of its kind to investigate the link between COVID-19 and PMS, and will contribute to understanding in variation in PMS, and increase awareness of female health as cyclical.
Clinical Applications of Evolutionary Medicine to Psychiatric Interviewing and Psychotherapy (Panel Discussion)	Chelsea Landolin, University of California, San Francisco; Randolph Nesse, Arizona State University, Tempe; Laith Al-Shawaf, University of Colorado, Colorado Springs; Mike Abrams, New York University, New York.	Despite several decades of theory development and research in evolutionary psychiatry and clinical evolutionary psychology, there has been limited progress in broad integration of evolutionary insights into day-to-day clinical practice. This is, in part, due to skepticism about its relevance to clinical psychiatry and psychology, which is currently dominated by symptom checklists, medication management, and evidence-based psychotherapies that have little to no evolutionary foundation. However, novel approaches developed in the past 5 years have promise to influence and transform diagnostic evaluation, case formulation, treatment, and patient education in a manner that improves patient care and contributes to the scientific advancement of psychiatry and clinical psychology. In this panel discussion, we bring together experts in evolutionary psychiatry and psychology to discuss specific methods that enable clinicians to apply evolutionary concepts to clinical practice. We will discuss (1) the evolutionary purpose of emotions, and how these can be productively discussed with patients and other clinicians; (2) an approach to psychiatric diagnostic evaluation that includes a review of social systems, situational analysis, and identification of problems that arise from goal pursuit, all with an evolutionary lens; and (3) integration of evolutionary insights into cognitive behavior therapy and other psychotherapies.

Title	Authors	Abstract
Evolutionary selection of alleles in melanophilin gene that impacts on prostate organ function and cancer risk	Luca Ermini, Institute of Cancer Research, London, UK; Jeffrey C. Francis, Institute of Cancer Research, London, UK; Gabriel S. Rosa, Institute of Cancer Research, London, UK; Alexandra J. Rose, Institute of Cancer Research, London, UK; Jian Ning, Institute of Cancer Research, London, UK; Mel Greaves, Institute of Cancer Research, London, UK; Amanda Swain, Institute of Cancer Research, London, UK.	Several hundred inherited genetic variants or SNPs that alter the risk of cancer have been identified through genome-wide association studies. In populations of European ancestry, these variants are mostly present at relatively high frequencies. To gain insight into evolutionary origins, we screened a series of genes and SNPs linked to breast or prostate cancer for genomic signatures of historical positive selection. Variants in only one gene, melanophilin (MLPH) and associated with risk of prostate cancer, showed genomic signatures of positive, evolutionary selection. MLPH protein has a role in skin pigmentation and these variants may have been historically selected for their impact on the skin tissue but MLPH is highly expressed in the prostate tissue. Functional depletion of MLPH in mouse prostate organoid cultures, by CRISPR/Cas9 mutation, produced alterations on epithelial cell growth and differentiation providing a possible explanation for the disease risk association. Our study suggests a potential functional mechanism via which MLPH and its genetic variants could influence risk of prostate cancer, as a serendipitous consequence of prior evolutionary benefits to another tissue.
Genetic ancestry effects on the response to viral infection are pervasive but cell type specific	Haley E Randolph, University of Chicago, Chicago, IL; Jessica K Fiege, University of Minnesota, Minneapolis, MN; Beth K Thielen, University of Minnesota, Minneapolis, MN; Clayton K Mickelson, University of Minnesota, Minneapolis, MN; Mari Shiratori, University of Chicago, Chicago, IL; João Barroso-Batista, University of Chicago, Chicago, IL; Ryan A Langlois, University of Minnesota, Minneapolis, MN; Luis B Barreiro, University of Chicago, Chicago, IL	Humans differ in their susceptibility to infectious disease, partly owing to variation in the immune response following infection. Genetic studies in immune cells have shown that certain polymorphisms drive variation in the response to influenza, including expression patterns of key antiviral regulators. Yet, relatively little is known about the underlying genetic factors that contribute to heterogeneity in the influenza response across different immune cell types. Here, we used single-cell RNA-sequencing to quantify genetic contributions to this variation in peripheral blood mononuclear cells across 90 individuals. We find that monocytes are the most responsive to infection but that all cell types mount a conserved interferon response, which is stronger in individuals with increased European ancestry. We show that genetic ancestry effects on expression are common, influencing 29% of genes, but highly cell type-specific, with over half detected in only one or two cell types. Further, we demonstrate that, on average, 53% of population-associated expression variation is explained by cis-expression quantitative trait loci. Finally, we provide evidence that genes associated with COVID-19 severity are strongly enriched among genes differentially expressed between African- and European-ancestry individuals, suggesting that immune response variation may compound known health disparities contributing to differences in COVID-19 susceptibility.
What we can and can’t predict about the evolutionary trajectory of SARS-CoV-2	C. Jessica E. Metcalf	After almost a year of relatively little phenotypic change, at the end of 2020, novel variants of SARS-CoV-2 began to emerge. There are three possible changes of concern: i) increases in transmissibility (or reductions in serial interval), ii) increases in capacity to overcome natural or vaccinal immunity, and iii) increases in virulence. The first two are associated with clear selective advantages; the last is unlikely to spread within populations unless also associated with transmission. Our ability to project the occurrence of these and future changes require progress in untangling many different dimensions of within-host biology and host to host transmission, for which an array of different approaches are possible.

Title	Authors	Abstract
Do pubes matter? Pubic hair removal as a risk factor for recurrent urinary tract infections in women.	Andrzej Galbarczyk, Jagiellonian University Medical College, Krakow; Urszula Marcinkowska, Jagiellonian University Medical College, Krakow; Grazyna Jasienska, Jagiellonian University Medical College, Krakow.	Objective Urinary tract infections (UTI) are the most common infections experienced by women. Previously, scalp and facial hair have been shown to inhibit the growth of pathogenic bacteria. Here we hypothesize that having hair down there might positively affect the genitourinary microbiome and, therefore, protect from UTI. Methods This study investigated grooming habits and diagnoses of UTI that had occurred in the past year in 2621 women (aged 18–45). Women who reported removing all their pubic hair at least weekly in the past year were defined as extreme groomers (67.4%). Results Extreme grooming was not associated with the risk of being diagnosed with UTI (OR = 1.25, 95%CI = 0.98–1.60), but was associated with a higher risk of recurrent UTI (OR = 2.77, 95%CI = 1.33–5.78), after controlling for age, history of UTI, and sexual practices. Conclusions Hygienic purposes are the most common motivations for pubic hair removal. The microbial communities that reside in many body sites are known to play key roles in maintaining host health. Presented results suggest that along with their pubes, women may get rid of important microbial niche and protection.
Ancient Darwinian replicators nested within eubacterial genomes	Frederic Bertels, Max Planck Institute for Evolutionary Biology, Plön; Paul Rainey, Max Planck Institute for Evolutionary Biology, Plön	Mobile genetic elements (MGEs), such as transposons and insertion sequences, propagate within bacterial genomes, but persistence times in individual lineages are short. For long-term survival, MGEs must continuously invade new hosts by horizontal transfer. Theoretically, MGEs that persist for millions of years in single lineages, and are thus subject to vertical inheritance, should not exist. Here I will present an exception — a class of MGE termed REPIN. REPINs are non-autonomous MGEs whose duplication depends on non-jumping RAYT transposases. Comparisons of REPINs and typical MGEs show that replication rates of REPINs are orders of magnitude lower, REPIN population size fluctuations correlate with changes in available genome space, REPIN conservation depends on RAYT function, and REPIN diversity accumulates within host lineages. From these data it follows that REPINs persist for millions of years within single host lineages. Such long-term persistence is expected to generate conflicts arising from the diverging effects of selection acting simultaneously on REPINs and host genomes. Evidence of conflict comes from analyses of REPIN abundance and diversity in two distantly related bacterial species. Taken together, the data leads to the conclusion that REPINs are ancient Darwinian replicators that have evolved enduring, beneficial relationships, with eubacterial genomes.
Gut mélange à trois: fluctuating selection modulated by microbiota, host immune system, and antibiotics	Hugo C. Barreto, Instituto Gulbenkian de Ciência, Oeiras, Portugal; Beatriz Abreu, Instituto Gulbenkian de Ciência, Oeiras, Portugal; Isabel Gordo, Instituto Gulbenkian de Ciência, Oeiras, Portugal.	Iron is critical in host-microbe interactions, and its availability is tightly regulated in the mammalian gut. Antibiotics and inflammation can perturb iron availability in the gut, which could alter host-microbe interactions. Here, we show that an adaptive allele of iscR, a major regulator of iron homeostasis of Escherichia coli, is under fluctuating selection in the mouse gut. In vivo competitions in immune-competent, immune-compromised, and germ-free mice reveal that the selective pressure on an iscR mutant E. coli is modulated by the presence of antibiotics, the microbiota, and the immune system. In vitro assays show that iron availability is an important mediator of the iscR allele fitness benefits or costs. We identify Lipocalin-2, a host's immune protein that prevents bacterial iron acquisition, as a major host mechanism underlying fluctuating selection of iscR. Our results provide a remarkable example of strong fluctuating selection acting on bacterial iron regulation in the mammalian gut.
Selection for resistance to glyphosate in enteric pathogen Salmonella Typhimurium: a trade-off between resistance, pathogenicity and persistence within host cells?	Fereshteh Ghazisaeedi, Freie Universitaet Berlin, Berlin; Benno Kuropka, Freie Universitaet Berlin, Berlin; Uwe Roesler, Freie Universitaet Berlin, Berlin; Olga Makarova, Freie Universitaet Berlin, Berlin and Vetmeduni Vienna, Vienna	Glyphosate is the most widely used herbicide in the world as well as a potent antimicrobial. Its traces are commonly be found in food and feed. Enteric pathogens such as Salmonella may come in contact with glyphosate in the animal gut, creating opportunities for glyphosate resistance development in bacteria. We recently demonstrated that it is possible to select for glyphosate resistance without any fitness costs in Samonella Typhimurium in vitro (Pöppe et al., 2020). Here, using host cell invasion and viability, and bacterial biofilm and motility assays in combination with global proteomics, we investigated fitness and pathogenicity of glyphosate-resistant Salmonella in host cells. Our results showed that the expression of pathogenicity-associated traits such as iron scavenging, motility and biofilm formation has been down-regulated in the glyphosate-resistant evolved mutant strain. At the same time, the mutant replicated to higher numbers in porcine intestinal epithelial cells and murine macrophages, with no significant alteration in the viability of the host cells. Our observations suggest that bacterial resistance to glyphosate results in a trade-off between pathogenicity and persistence, which provides a fitness advantage for bacteria within the host cells and may create potential reservoirs for dissemination of glyphosate resistance.

Title	Authors	Abstract
Profiles and Characteristics of Patients with Mild to Moderate COVID -19 Phenotypes in a Teaching Hospital in Kano, Northern Nigeria	Mahmoud Habib Maje, MScPH; Musa Baba Maiyaki, MBBS, MPH; Garba Dahiru, MBBS; Amina Abdullahi, MBBS, MPH; Tijjani Hussaini, MBBS, MPH; Sabitu Shuaibu, MBBS; Mohammed Auwal Ibrahim, MSc; Auwal Adamu, MSc; Nura Mohammed, MScPH; Hamisu M. Salihu, MD, PhD Corresponding author email: mahmoudmaje@yahoo.com	Background: COVID-19 has affected almost 180 million people globally, with the death of about 5 million persons, as of November 16, 2021. The disease presents with a plethora of pulmonary and extra-pulmonary symptoms of varying severity. After an exhaustive review of the literature, we found no data on the mild and moderate COVID-19 disease phenotypes in Northern Nigeria. Our objective is to describe the clinical characteristics of non-severe COVID -19 disease phenotypes in Kano State. Methods: A retrospective cohort study at the COVID-19 Isolation Centre of Muhammad Buhari Specialist Hospital Kano, Nigeria. For all patients admitted from May 2020 to December 2020 medical records were assessed and evaluated to describe the clinical characteristics at presentation. We explored time to discharge between patients aged ≤ 50 years old versus those >50. We applied the Kaplan-Meier product-limit estimator to generate cumulative probabilities of discharge over time and used the Log-rank test to determine differences between the two age groups. We applied Cox Proportional Hazards to identify predictors of time to discharge among the patients in the study. The study variables comprised time of viral clearance and time to discharge as outcome variables, while the main exposure variables included, age, sex, occupation, mode of exposure, presence of co-morbidity, and duration of hospitalization. Results: A total of 187 COVID-19 patients were reviewed. The commonest symptoms were fever, breathing difficulty, and dry cough. There was no recorded death. Contact with a confirmed COVID-19 positive person was the source of infection in 167(89.3%) of patients. We noted a faster time to viral clearance in patients on lopinavir compared to those on chloroquine (Log-rank test p-value = 0.048). There were no significant differences in time to discharge between younger (< 50 years) versus older patients (≥ 50 years) [24 days vs. 26 days respectively; Log-rank test p-value = 0.082]. Age, sex, and source of infection did not appear to be predictors of infection phenotype.
Effect of social microbiomes on the pattern of gut bacterial evolution	Nelson Frazão and Isabel Gordo	Social networks can influence the ecology of gut bacteria shaping the species composition of the gut microbiome. Gut commensals evolve and adapt at a fast pace when colonizing healthy hosts. Here, we aimed at assessing the impact of the host social regime on bacterial evolution in the mammalian gut. Using an in vivo experimental evolution approach, we investigated how the pattern of genetic adaptation of Escherichia coli colonizing the mouse gut is influenced by host-to-host bacterial transmission. We found high transmission rates of newly colonizing E. coli strains in mice inhabiting the same environment, with horizontal gene transfer (HGT) events between phylogenetic distinct E. coli strains being pervasive. A simple population genetics model of mutation-selection-migration predicts that, after hundreds to thousands of generations of gut adaptation, the level of shared evolutionary events is enhanced in social animals. The observed pattern of shared mutation and HGT events under sociality is consistent with a massive role of migration shaping the adaptive evolution of new strains that invade the gut microbiomes of healthy hosts. Selection of biofilm-defective E. coli was only observed in the social regime, which may have important implications for the antibiotic resistance profile of bacteria transferring across mammalian microbiomes.
Investigating genotypic and phenotypic co-adaptation of simulated microgravity and silver on Streptococcus mutans using experimental evolution.	Mizpha C Fernander, North Carolina A&T State University, Greensboro NC; Kelyah Spurgeon, North Carolina A&T State University, Greensboro NC; Jada Graves, North Carolina A&T State University, Greensboro NC; Wynter Guess, North Carolina A&T State University, Greensboro NC; Chanell Mangum, North Carolina A&T State University, Greensboro NC; Jordan Miller, North Carolina A&T State University, Greensboro NC; Joseph L Graves, PhD, North Carolina A&T State University, Greensboro NC; Misty Thomas, PhD, North Carolina A&T State University, Greensboro NC	Sustaining life on extended missions in space is a priority for NASA. Space travelers' immune system undergoes dysregulation, causing susceptibility to opportunistic infections. Decreased saliva flow and low bone density increase infections by dental caries and plaque causing Streptococcus microorganism. NASA intends to switch to silver into PWD on the ISS. S. mutans are well studied on earth; however it's not studied on extended space exploration. This research study aims to examine the evolutionary co-adaptation of S. mutans under simulated microgravity (SMG) and SMG and silver (Ag). The study tested if extended (100-day) exposure leads to a virulent strain. Populations of S. mutans were propagated (x4) under both (MG) and (MGAg) using High Aspect Ratio Vessels (HARVs') to simulate co-adaptation to MG and Ag. Virulence was assessed using MIC silver assays to evaluate antibiotic resistance, acid stress tests, and adherence/biofilm assays. Genetic adaptations of S. mutans were evaluated using DNA sequencing. DNA sequencing identified mutations in Domain Containing Protein (DQM59_RS04335→) involved in metal resistance; and two component response CiaR/H gene mutations involved in biofilms, acid stress, and fitness. Adaptation is seen in planktonic populations; but single species biofilm in HARVs could provide insight into the pathogenic state of the organism.

Title	Authors	Abstract
Stress exposure in specific growth periods associates with children's weight, height and BMI	Daniela Rodrigues, CIAS – Research Centre for Anthropology and Health, University of Coimbra, Coimbra, Portugal & Department of Life Sciences, University of Coimbra, Coimbra, Portugal; Aristides M. Machado-Rodrigues, High School of Education, Polytechnic Institute of Viseu, Viseu, Portugal; Helena Nogueira, CIAS – Research Centre for Anthropology and Health, University of Coimbra, Coimbra, Portugal; Augusta Gama, Department of Animal Biology, Faculty of Sciences of the University of Lisbon, Portugal; Maria-Raquel G. Silva, Faculty of Health Sciences, University Fernando Pessoa, Porto, Portugal; Barry Bogin, UCSD/Salk Center for Academic Research and Training in Anthropogeny (CARTA), USA & School of Sport, Exercise & Health Sciences, Loughborough University, UK; Cristina Padez, CIAS – Research Centre for Anthropology and Health, University of Coimbra, Coimbra, Portugal & Department of Life Sciences, University of Coimbra, Coimbra, Portugal.	We test the hypothesis that exposure to stressful events at different ages in early life is related to children's current weight, height, and body mass index (BMI), even after controlling for family socioeconomic status and for child characteristics. Data from 8430 Portuguese children (3367 exposed to at least one stressful event during their lifetime; 50.2% males; 7.21±1.85 years) were included in the analysis. Boys and girls who experienced a stressful event had significantly lower weight and height, particularly when the event took place in the first 2 years of life ($p<0.001$). After adjustment for child's age, birthweight, gestational age, breastfeeding, number of siblings, and father education, child's height and weight were affected by stress, particularly when the event was related with health of a family member. Family stress during the first years of life was significantly and independently associated with shorter stature and lower weight in childhood. The COVID-19 outbreak might increase parents' difficulties, particularly stress both at the individual and the dyadic level, with a consequent negative impact on children's growth.
Does the death of a close relative influence effort in looking after death?	Mona Joly, WZB Berlin Social Science Center, Berlin; Daniel Nettle, Newcastle University, Newcasle-upon-Tyne; Jan Paul Heisig, WZB Berlin Social Science Center, Berlin	Within affluent societies, socioeconomic disparities in health and mortality are large, and substantially driven by differences in behaviours. One explanation could be that disadvantaged people perceive a large part of their mortality risk to be beyond their control, making them less willing to look after their health. We hypothesise that the death of close relatives serves as a cue of perceived uncontrollable mortality risk (PUMR). We thus expect the death of close relatives to impact PUMR and health behaviours. In a first pre-registered exploratory study, we surveyed 600 representative UK adults for their family mortality history, effort in looking after health and PUMR using self-report measures. We found that the number of deaths in the close family was significantly associated with PUMR, effort in looking after health and more specifically smoking status. To remove the confounding effect of age and replicate our findings, we will further examine these associations in a second age-homogeneous larger sample (n=1000 UK participants).

Title	Authors	Abstract
Key features of the genetic architecture and evolution of host-microbe interactions revealed by high-resolution genetic mapping of the mucosa-associated gut microbiome in hybrid mice	Shauni Doms, Max Planck Institute for Evolutionary Biology, Plön, Germany; Hanna Fokt, Max Planck Institute for Evolutionary Biology, Plön, Germany; Malte Christoph Rühlemann, Kiel University, Kiel, Germany; Cecilia J. Chung, Max Planck Institute for Evolutionary Biology, Plön, Germany; Axel Künstner, University of Lübeck, Lübeck, Germany; Saleh Ibrahim, University of Lübeck, Lübeck, Germany; Andre Franke, Kiel University, Kiel, Germany; Leslie M. Turner, Milner Centre for Evolution, Bath, UK; John F. Baines, Kiel University, Kiel, Germany	Determining the forces that shape diversity in host-associated bacterial communities is critical to understanding the evolution and maintenance of metaorganisms. To gain deeper understanding of the role of host genetics in shaping gut microbial traits, we employed a powerful genetic mapping approach using inbred lines derived from the hybrid zone of two incipient house mouse species. Further, we uniquely performed our analysis on microbial traits measured at the gut mucosal interface, which is in more direct contact with host cells and the immune system. A high number ofSeveral mucosa-associated bacterial taxa have high significant heritability estimates; heritabilities are greater for 16S rRNA transcript- compared to gene copy-based traits, and interestingly, 16S rRNA transcript-based heritability estimates are positively correlated with cospeciation rate estimates. Genome-wide association mapping identifies 42843 loci influencing 1203 taxa, with narrow genomic intervals pinpointing promising candidate genes and pathways. Importantly, we identified an enrichment of candidate genes associated with several human diseases, including inflammatory bowel disease, and functional categories including innate immunity and G-protein-coupled receptors. These results highlight key features of the genetic architecture of mammalian host-microbe interactions and how they diverge as new species form.
Patellofemoral Pain Syndrome as a Consequence of Gene-Culture Coevolution	Priyanka Tiwari, New York Medical College, New York; Dr. Nasreen Haque, New York Medical College, New York	Patellofemoral pain syndrome (PFPS) is a knee overuse injury that is one of the most common causes of knee pain worldwide. Despite evolutionary evidence indicating that the human body has been specialized for long-distance running, PFPS continues to affect multiple populations, including physically active adolescents and adults. This brings into question the lack of resiliency of the patellofemoral joint to extensive forces, despite thousands of years of evolution. Previous studies have shown long gaps between human dispersals with increasing tool use and societal development over time. To offer an evolutionary explanation for the high prevalence of PFPS, this review hypothesizes a trade-off mechanism wherein development of the hand was prioritized over the development of the knee. Tracking human dispersals compared to human tool use, as well as differences in patellar morphology of the Hadza (hunter-gatherer), Tsimane (farmer-forager), and modern Western population would support this model. Ultimately, this model based on gene-culture coevolution may hold insights for the future of human development, as different anatomical features are prioritized throughout history.
Bacterial evolution during chronic inflammation in the intestine	Nadia Andrea Andreani, Max Planck Institute for Evolutionary Biology, Plön & Kiel University, Kiel, Germany; Rahul Unni, Max Planck Institute for Evolutionary Biology, Plön & Kiel University, Kiel, Germany; Marie Vallier, Max Planck Institute for Evolutionary Biology, Plön & Kiel University, Kiel, Germany; Silke Heinzmann, Helmholtz Zentrum München, Germany; Daniel Unterweger, Max Planck Institute for Evolutionary Biology, Plön & Kiel University, Kiel, Germany; John F. Baines, Max Planck Institute for Evolutionary Biology, Plön & Kiel University, Kiel, Germany.	Inflammatory bowel disease (IBD) comprises disorders characterized by chronic inflammation of the digestive tract and an altered gut microbiome. With the aim to test the hypothesis that disease-mediated changes in the intestinal environment impose different selection pressures on the microbiome, we performed an evolution experiment with Escherichia coli NC101 in a mouse model of IBD to study the adaptation of the gut microbiome to chronic inflammation within a host's lifetime. Bacteria were allowed to adapt to two alternative mouse intestinal environments (healthy wild-type vs. inflamed Il10-/-) for a period of three months. Fecal samples were collected during the experiment and investigated using multi-omics approaches. Evolved populations were studied by shotgun sequencing, and individual candidate mutations were investigated with a combination of gene expression and phenotypic analysis. The metabolic capabilities of the evolved populations were investigated with Biolog GEN III MicroPlates and the difference in metabolites in the fecal samples were investigated by 1H-NMR metabolomics. Our results suggest that adaptation of bacterial populations to the inflamed intestinal environment could lead to changes in their metabolic repertoire, which in turn may provide new opportunities for therapeutic interventions.

Title	Authors	Abstract
Reproductive plans of childless women in Poland during COVID-19 pandemic	Urszula M. Marcinkowska, Jagiellonian University Medical College; Ilona Nenko, Jagiellonian University Medical College	During the COVID-19 pandemic life of women worldwide changed. Among restrictions introduced in all countries around the globe, some had put women's work-life balance under stress and further increased the anxiety related to the health complications. This study focuses on exploration how women's reproductive plans changed due to pandemic and whether direct contact with and fear of the virus, living circumstances and family situation had a modifying effect on the pre-pandemic reproductive plans. We interviewed online 1340 heterosexual women between 18 and 50 years (Mean = 30.45, SD = 4.5) living in Poland. Preliminary analyses showed, that 38.7% of women changed reproductive plans during the pandemic – for 35.3% they decreased, for 3.4% they increased. Further exploration will focus on possible reasons for the change and will broaden the analysis with additional confounding variables that could have mediated the change, e.g.: socio-economic status, direct contact with the virus, fear of the pandemic, attitudes to fertility and childbearing. The pandemic provides a novel setting for investigating the biological and cultural bases for evolution of women's reproductive incentives, and a large sample size and open questions will allow for a better understanding of the topic.
Teaching Evolutionary Medicine to Medical Students: A Brazilian experience during the COVID-19 pandemic	Thais de Souza Oewel, University of Sao Paulo, Brazil; Anna Carolina Berkenbrock Mendes, University of Sao Paulo, Brazil; Alexandre Archanjo Ferraro, University of Sao Paulo, Brazil.	Evolutionary Medicine (EM) can help enlighten the complexity of human biology, and aims to better understand diseases and its implications on health. Being a new field of study, there is a challenge to incorporate it into medical school curricula, and to educate students to apply its critical thinking throughout their academic and professional career. This article explains the experience of the first EM course at University of São Paulo Medical School. Educational strategies during the COVID-19 pandemic included synchronized and asynchronous short lectures followed by interactive activities. The course was positively perceived by the students. They reported having obtained a different approach to evaluating health and disease, although they manifested an insecurity to conceptualize further clinical applications of EM. As a final evaluation, students reflected together on their experiences and, individually, wrote an original case report using EM. The results were engaging cases that challenge the traditional standpoint of medicine. One difficulty faced during the elaboration of this course was to actively bring an evolutionary perspective to everyday medical practices. Despite being an emerging area, it is of extreme importance to bring EM to medical school programs, in order to prepare physicians for a broader approach on human health.
Can we eat sugar in space? Adaptation of the oral microbe Streptococcus mutans to simulated microgravity.	Misty Thomas, Mizpha Fernander, Billal Khaled, Amina Bradley, Paris Parsons, Joseph L. Graves Jr.	Long-term space missions have shown an increased incidence of oral disease in astronauts' and as a result, are one of the top conditions predicted to impact future missions. Here we evaluated the adaptive response of Streptococcus mutans (etiological agent of dental caries) to simulated microgravity. This organism has been well studied on earth and treatment strategies are more predictable. Despite this, we are unsure how the bacterium will respond to the environmental stressors in space. We used experimental evolution for 100-days in high aspect ratio vessels followed by whole genome resequencing to evaluate this adaptive response. Our data shows that planktonic S. mutans evolved variants in three genes that can be uniquely attributed to simulated microgravity. In addition, collection of data at multiple time points showed mutations in three additional genes earlier in simulated microgravity populations. Comparison of virulence-related phenotypes showed few changes in antibiotic susceptibility, while acid tolerance and adhesion varied significantly between biological replicates and decreased as compared to the ancestral populations. Most importantly, our data is novel for simulated microgravity studies by showing the importance of a parallel normal gravity control, sequencing at multiple time points and the use of biological replicates for appropriate analysis of adaptation.

Title	Authors	Abstract
Biocultural Characteristics as Predictors of Birth Delivery Mode Among Indigenous and Non-Indigenous Mothers in Yucatan Mexico, 2019	Joseph Ruffle1, Hugo Azcorra2, Nina Méndez-Domínguez3, Federico Dickinson4, Graciela Valentín4, and Maria Inês Varela-Silva1 1School of Sport, Exercise and Health Sciences, Loughborough University, Loughborough, UK 2 Centro de Investigaciones Silvio Zavala, Universidad Modelo, Merida, Mexico 3 Hospital Regional de Alta Especialidad de la Peninsula de Yucatan, Mérida, México 4 Departamento de Ecología Humana, Cinvestav, Mérida, México	We analyse biocultural predictors of mode of birth (vaginal versus caesarean delivery), among indigenous and non-indigenous mothers in Yucatan, in 2019. Yucatan reported high caesarean delivery rates (~50.0%) which tend to be associated with negative health consequences later in life (e.g. obesity and non-communicable diseases). The sample was composed of 26,582 mothers. The outcome variable was mode of delivery (vaginal birth vs caesarean), and the predictors included in the analysis were indigenous status, age, education, number of previous births, ante-natal care (ANC) and hospital type (public vs private). More indigenous mothers gave birth in public hospitals. Indigenous mothers were older, more likely to have a partner, with higher rates of illiteracy, higher number of previous births, and tended to deliver longer babies. A smaller percentage of indigenous mothers gave birth by caesarean delivery, received ANC in the first trimester and delivered lighter babies. Maternal age, indigenous status, number of previous births, maternal education, and trimester of first ANC predicted mode of delivery. Higher maternal age and higher education increased the likelihood of caesarean delivery. Lower education level, later ANC and belonging to an indigenous group decreased the odds of caesarean delivery.
Association between diet, physical activity and body composition	Nima Hosseini, University of Zurich, Switzerland; Bahri Bektashi, University of Zurich; Luana Giacone, ETH Zurich, Switzerland; Cynthia Sob, ETH Zurich, Switzerland; Christina Hartmann, ETH Zurich, Switzerland; Katarina Matthes, University of Zurich, Switzerland; Frank Rühli, University of Zurich, Switzerland; Kaspar Staub, University of Zurich, Switzerland; Nicole Bender, University of Zurich, Switzerland.	Obesity is among the main health risk factors worldwide and is discussed in the framework of evolutionary mismatch. The influence of diet and physical activity on body composition is well studied, but the interaction of sex specific associations of specific diet components and physical activity are less well understood. We assessed nutrition, physical activity, socioeconomic variables and body composition in a sample of 431 adults from the Swiss general population, including both sexes (age range 19-84 years). Body composition measures differed between the sexes and age groups. In women, only meat and fruit were associated with body composition measures such as BMI, skeletal muscle mass (SMI), fat mass (FMI) and visceral adipose tissue (VAT). In men meat, wholegrain products, and fruit consumption was associated with body composition. In both sexes there was an inverse association between physical activity and body composition, while in women physical activity was positively associated with SMI. The sex differences could be due to the influence of sex hormones on female body composition. Interestingly, the consumption of modern unhealthy foods like alcohol, sweet or salty snacks was not associated with body composition in our sample. These results demand further investigation in the light of evolutionary theory.

Title	Authors	Abstract
The Mummy Explorer - an interactive online teaching tool for Evolutionary Medicine	Anja Furtwängler, University of Zurich, Switzerland; Chris Baumann, University of Tübingen, Germany; Kerttu Majander, University of Zurich, Switzerland; Shevan Wilkin, University of Zurich, Switzerland; Nadja Tomoum, University of Zurich, Switzerland; Frank Rühli, University of Zurich, Switzerland; Adrian V. Jäggi, University of Zurich, Switzerland; Patrick Eppenberger, University of Zurich, Switzerland; Nicole Bender, University of Zurich, Switzerland; Verena J. Schuenemann, University of Zurich, Switzerland.	Teaching evolutionary medicine covers different fields, such as genetics, life history theory, or diseases of evolutionary mismatch. This renders it difficult to transmit the connections between the single subtopics to the students. To date there is no specific online teaching tool that can be adapted to different subtopics in this field. We developed a self-explanatory, online educational tool, the Mummy Explorer. With a virtual journey through a paleopathological examination of a mummy, we explain the logical sequence of the individual examination steps and how the collected data can be interpreted in its historical and cultural context. Images, hyperlinks, and text elements are added at each step, to visualize and explain the methods. All subtopics are interlinked with each other. The online tool can be used as a red thread for lectures, or as a self-learning repeating source. The online tool is open access and has a modular structure. Lecturers can replace the image and text elements and thus adapt them to their own subject. Instead of the mummy, a patient, a child, an ape, or even a theoretical concept can be placed in the center and several different subfields can be linked to the central element and between each other.
EvoMedEd: Piloting Evolutionary Medicine Cases in Lower- and Upper-Year Undergraduate Courses	James J. Smith, Michigan State University, East Lansing David C. S. Filice, Michigan State University, East Lansing Merle K. Heidemann, Michigan State University, East Lansing Joseph J. Riedy, Michigan State University, East Lansing Peter J. White, Michigan State University, East Lansing	Case-based pedagogies, in which students synthesize ideas and concepts across disciplinary boundaries, provide opportunities for teaching excellence. Over the past 18 months, we developed case-based evolutionary medicine teaching resources for biology educators, which are available on our project website (www.evo-ed.org). These case-based materials are framed in the context of Cancer, Mental Health, Addiction, Sleep, and Infectious Disease as viewed through an evolutionary lens. The materials include descriptive summaries, decks of content slides and YouTube videos describing the biology and human dimensions of various aspects of each case (e.g., Neurobiology of Sleep; Ethics of Cancer Treatment), and discussion question sets with activities that can be adapted for instructors' use. In spring 2022, we implemented EvoMedEd materials in two courses at Michigan State University. In an Introductory Cell and Molecular Biology course, EvoMedEd was used to introduce basic cell and molecular biology concepts in the context of breast cancer and COVID-19. Then, in a Capstone Seminar course on Evolutionary Medicine, students explored all five cases, with an emphasis on learning and applying core evolutionary medicine concepts (antagonistic pleiotropy, trade-offs, mismatch, etc). Students in both courses reported that the EvoMedEd materials were useful, accessible, and contributed to their learning.
Influence of the adaptive immune system on the evolution of gut microbiota	Camille Ameline, IGC, Oeiras; Nelson Frazão, IGC, Oeiras; Elsa Seixas, IGC, Oeiras; Isabel Gordo, IGC, Oeiras.	Gut microbiota is hypothesized to be a major driver of evolution in vertebrates. The diversity and evolution of gut microbiota have been shown to influence speciation, development, and immunity in the host. Because the microbial community in the gut is complex, it remains challenging to study the influence of host traits on the diversity and evolution of gut microbiota. The evolutionary dynamics of commensal bacteria during colonization of the gut is of particular interest in the context of immune and inflammatory bowel diseases (IBD), where the natural balance of the gut microbiota is disrupted. While the composition of the gut ecosystem has been characterized, little is known about evolution within species. We use the host–bacterium model system Mus musculus–Escherichia coli to unravel the emergence of intra-species diversity and the dynamics of bacterial mutations while colonizing the host gut. We conduct experimental evolution of E. coli in immune-deprived and IBD mutant mice in germ-free conditions, to remove the environmental factor of the surrounding microbiota. We track major evolutionary changes and investigate the tempo and mode of E. coli evolution, measuring rates of mutation accumulation and horizontal gene transfer, and determining evolution predictability across hosts with distinct immune status.

Title	Authors	Abstract
‘More passive than the foetus ever was…’: an evolutionary perspective on swaddling.	Helen Ball, Durham University, Durham, UK; Allison Dixley, Durham University, Durham UK.	A global practice implemented to restrain and pacify infants, swaddling has experienced a popular resurgence in WEIRD societies as a tool to promote infant sleep and suppress crying. While often characterised as a benign practice that replicates the uterine environment for the new-born infant, swaddling exposes the infant’s body to constant mechanical pressure and insulation which contrasts with the flexible living wall of the uterus. The swaddle is a physical barrier separating the infant from the mother’s body, decoupling mother-baby physiological synchrony, and suppressing a range of postnatal infant reflexes that serve key survival functions. When guidance to ‘swaddle for every sleep’ is followed, infants can spend up to 18 hours per day under conditions of motor restraint which reduces infants’ normally frequent sleep arousals. In reviewing its effects via an evolutionary lens we conclude that swaddling neither replicates the womb environment, nor provides an appropriate developmental environment for the new-born human infant. Through swaddling an “active foetus is turned into a passive creature, more passive than the foetus ever was” (Frenken 2011 p238). The sensory experience of swaddling is mismatched with the human infant’s need for freedom of movement for communication, food consumption, and survival.
Exploring evolutionary potential in the clinically-relevant carbapenemase KPC-2	Laura Dabos, Polytechnic University of Madrid, Spain; Alejandro Couce, Polytechnic University of Madrid, Spain	KPC-2 is an antibiotic-resistance enzyme well-known for its ability to hydrolyze carbapenems, although it also has activity against other β-lactam. With over 100 allelic variants reported to date, it represents an important case study due to its staggering evolutionary success: described in 2001, went global in less than a decade. Here we used directed evolution to characterize the mutational pathways that lead KPC-2 to extend its activity against ceftazidime, an important β-lactam of the cephalosporin class. We recovered several mutations commonly observed in clinical settings, but also previously unknown large-effect ones. Importantly, strong epistatic constraints largely determined evolutionary outcomes in this system: we uncover at least four distinct adaptive pathways in which the identity of the first mutation markedly affected the identity of subsequent adaptive steps. Of note, after several rounds of evolution, each pathway seemed to converge to a distinct plateau, most probably representing different solutions to the activity-stability trade-off. These solutions, moreover, display idiosyncratic activities against other β-lactam classes. Taken together, our results illustrate how strong epistasis imposes a high degree of historical contingency in this system, with the long-term properties of a given lineage hinging on the probabilistic choice among a few first-step, beneficial mutations.
The metabolic consequences of antibiotic resistance plasmid acquisition on their bacterial hosts.	Kathryn Billane, University of Sheffield Duncan Cameron, University of Sheffield Ellie Harrison, University of Sheffield Michael Brockhurst, University of Manchester	Conjugative plasmids carrying antimicrobial resistance genes play an important role in the widespread antimicrobial resistance crisis. Plasmid persistence in the bacterial community is at odds with their detrimental costs of carriage from an evolutionary fitness perspective, this is known as the ‘plasmid paradox’. Studies have demonstrated genetic mutations can ameliorate costs. There is increasing evidence for plasmid driven manipulation of the expression of genes in their bacterial hosts, and this frequently affects the metabolism. This research examines the relationship between a number of Escherichia coli strains from different clinical and environmental sources and a multidrug resistance plasmid derived from Klebsiella pneumoniae through the lens of untargeted metabolomics. This method of analysis allows direct comparison of the whole metabolome both between strains, and between strains carrying the plasmid and those that are plasmid free. The impacts of the plasmid are subtle, indicating a limited negative effect and challenging the theory of the paradox. The results suggest a shift in how the bacteria utilise and produce energy towards the glutamate pathway. The plasmid may be causing a rerouting of E.coli’s malleable metabolic network to enable coexistence.
The effect of bottleneck size and antibiotic-induced selection on antibiotic resistance evolution	Ernesto Berríos-Caro, Max Planck Institute for Evolutionary Biology, Plön, Germany; Hildegard Uecker, Max Planck Institute for Evolutionary Biology, Plön, Germany; Hinrich Schulenburg, Christian-Albrechts-University of Kiel, Kiel, Germany	Bacterial populations undergo several bottlenecks during infection of host populations, imposed by the transmission of pathogens between hosts, an activated host immune response, or the antibiotic treatment employed. Bottlenecks—drastic reductions in bacterial population size—can increase the influence of random effects during bacterial evolution, directly affecting the diversity of resistance alleles. Despite the relevance and presence of bottlenecks in antibiotic resistance evolution, their effect, along with other relevant factors (e.g., the strength of antibiotic-induced selection or competition), has been largely ignored in the literature. Recent evolution experiments have demonstrated that bottleneck size and antibiotic-induced selection reproducibly impact the evolutionary path to resistance in pathogenic Pseudomonas aeruginosa. In particular, these experiments found that resistance is favoured —expectedly—under high antibiotic selection and weak bottlenecks, but—unexpectedly—also under low antibiotic selection and severe bottlenecks. In this talk, I will present progress made in the theoretical modelling of these evolution experiments to explain their outcome. Results from this modelling can be a critical stepping stone in the transfer between experiment and clinical reality and, thus, the design of evolution-informed effective therapy. At the end of the talk, I will discuss several model extensions that may inspire new experiments.

Title	Authors	Abstract
Role of bacterial motility in evolutionary mechanisms for acquired antimicrobial resistance	Lisa Stabryla, NIST, Gaithersburg, MD; Kathryn Johnston, Corning, NY; Nathan Diemler, NETL, Pittsburgh, PA; Vaughn Cooper, University of Pittsburgh, Pittsburgh, PA; Jill Millstone, University of Pittsburgh, Pittsburgh, PA; Sarah-Jane Haig, University of Pittsburgh, Pittsburgh, PA; Leanne Gilbertson, University of Pittsburgh, Pittsburgh, PA; Jason Kralj, NIST, Gaithersburg, MD	The first part of this work explores the evolution of bacterial resistance towards silver nanoparticles (AgNPs). A classic laboratory evolution approach was adopted where Escherichia coli (E. coli) K-12 strains were repeatedly exposed to sub-inhibitory concentrations of AgNPs. Results showed that a hyper-motile E. coli strain evolved resistance to AgNPs and was conferred by a permanent mutation in cusS, a gene encoding a sensory kinase associated with copper and silver ion efflux. This mutation was found within the active site of the phosphoacceptor region and suggests a direct mechanism of resistance through increased silver efflux resulting from autophosphorylation of the CusS cytoplasmic domain. Resistance did not evolve to Ag(I) ions alone, indicating a nanoparticle-specific resistance response that likely arose from the intracellular Ag delivered by the AgNPs. Further, non-motile E. coli demonstrated no resistance to AgNPs, underscoring the potentially important role of motility in the evolution of resistance. The second half of this work discusses current research at NIST that aims to understand evolutionary mechanisms for acquired antibiotic resistance (ABR) and genetic determinants of ABR (e.g., non-synonymous SNPs) in pathogenic environmental and clinical microbiota, and whether an organism's evolutionary landscape and its genetic basis for resistance links to its motility.
Pneumococcus and the stress-gradient hypothesis	Ermanda Dekaj, Center for Computational and Stochastic Mathematics, Instituto Superior Tecnico, University of Lisbon, Lisbon Portugal Erida Gjini, Center for Computational and Stochastic Mathematics, Instituto Superior Tecnico, University of Lisbon, Lisbon Portugal	Modern molecular technologies have revolutionized our understanding of bacterial epidemiology, but reported data across studies and different endemic settings remain under-integrated in common theoretical frameworks. Pneumococcus serotype co-colonization, caused by the polymorphic bacteria Streptococcus pneumoniae, has been increasingly investigated and reported in recent years. While the global genomic diversity and serotype distribution of S. pneumoniae have been characterized, there is limited information on how co-colonization patterns vary globally, critical for understanding the evolution and transmission dynamics of the bacteria. Gathering and analyzing a rich dataset of cross-sectional pneumococcal colonization studies in the literature, we quantified patterns of transmission intensity and co-colonization prevalence variation in children populations across several geographic locations. Fitting these data to an SIS model with cocolonization and similar strains, our analysis reveals strong patterns of negative co-variation between transmission intensity (R0) and susceptibility to co-colonization (k). In line with expectations from the stress-gradient-hypothesis in ecology (SGH), pneumococcus serotypes appear to compete more in co-colonization in high-transmission settings and compete less in low-transmission settings, a trade-off which ultimately leads to a conserved ratio of single to co-colonization $\mu = 1/(R0 - 1)k$. Such conservation suggests preservation of 'stability-diversity-complexity' regimes in multi-strain coexistence.
Microbial evolutionary signatures associated with longevity in the gut of very old	Rita Melo-Miranda, Department of Medical Sciences, Institute for Biomedicine (iBiMED), University of Aveiro; Ana Sousa, Department of Medical Sciences, Institute for Biomedicine (iBiMED), University of Aveiro	Aging is accompanied by numerous events, including an increase in inflammation and gut dysbiosis. This contributes to aging by increasing intestinal permeability and inflammation, but how it influences microbiota evolution and pathobiont selection remains unknown. Here we approach this question by comparing microbial evolution in the guts of three sets of mice: young (6-9 weeks old), old (19 months old), and very old (25 months old). Previous studies have described the adaptation of a commensal strain of E. coli to the guts of young animals and shown that it acquires metabolic-related mutations whereas, in old mice, the pattern shifts towards stress-related mutations, and metabolic adaptations arise slower. Yet, aging is a discontinuous process and as such, other age groups should also be characterized. So, we compared frailty, intestinal inflammation, and microbiota composition of very old animals to younger ones. These were the frailest but not more locally inflamed than the old. Interestingly, compared with the others, they showed an increase in health-associated bacteria, e.g. Akkermansia muciniphila, and E. coli displayed more metabolic than stress-related mutations, resembling young animals. These data suggest that microbiota alterations during aging may not be exclusively dysbiotic and may be associated with longevity.
The rugged fitness landscape of the carbapenemase KPC-2.	Nedjari Zahia Inssaf, Laura Dabos, Alejandro Couce.	The antibiotic resistance enzyme KPC-2 represents a dramatic, contemporary example of evolutionary success, rising to worldwide prevalence in less than a decade since it was first described in the early 2000s. In a companion submission, we used in vitro evolution to characterize the mutational pathways that lead KPC-2 to extend its activity against ceftazidime, an important β-lactam antibiotic of the cephalosporin class. A major result from this study was the existence of independent adaptive pathways involving different first-step mutations – a clear signature of epistasis. To gain further insight into the patterns of epistasis, here we took the 6 most common mutations observed in the experiment and created all their possible 64 combinations via site directed mutagenesis. We uncovered the full range of epistasis types, with magnitude epistasis (i.e., synergistic or antagonistic effects) being the most prevalent. However, the small but sizable fraction of sign epistasis interactions (i.e., the sign of the effect, beneficial, neutral or deleterious, changes with the genetic background) was sufficient to dictate the overall shape of the fitness landscape, with a global optimum but several isolated local maxima (i.e. "rugged"). Our results illustrate how just a few genetic interactions can have an outsize impact on evolutionary outcomes.

Title	Authors	Abstract
Investigating and modeling the regulation of extracellular antibiotic resistance gene bioavailability by naturally occurring nanoparticles	Nadratun Chowdhury, National Institute of Standards and Technology, Gaithersburg, MD, USA Mark Wiesner, Duke University, Durham, NC, USA Samuel Forry, National Institute of Standards and Technology, Gaithersburg, MD, USA Scott Jackson, National Institute of Standards and Technology, Gaithersburg, MD, USA	Widespread environmental extracellular antibiotic resistance genes (eARGs) can contribute to the evolution of bacteria and increase the propagation of antibiotic resistance, which is one of the largest current public health issues. The role of environmentally relevant nanoparticles (NPs) in regulating eARG transfer was examined. eARGs extracted from antibiotic-resistant B. subtilis were incubated with non-resistant recipient B. subtilis cells. In the mixture, particle type (either humic acid coated nanoparticles (HASNPs) or their micron-sized counterpart (HASPs)), DNase I concentration, and eARG type were systematically varied. Transformed bacteria were counted on selective media. Particles decreased bacterial growth and eARG bioavailability in sterile systems without nuclease. When DNase I was present (≥5 ug/mL), particles increased transformation via chromosomal eARGs. HASNPs increased transformation more than HASPs, indicating that the nanoscale increases eARG bioavailability. These results were also modeled via particle aggregation theory, which represented eARG-bacteria interactions as transport leading to collision, followed by attachment. Using attachment efficiency as a fitting factor, the model predicted transformed bacterial concentrations within 35% of experimental data. These results confirm the ability of NPs to increase eARG bioavailability and suggest that particle aggregation theory may be a simplified and suitable framework to broadly predict eARG uptake.
Cross-Species Comparisons Reveal a Core Signature of Social Adversity on Immune Cell Gene Expression	C. Ryan Campbell, Duke University, Durham, NC, USA; Noah Simons, Duke University, Durham, NC, USA; Paul Maurizio, University of Chicago, Chicago, IL, USA; Joao Batista, University of Chicago, Chicago, IL, USA; Vasiliki Michopoulos, Emory University School of Medicine, Atlanta, GA, USA; Allison Aiello, University of North Carolina at Chapel Hill, Chapel Hill, NC, USA & Columbia University, New York, NY, USA; Luis Barreiro, University of Chicago, Chicago, IL, USA; Jenny Tung, Duke University, Durham, NC, USA & Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany	The relationship between social adversity and gene expression has been studied in both observational and experimental contexts, in both humans and other social mammals. This work suggests a consistent relationship between social adversity and gene regulation in the immune system, but the magnitude and directionality of these effects, as well as their sensitivity to the local cellular environment, appear to be more variable. To investigate the potential for a conserved, core signature of social advantage and adversity, here we compared the effects of social adversity on gene expression in peripheral blood cell gene expression levels in rhesus macaques, baboons, and humans, in both baseline and immune-challenged conditions. In females of all three species, we observe consistently elevated activity of interferon signaling and inflammation-related pathways in socially disadvantaged individuals, at baseline and after immune stimulation. In comparison, male baboons and male humans tend to activate the same pathways in conditions that predict social advantage. Our results point to similar responses to social adversity that transcend millions of years of evolution–but nevertheless exhibit substantial sex-specific differences within species. They therefore illustrate how cross-species comparisons can help disentangle the biological pathways that mediate social gradients in fitness and health.
Relationships between Behavioral Immune System Activity, COVID-19 Case Counts, and Immune Function	Jeffrey Gassen, Baylor University, Waco, TX; Tomasz Nowak, Baylor University, Waco, TX; Alexandra Henderson, Baylor University, Waco, TX; Edward Thum, Baylor University, Waco, TX; Sally Weaver, Waco Family Medicine, Waco, TX; Erich Baker, Baylor University, Waco, TX; Michael Muehlenbein, Baylor University, Waco, TX.	The selection pressures exerted by pathogens have played an important role in shaping the biology and behavior of animals, including humans. Immune systems recognize and respond to cues of infection or damage by coordinating cellular, humoral, and metabolic shifts that promote recovery. Moreover, animals also possess a repertoire of behavioral tools to help combat the threat of pathogens, often referred to as the behavioral immune system. Recently, researchers have begun to examine how cognitive, affective, and behavioral disease avoidance mechanisms interact with the biological immune system. The current research examined relationships among individual differences in behavioral immune system activity (e.g., trait pathogen disgust), shifts in SARS-CoV-2 infection risk (i.e., 7-day case averages), and immune function (serum levels of IFN-γ, TNF-α, IL-2, and IL-8, as well as serum Escherichia coli killing ability) in a community cohort from McLennan County, TX (n = 387). Results revealed that trait levels of disease concern were not consistently related to immune markers, even though each varied with case counts. Additional analyses suggest that these effects may be mediated, in part, by changes in stress physiology. The present results add to the growing body of research finding links between behavioral and biological pathogen management strategies.

Title	Authors	Abstract
Fear of birth, knowledge confidence and preference for cesarean section among Polish women	Ilona Nenko, Jagiellonian University Medical College; Agnieszka Micek, Jagiellonian University Medical College; Katarzyna Kopeć-Godlewska, Jagiellonian University Medical College; Kathrin Stoll, University of British Columbia.	Rising rates of cesarean sections (CS) are a worldwide phenomenon. In Poland, 43 in 100 babies is born by CS which is among the highest rates of CS birth in OECD countries. Fear of childbirth is defined as important predictor for elective CS. However, the factors that impact childbirth fear prior to pregnancy are not well known. We recruited 782 women aged 18 – 35 (mean 24.7, sd = 3.19) who had never been pregnant but wished to have at least one child in the future. Almost one in four women (22.1%) preferred CS in a hypothetical low-risk pregnancy. Participants with high levels of childbirth fear were 10 times as likely to prefer a CS (95%CI = 5.61 – 18.91) compared to those with low levels of fear. There was a significant association between confidence in their knowledge of pregnancy and birth and childbirth fear i.e. there was a higher percentage of women with low fear of childbirth among those with low confidence in their knowledge of pregnancy and birth. Increasing knowledge about pregnancy and labour among young women might lower childbirth fear and thus, indirectly, achieve lower rates of CS in the future.
Attitude-Behavior Incongruency and Possible Infectious Disease Transmission Between Monkeys and Tourists	Edward Thum, Baylor University, Waco, Texas; Kerry Dore, Baylor University, Waco, Texas, Ross University School of Veterinary Medicine, St. Kitts; Jeffrey Gassen, Baylor University, Waco, Texas; Vy Nguyen, Baylor University, Waco, Texas; O. Grace Jolley, Baylor University, Waco, Texas; Rebecca Friedel, University of Texas, San Antonio; Victoria Ingalls, University of Texas, San Antonio; Alexandra Holdbrook, University of Texas, San Antonio; Christa Gallagher, Ross University School of Veterinary Medicine, St. Kitts; Eric Shaw, Helping Hand Trust, Gibraltar; Michael Muehlenbein, Baylor University, Waco, Texas	Despite concern about environmental protection, travelers often underestimate the contribution they may have to disease transmission to other species, as well as the risk of becoming infected themselves. To better understand environmental attitudes and travel health knowledge and behaviors, surveys of adult tourists were distributed in St. Kitts (n = 1097) and Gibraltar (n = 980), which are both home to wild monkey populations. Even though individuals with more positive environmental attitudes were more willing to take steps to mitigate tourism-related disease transmission, they were also more likely to report wanting to touch or feed a monkey. Similarly, those more willing to prevent the spread of diseases (e.g., wear a mask) were actually more likely to want to touch or feed a monkey. The attitude-behavior incongruency identified here may be explained through cognitive-affective inconsistency: environmentally-oriented individuals wish to take steps to prevent zoonotic disease transmission (part of our behavioral immune system), but also desire to touch or feed exotic species as it may be emotionally rewarding (i.e., expression of biophilia via the somatosensory haptic system). Techniques aimed at appealing to peoples' emotions may be more effective than logical appeals to combat this evolutionary mismatch between attitudes and behaviors.

Title	Authors	Abstract
Th1/Th2 Paradigm, Reproductive Status, and Estradiol Concentrations	Tomasz Nowak, Baylor University, Waco, Texas, USA Jeffrey Gassen, Baylor University, Waco, Texas, USA Alexandra Henderson, Baylor University, Waco, Texas, USA Brooke Morris, Baylor University, Waco, Texas, USA Edward Thum, Baylor University, Waco, Texas, USA Sally Weaver, Waco Family Medicine, Waco, Texas, USA Erich Baker, Baylor University, Waco, Texas, USA Michael Muehlenbein, Baylor University, Waco, Texas, USA	A coordinated change in immune parameters arises during reproductive events in women, such as pregnancy, to accommodate the needs of the mother and fetus. Immunological changes throughout the menstrual cycle are also common. T helper cells (Th) are a particular part of the adaptive immune response, with Th1/Th2-related cytokines fluctuating across the menstrual cycle. In particular, the Th1/Th2 cytokine ratio has been associated with fecundity and fertility. The present research examined relationships among the Th1/Th2 (IFN-γ/IL-10) cytokine ratio, reproductive status, and estradiol concentrations in cross-sectional sample of healthy women from Texas, USA (n = 243). Overall results reveal a Th1/Th2 ratio negatively correlated with estradiol and positively correlated with the number of children, a relationship that disappears in only women with regular menstrual cycles. In women with irregular menstrual cycles, the Th1/Th2 ratio is highly correlated with estradiol (Pearson r = 0.889, p < 0.01, n = 9). The Th1/Th2 ratio is positively correlated with the number of biological children among postmenopausal women. Overall, changes in immune status during reproductive events may affect trade-offs between highly demanding functions of reproduction and immunity.
Microchimerism: frequency and distribution from an evolutionary perspective	Janne Rozemarijn Buwalda-Smit, University of Groningen, Groningen, NL; Michael G. Elliot, University of Groningen, Groningen, NL.	Microchimerism is perhaps the most mysterious epigenetic phenomenon of pregnancy, where cells of fetal origin establish themselves as permanent or temporary colonies in maternal tissues and vice versa. Although microchimerism has been a subject of interest and study for several decades, little is known about the frequency, distribution and function of these cells throughout the body. We here describe a sensitive way to identify fetal and maternal microchimeric cells in the host's tissues, with an emphasis on tissues involved in (maternal) energetics and behaviour, as we hypothesize that fetal cells should be selected to provoke responses in the mother that benefit the fetus (e.g. increase nutrition transfer or care behaviour) and vice versa. Fetal and maternal microchimeric cells will be detected by digital PCR, FACS and FISH, using a mouse model that expresses eGFP ubiquitously. We here focus on (sub-areas of) tissues involved in nutrient transfer and maternal behaviour, such as the maternal blood, mammary glands, liver, fat tissue and brain. Results from this experiment will be presented as frequency and distribution of microchimeric cells per tissue, as counted by digital PCR, FACS and FISH. Other data on functional properties of microchimeric cells in (other) tissues may also be presented.
Physical contact with alloparents is associated with composition of the infant gut microbiome across the first of year of life	Kyle S. Wiley, University of California, Los Angeles; Andrew M. Gregg, University of California, Los Angeles; Molly Fox, University of California, Los Angeles; Venu Lagishetty, University of California, Los Angeles; Curt A. Sandman, University of California, Irvine; Jonathan P. Jacobs, University of California, Los Angeles; Laura M. Glynn Chapman University, Orange	The human cooperative breeding strategy is based on the premise that alloparents benefit mother-offspring fitness. However, the biosocial mechanisms by which alloparents confer benefits remains unknown. We investigated a novel hypothesis that contact with alloparents may contribute to seeding a diverse microbiome in infancy. We examined if infant contact with alloparents at birth and within the first three weeks of life were associated with gut microbiome composition assessed at newborn, 2, 6, and 12 months. Stool samples were sequenced using the 16S Illumina MiSeq platform. Newborn beta diversity was associated with the number of hours infants spent in physical contact with alloparents per day for neonates. The number of people in physical contact at birth was associated with beta diversity at 2 months while the total number of people in physical contact at delivery was associated with beta diversity at 6 months. On the day of birth, skin-to-skin contact and number of alloparents that held the baby were associated with the relative abundance of specific genera. The results of this study contribute to the literature on skin-to-skin contact, pointing to a potential mechanism by which alloparents benefit infants. These findings contribute to work exploring the social transmission of microbes.

Title	Authors	Abstract
In the Light of Evolution: Evaluating the Effects of Evolutionary Adaptations in Two-Component Response Systems (CusS-CusR)	Maria Ford, North Carolina A & T University, USA; Sydney Townsend North Carolina A & T University, USA; Joseph L Graves North Carolina A & T University, USA, Misty Thomas,North Carolina A & T University, USA	Bacteria are continuously interacting with their environment and must quickly respond to changes in a wide range of environmental niches. Therefore, bacteria have evolved two component response systems to help regulate cellular homeostasis, allow them to survive under changing environmental conditions. TCRS are among the best studied genetic elements for environmental acclimation in bacteria but very little is known about their role in adaptations. We aim to understand the role TCRS play in environmental adaptation and their fitness costs. We hypothesize that, mutations in the TCRS CusS/R will lead to adaptation to high levels of silver will decrease the overall fitness of the bacteria characterized by a decreased growth rate, and quick reversion when the stressor is removed. To investigate adaptations within TCRS we used in vivo recombineering to insert chromosomal mutations in the cusS gene known to be associated with silver resistance in Escherichia coli K12 MG1655. Bacterial fitness was determined by comparative growth curves, competition assays and reverse selection experiments. Growth assays showed an increase in resistance to silver, their overall growth rate in absence of the stressor was decreased. Based on this, we believe our competition assays will show that the WT will outcompete the adapted mutants.
Predictors of Global Neonatal Hyperbilirubinemia	Catherine Kitrinos, University of Massachusetts Amherst, Amherst, USA	Over 1 million infants globally experience severe hyperbilirubinemia that is associated with increased mortality and morbidity. However, the causes of this potentially fatal condition are not well understood. In this study, I asked whether biocultural, biogeographical, or geopolitical factors best predict the prevalence of severe hyperbilirubinemia in neonates across 83 countries. I used data on neonatal hyperbilirubinemia and malaria prevalence from the Institute for Health Metrics and Evaluation, data on breastfeeding from Unicef, altitude data from Tremblay & Ainslie, 2021, data on GDP per capita from the United Nations, and data on relative country stability from the Global Peace Index. I used linear models to test for associations between hyperbilirubinemia and my predictors while controlling for confounding between predictors, and the Sum of AICc weights to determine which factors most strongly predict neonatal hyperbilirubinemia. I found that the Global Peace Index is the strongest predictor of neonatal hyperbilirubinemia, followed by longitude. Altitude, breastfeeding, GDP per capita, and malaria were comparatively weak predictors. These results suggest that maternal stress may play a bigger role in neonatal hyperbilirubinemia than access to healthcare, and that severe hyperbilirubinemia may be an adaptive response to signals of stress in the intrauterine environment.
Searching for the optimum sleep quota. Is adolescent sleep in non-WEIRD contexts optimal?	A Silva-Caballero, Department of Anthropology, Durham University, Durham, UK; HL Ball, Department of Anthropology, Durham University, Durham, UK; KL Kramer, Anthropology Department, University of Utah, Salt Lake City, Utah, US; RD Greaves, Anthropology Department, University of Utah, Salt Lake City, Utah, US; GR Bentley, Department of Anthropology, Durham University, Durham, UK	Since the late 1970s, sleep researchers in WEIRD societies have warned against short sleep quotas among adolescents and their adverse short- and long-term effects on health. We reexamined the Social Jetlag Hypothesis (SJH) among 145 teenagers (aged 11-16, $\bar{x}$=13.7 ± 1.21) who were: 1) Totonac agriculturalists, 2) Maya agriculturalists, and 3) urbanites from Mexico City, arguing that adolescents living in “traditional,” non-industrial environments will more closely fulfil their “biological/natural” sleep requirements. We collected 1405 sleep observations from February-November, 2019, using actigraphy, sleep diaries, interviews, and ethnographic observations. We employed three-level mixed-effects models to examine bio-socio-ecological predictors of nightly sleep duration. Short sleep quotas were common in both of the agricultural societies, with over 75% of adolescents in each group sleeping <9hrs per school day. Sleep duration was consistently influenced by gender across all study sites and weekdays, with girls sleeping more than boys. Meanwhile, advanced puberty negatively affected sleep duration exclusively among non-urban adolescents (95% CI). These findings undermine the SJH since they indicate that adolescents from natural, traditional societies also express short sleep quotas given certain socio-cultural and ecological factors. These findings bring into question current presumptions about sufficient sleep and how adolescents slept before the modern era.

Title	Authors	Abstract
No significant adverse outcomes reported with COVID-19 mRNA vaccines in a cohort of lactating mothers and their infants: a cross sectional analysis.	Renuka Ananth Kalyan Kadali, Harnett Health System and Campbell University, Lillington, NC, USA; Alok Arora, Advocate Aurora Health, Marinette, WI, USA; Ravali Janagama, Kidzcare Pediatrics, Sanford, NC, USA; Viswanath Gajula, The University of Mississippi Medical Center, Jackson, MS, USA	Abstract Background: The safety of COVID-19 messenger RNA vaccines in breastfeeding mothers has not been studied widely and following the United States Food and Drug Administration (US FDA) and Centers for Disease Control and Prevention (CDC) Emergency Use Authorization (EUA) for COVID 19 vaccination for breastfeeding mothers, we need evidence about its safety and effectiveness including any potential risks. Phase 3 clinical trials for the COVID-19 vaccines currently used in the United States did not include people who are breastfeeding [13, 15, 16]. Hence, there is limited data available on the safety and efficacy of COVID-19 vaccines in population who is breastfeeding, the breastfed baby, its effects on milk production or excretion. This succinct practical study seeks to compare the adverse effects profiles for the two available messenger RNA vaccines (m-RNA) for SARS-CoV-2 in female Health Care Workers (HCW). Methods: A cross-sectional study was conducted using an online questionnaire to evaluate the effects of new mRNA vaccines among lactating women. The study describes the responses of 72 female HCWs who were lactating when they received a dose of COVID-19 m-RNA vaccine. Results: The data from the sample group shows no statistical difference in vaccination-related symptoms between breastfeeding and non-breastfeeding women. No significant adverse outcomes were reported in breastfeeding infants either in this study. Conclusions: COVID-19 m-RNA vaccines did not cause any noticeable effects on breast feeding infants per this study. The cessation of breastfeeding is not recommended during the post-vaccination phase and lactating mothers should discuss the risks and benefits of vaccination with their or their infant’s health care provider. The non-life-threatening risks associated with COVID-19 m-RNA vaccination should not outweigh the benefits of mRNA vaccines. A longitudinal follow up is recommended for the lactating mothers participating in the CDC’s v-safe program for evaluation of latent effects.
Menstrual bleeding in healthy humans: variability, impacts on health and sexual behavior, and evolutionary trade-offs	Virginia J. Vitzthum, Indiana University; Amanda A. Shea, Clue by Biowink GmbH, Berlin; Jonathan Thornburg, Indiana University; Fiorella Wever, University of Amsterdam; Georgina Denis, Clue by Biowink GmbH, Berlin; Cecile Ventola, Clue by Biowink GmbH, Berlin.	Menstrual bleeding is the most easily recognized and widely used biomarker of human female reproductive functioning. However, periods in healthy women are not necessarily preceded or followed by ovulation. Compared to other primates, menses in humans is typically copious. Menses duration varies more than two-fold across human populations, and burdensome heavy bleeding occurs in perhaps a third of women in high income countries. Concerns that COVID infection and/or vaccination may change menstrual cycling and fertility have heightened interest in identifying abnormal cycling and excessive bleeding, but a lack of data on variability in menstruation in healthy women has impeded such efforts. Drawing on questionnaire responses and tracked data from >6500 healthy users of a period-tracking app, we quantified natural variation in bleeding, and how duration and volume relate to the severity of physical impairments and impact sexual and other behaviors. We consider possible evolutionary trade-offs that may contribute to excessive menstrual bleeding
Antioxidative potential and masculinity – testing oxidative handicap hypothesis in men.	Agnieszka Żelaźniewicz, University of Wrocław, Wrocław, Poland; Judyta Nowak-Kornicka, University of Wrocław, Wrocław Poland; Bogusław Pawłowski, University of Wrocław, Wrocław, Poland.	The immunocompetence handicap hypothesis (ICHH) proposes that high testosterone levels (T), necessary for the development of masculine traits, may also entail a cost related to the immunosuppressive properties of T. The limited studies on the relationship between oxidative stress and masculinity in men have shown mixed results. However, increased oxidative stress may result from the pro-oxidative properties of testosterone but also from the lowered antioxidant defense. Thus, the aim of this study was to verify if antioxidant potential, determining an individual's ability to deal with oxidative imbalance, correlates positively with morphological masculinity in men. 183 healthy men aged 26.56-44.29 years (X = 35.24, SD = 3.54) participated in the study. Serum levels of antioxidants (CAT, SOD, vitamin C), total antioxidant capacity, and OS markers (8-isoepiprostaglandin, RNA / DNA, PCs) were determined. Testosterone, cortisol, hsCRP levels, and body adiposity were controlled. Masculinity was measured based on facial measurements, shoulder-to-hip ratio, 2D:4D, muscle mass, upper-torso and grip strength. The result of the study showed no relationship between antioxidant capacity and morphological masculinity in men, also when controlled for potential confounders. The results suggest that morphological masculinity is not a cue of a man’s antioxidant capacity in men.

Title	Authors	Abstract
Adaptive perspectives on factors affecting child growth	Nuzhat Choudhury, Department of Anthropology, Durham University, Durham, UK; Gillian R Bentley, Department of Anthropology, Durham University, Durham, UK; Dimitrios Vallis, Department of Anthropology, Durham University, Durham, UK; Malay Kanti Mridha, Centre for Non-communicable Diseases and Nutrition, BRAC James P Grant, School of Public Health, BRAC University, Dhaka, Bangladesh; Md. Mokbul Hossain, Centre for Non-communicable Diseases and Nutrition, BRAC James P Grant, School of Public Health, BRAC University, Dhaka, Bangladesh; Barry Bogin, School of Sport, Exercise and Health Sciences, Loughborough University, Loughborough, UK; Nasima Akhter, Department of Anthropology, Durham University, Durham, UK	While nutrition is essential for ensuring adequate child growth, a primary determinant of height may lie in relative social position (RSP) within hierarchical human societies. Explanatory mechanisms point to dominance effects exerted through the hypothalamic-pituitary-adrenal (stress) axis. Child growth and relative final adult height may be adaptively mediated through complex social pathways in addition to just nutrition. To assess this perspective, we used data from 35,106 mother-child (<5 years) dyads from a Bangladeshi national surveillance project. RSP was constructed using Principal Component Analysis (PCA); nutritional factors (NF) included minimum dietary diversity (MDD) and child morbidity. Multiple linear regression examined associations between RSP and NF against height-for-age Z-scores (HAZ) controlling for other covariates. Standardised beta coefficients compared effects of RSP and NF. Results showed RSP had a greater effect on HAZ than MDD or morbidity. Our findings suggest social inequalities have strong effects on height differences within human groups and have follow-on implications for how developmental and nutritional aid to LMICs should be allocated. The results also raise questions about evolved primate (including human) responses to perceived dominance. Smaller body size, for example, may have been adaptive in our evolutionary past for subordinate individuals with less access to reliable food sources.
Body mass index vs visceral fat and its relation to selected health measures and immunity markers in non-obese healthy men and woman	Judyta Nowak-Kornicka, University of Wroclaw, Poland; Agnieszka Żelaźniewicz, University of Wroclaw, Poland; Bogusław Pawłowski, University of Wroclaw, Poland.	Body adiposity might be a cue of various components of biological condition, including health and immunity. However, adipose tissue differs in terms of their metabolic activity. As such visceral fat (VAT) might be a better indicator of biological condition than markers of total adiposity such as BMI. This study try to verify if VAT is a better predictor of immunity and health than BMI and also if these relationships are stronger in women. 81 healthy non-obese men (aged 30-44) and 163 women (aged 25-34) were included in the analyzes. VAT was measured by bioimpedance, BMI was calculated using height and weight. Antibody response to vaccine, inflammation markers, and lipid profile were measured. Participants' age and sex hormone levels were controlled. The results suggest that VAT and BMI were not related to immunity. VAT was more strongly associated with markers of general health than BMI, while the latter tended to be a better predictor of sex hormones levels than the former. These results only partially support the hypothesis that VAT is a better marker of biological condition than BMI in non-obese individuals. No sex difference in the relationship between VAT and health markers was confirmed in our study population. Funding NCN grant no2017/27/B/NZ8/00500

Title	Authors	Abstract
The effectiveness of pulmonary rehabilitation in COPD is associated with specific shifts in oral microbiota	Sara Melo-Dias, University of Aveiro, Portugal; Miguel Cabral, University of Aveiro, Portugal; Andreia Furtado, University of Aveiro, Portugal; Sara Souto-Miranda, University of Aveiro, Portugal; Catarina Almeida, University of Aveiro, Portugal; Alda Marques, University of Aveiro, Portugal; Ana Sousa, University of Aveiro, Portugal	Pulmonary Rehabilitation (PR) is the most cost-effective therapy for chronic obstructive pulmonary disease (COPD), but not all patients are responsive. The reasons behind this and the role of the airway microbiota in PR effectiveness are currently unknown. Here, we explored the effects of PR on oral microbiota and inflammatory markers and the associations of observed changes with responsiveness to PR. 456 saliva samples and data on exercise capacity, dyspnoea, and health-related quality of life were collected from 76 patients, of whom half participated in a 12-weeks PR programme. PR responsiveness was defined as overcoming the minimal clinically important difference of the measure assessed. PR modulated patients' microbiota composition as well as the levels of IL-1β, TNF-α, and IL-10. Distinct patterns of longitudinal correlation between bacteria and inflammatory markers were also observed among responders (R) and non-responders (NR). Particularly, the longitudinal dynamic of Lautropia (Burkholderiaceae family) was significantly different between R and NR to exercise capacity, with NR having higher frequencies by the end of PR. Additionally, Lautropia was highly positively correlated with most of the inflammatory markers quantified (e.g., TNF- α, IL-6, IL-18) in NR to exercise capacity. Future studies should address the implications and stability of these microbiota modifications.
Evolutionary Model of Depression as an Adaptation for Blocked Social Mobility	Hanson Park, Seoul National University, Seoul, South Korea; Sunyoung Pak, Seoul National University, Seoul, South Korea.	Objectives In regard to the social competition hypothesis, depression is viewed as an involuntary defeat strategy. A previous study has demonstrated that adaptation in microenvironments can result in a wide range of behavioural patterns including defense activation disorders. Using a simulation model with evolutionary ecological agents, we explore how the fitness of various defence activation traits has changed over time in different environments with high and low social mobility. Method The Evolutionary Ecological Model of Defence Activation Disorder, which is based on the Marginal Value Theorem, was used to examine changes in relative fitness for individuals with defensive activation disorders after adjusting for social mobility. Result Our study examined the effects of social mobility on fitness by varying the d-values, a measure of depression in the model. With a decline in social mobility, the level of fitness of individuals with high levels of defense activation decreased. We gained insight into the evolutionary influence of varying levels of social mobility on individuals' degrees of depression. In the context of a highly stratified society, the results support a mismatch hypothesis which states that high levels of defence are detrimental. Conclusion Despite the fact that niche specialization in habitats composed of multiple microenvironments can result in diverse levels of defensive activation being evolutionary strategies for stability, decreased social mobility may lead to a decrease in fitness of individuals with highly activated defence modules. There may be a reason behind the epidemic of depression in modern society.

Title	Authors	Abstract
Phylogenomics and accessory genome diversity of Streptococcus dysgalactiae uncover host specializations	Cinthia Alves-Barroco1,2, Patrícia H. Brito1,2,3*, Alexandra R. Fernandes1,2* 1. Applied Molecular Biosciences Unit (UCIBIO), Dept. Ciências da Vida, NOVA School of Science and Technology, Portugal 2. i4HB, Associate Laboratory - Institute for Health and Bioeconomy, Faculdade de Ciências e Tecnologia, Universidade NOVA de Lisboa, Portugal 3. NOVA Medical School, Faculdade de Ciências Médicas, Universidade NOVA de Lisboa, Portugal *Corresponding author: phbrito@fct.unl.pt (PHB), ma.fernandes@fct.unl.pt (ARF)	Streptococcus dysgalactiae (SD) is a gram-positive bacterium capable of infecting both humans and animals and causing a wide range of invasive and non-invasive infections. With two subspecies, the taxonomic status of SD remains controversial. Subspecies equisimilis (SDSE) is an important human pathogen, while subspecies dysgalactiae (SDSD), the cause of bovine mastitis and infectious arthritis, has been considered an emerging zoonotic pathogen. Adaptation of SDSD to the different hosts is still understudied, and the failure to distinguish SDSD from SDSE in routine laboratory tests results in a global underestimation of the incidence of SDSD human infections. In this work, we provide a phylogenomic analysis of 115 isolates from both subspecies and different infected hosts. Our analysis reassesses previous taxonomic identifications and recovers an evolutionary history that is not compatible with current taxonomy. Core genome phylogenetic relationships segregate all human SDSE in a single cluster separated from all other SDSD and non-human SDSE isolates. The subgroup of bovine SDSD evolved from this later clade and harbors a specialized accessory genome characterized by the presence of specific virulence determinants (e.g. cspZ) and carbohydrate metabolic functions (e.g. fructose operon). Together our results indicate a host-specific SD and opportunistic human infections from non-human SDSD.
Understanding the Psychological and Physiological Impacts of Assisted Reproductive Technology-Related Stress	Zaneta Thayer, Dartmouth College, Hanover; Aditi Gupta, Dartmouth College, Hanover; Emily Lu, Dartmouth College, Hanover	The Developmental Origins of Health and Disease hypothesis suggests maternal stress can adversely impact fetal health and development; yet, the impacts of fertility-related stress on maternal and fetal health remain poorly understood. As a first step toward understanding the potential importance of infertility-related stress to offspring development, we evaluated the relationship between fertility-related stressors, perceived stress, and depression symptoms among individuals (n = 290) considering, undergoing, or having recently undergone assisted reproductive technologies (ART), such as IVF. Across all sample groups, 42.51% of individuals (n=287) had clinically-significant depression scores; 88.92% of individuals (n=280) reported medium or high levels of perceived stress. Financial stress was positively associated with perceived stress score ($r = .1871$, $p < .0017$), but not with depression. Shame about infertility and concerns about treatment success were also correlated with higher stress and depression scores (both $p < 0.05$). In sum, participants were highly stressed about their financial situation, shame around infertility, and the likelihood of treatment success. These stressors were associated with greater perceived stress and depression. Forthcoming analyses of hair cortisol levels in the study sample will evaluate whether ART-related stress is associated with variation in maternal hypothalamic-pituitary-adrenal function in the perinatal period.

Title	Authors	Abstract
Purifying selection and adaptive evolution spanning the zoonosis of SARS-CoV-1 and SARS-CoV-2	Alex Dornburg, University of North Carolina at Charlotte, Charlotte; Stephen Gaughran, Princeton University, Princeton; Hayley B. Hassler, Yale University, New Haven; J. Nicholas Fisk, Yale University, New Haven; Mofeed Nagib, Yale University, New Haven; Yinfei Wu, Yale University, New Haven; Jaiveer Singh, Yale University, New Haven; Yaning Wang, Yale University, New Haven; Zheng Wang, Yale University, New Haven; Alison P. Galvani, Yale University, New Haven; Jeffrey P. Townsend, Yale University, New Haven.	COVID-19 is the third major zoonotic disease of the past two decades resulting from spillovers of an animal coronavirus to humans. How the virus evolved proximate to zoonosis is crucial knowledge to aid in the prevention and suppression of future zoonoses. However, key genomic changes in SARS-CoV-2 that may have enabled human infection and transmission remain unclear. Here we test competing hypotheses regarding adaptive evolution during the zoonosis of SARS-CoV-2 and SARS-CoV-1 using molecular-evolutionary and population-genetic approaches to quantify region-specific selection within both SARS-CoV genomes. We find strong purifying selection across each genome at the time of zoonosis and little evidence of positive selection—even in the fast-evolving antigenic viral surface protein Spike. These findings suggest that zoonotic transmission is primarily mediated by human interactions with reservoir populations. One notable exception exhibiting signs of adaptive selection proximate to zoonosis occurs within ORF7a in both SARS-CoV-1 and SARS-CoV-2. Selection on ORF7a indicates an important and underappreciated role of this immunomodulatory accessory protein in the transmission of SARS coronaviruses to human hosts. Our results reveal that molecular evolution proximate to the zoonosis of SARS coronaviruses is characterized by strong purifying selection complemented by only a trace of targeted adaptation in specific gene regions.
Back-to-Africa introductions of Mycobacterium tuberculosis as the only cause of Tuberculosis in Dar es Salaam, Tanzania	Michaela Zwyer, Swiss TPH, Switzerland; Liliana Rutaihwa, FIND, Switzerland; Jerry Hella, Ifakara Health Institute, Tanzania; Mohamed Sasamalo, Ifakara Health Institute, Tanzania; Sebastien Gagneux, Swiss TPH, Switzerland; Daniela Brites, Swiss TPH, Switzerland	Dar es Salaam is a high-endemic tuberculosis (TB) setting in East Africa and has the highest TB notification rate in Tanzania. We investigated the TB epidemic in Dar es Salaam by analyzing 1,082 genomes of Mycobacterium tuberculosis (Mtb) isolated from patients and their clinical data collected between 2013 and 2019. We found a high diversity of Mtb strains circulating in Dar es Salaam. Mtb is thought to have evolved in East Africa, however we found that the epidemic in Dar es Salaam was exclusively driven by strains introduced from other parts of the world during the last 300 years. Evolutionary success, as measured by abundance, was not correlated with clinical variables related to virulence such as extent of cavitary disease, or bacterial load. However, we show that different bacterial strains differed in transmission. Abundance of some genotypes could be explained as a composite of early introduction and enhanced transmissibility. These results suggest that despite being genetically very strongly related and having contacted with a similarly sensitive host population upon being introduced to Dar es Salaam, different Mtb strains have most likely evolved different life history traits leading to different extant epidemiological characteristics.
Characterizing the impact of local adaptations to ancestry-associated differences in transcriptional responses to environmental challenges	Joao Barroso-Batista, University of Chicago, Chicago; Cary Brandolino, University of Chicago, Chicago; Neha Joshi, University of Chicago, Chicago; Luis Barreiro, University of Chicago, Chicago.	When human populations migrated out of Africa, they encountered markedly different environments, likely resulting in population-specific adaptive events. Substantial evidence supports this hypothesis at the genetic level, with many reported cases of population-specific signatures of natural selection around immunity genes and other genes directly responsive to environmental cues. However, we still know little about the extent to which neutral or adaptive inter-population genetic differences affect phenotypic variation at the population level and what molecular pathways are the most divergent across populations. Addressing this gap is not only important for understanding recent human evolution, but may also help reveal the molecular basis of ancestry-related differences in disease susceptibility. Here, we analyzed gene expression responses in EBV-immortalized B cells (lymphoblastoid cell lines, LCLs) derived from a panel of 100 individuals with varying degrees of African- and European-ancestry. Specifically, we performed transcriptional profiling of LCLs upon challenge with a large array of stimuli, including bacterial and viral agents as well as common environmental compounds for a total of over three thousand transcriptional profiles. By combining gene expression responses with genotype data from the same individuals we expect to uncover conserved and divergent patterns of gene expression responses to different environmental triggers, identify the genetic basis of such differences, and characterize the evolutionary mechanisms (neutral genetic drift versus positive selection) that led to their establishment in modern human populations.

Title	Authors	Abstract
Protein Moonlighting: A Novel Potential Basis for Functional Hitchhiking During Cancer Cell Selection?	R. Brooks Robey, United States Veterans Administration and Geisel School of Medicine at Dartmouth, Hanover, NH, USA	Beadle's original One Gene-One Enzyme Hypothesis has now been supplanted by the widespread recognition that individual gene products can have multiple discrete molecular functions, including both canonical and so-called "moonlighting" functions. Hexokinase 2 (HK2), which is overexpressed in many cancers, is illustrative of this concept. In addition to its canonical ability to catalyze the first committed step of all glucose utilization pathways within the cytosol, physical and functional interactions between HK2 and mitochondria directly couple intra- and extra-mitochondrial metabolism through the control of anionic metabolite entry and exit at mitochondrial contact sites. Mitochondria-bound HK2 also directly antagonizes proapoptotic Bcl-2 protein family signaling. In addition, HK2 can serve as a molecular scaffold for the integration of signal transduction involving PKA and GSK3beta. These discrete functions of HK2 can individually contribute to characteristic hallmarks of cancer, thereby potentially serving as both cellular fitness determinants and a basis for cancer cell selection. Indirect selection of one or more moonlighting functions could also lead to "functional hitchhiking" in cancer development and progression. Conversely, selectable fitness advantages conferred by favorable molecular functions could be partially or completely offset by indirect co-selection of non-favorable moonlighting functions. Both scenarios have obvious biological, clinical, therapeutic, and evolutionary implications.
Unrealistic Optimism and COVID-19 Risk among an Autoimmune Disease Cohort	Alexandria Henderson, Baylor University, Waco, Texas, USA; Jeffrey Gassen, Baylor University, Waco, Texas, USA; Tomasz Nowak, Baylor University, Waco, Texas, USA; Brooke Morris, Baylor University, Waco, Texas, USA; Edward Thum, Baylor University, Waco, Texas, USA; Sally Weaver, Waco Family Medicine, Waco, Texas, USA; Erich Baker, Baylor University, Waco, Texas, USA; Michael Muehlenbein, Baylor University, Waco, Texas, USA.	Higher risk score for COVID-19 is associated with lower perceived likelihood of infection. This is explained through unrealistic optimism, a phenomenon that can provide short-term psychological benefits to individuals at high risk of illness. Chronic conditions, such as autoimmune diseases, are shown to increase a person's risk of severe illness from COVID-19. Autoimmune diseases are often treated with immunosuppressive medication, some of which have been shown to impact seroconversion rates negatively following vaccination against COVID-19. The complexity of infection from SARS-CoV-2 with autoimmune comorbidities warrants concern for risk perception among these groups. A cohort of women in McLennan County, TX, USA who self-report a diagnosis of an autoimmune disease showed higher perceived infectability and perceived severity of disease, if infected when compared with age- and BMI-matched controls. These results contrast broader analyses of high-risk participants, who reported similar perceived severity of illness if infected, but lower perceived likelihood of being infected in the first place. There was no significant effect found between diagnosis of autoimmune disease and perceived stress during the COVID-19 pandemic. These results suggest women with an autoimmune disease in this cohort do not exhibit unrealistic optimism for COVID-19.
Do microbes gain when there is no pain?	Kevin Lozo, University of Pittsburgh Medical Center; Athena Aktipis, Arizona State University, Tempe AZ; Joe Alcock, University of New Mexico, Albuquerque	Pain is among the most common reasons a patient seeks medical care. However, pain itself is not always problematic. Responding to painful stimuli protects an organism from physical harm. Here we suggest another function: pain protects organisms from pathogens. Protection from infection is orchestrated by local effects of pain neuron activation, regulation of pain at the CNS, and subjective experience of pain. Mechanisms underlying the regulation of pain and immunity overlap considerably, suggesting that pain may be another arm of the immune system. Notably, pain is used by clinicians as a sign of likely infection in wounds and after surgery. Some pain neurons express receptors that detect pathogens; when activated, these neurons initiate immune responses against pathogens. One prediction of this hypothesis is that pathogens should engage strategies to block pain. Accordingly, SARS-CoV2 recently was shown encode peptides that interfere with pain. Other parasites and bacteria also disrupt pain signaling, including M. leprae which destroys pain neurons. Because some pathogens block pain, it could be adaptive for hosts to have an anticipatory counter-response against microbial manipulation of the pain system. This could lead to higher pain sensitization. We discuss treatment implications for chronic pain, long COVID, and opioid dependence.
Evaluating the effect of copper and copper dependent compounds on meropenem resistant bacteria	Sada M. Boyd, Portia Mira, Nghi Nguyen, Brian Bui, Pamela Yeh	Antibiotic resistance is a growing worldwide public health concern. To combat this issue there is a need for new antimicrobials, however development has been almost non-existent in the last 30 years. Copper has received particular attention due to its inherent antibacterial properties. Another alternative is to repurpose already available drugs. Disulfiram, originally purposed as an Antabuse treatment has been shown to have antibacterial properties in the presence of copper. Here we evaluate the combined effect of disulfiram and copper on eight individually evolved meropenem-resistant Escherichia coli populations in the presence and absence of meropenem. Additionally, we determine which genotypes lead to increased meropenem resistance in Escherichia coli. Preliminary results suggests that the combined effect of disulfiram and copper restores meropenem sensitivity in meropenem-resistant populations. Our experiments are ongoing.

Title	Authors	Abstract
The durability of immunity against reinfection by SARS-CoV-2	Jeffrey P. Townsend, Yale University, New Haven; Hayley B. Hassler, Yale University, New Haven; Zheng Wang, Yale University, New Haven; Sayaka Miura, Temple University, Philadelphia; Jaiveer Singh, Yale College, New Haven, Sudhir Kumar, Temple University, Philadelphia; Nancy H. Ruddle, Yale University, New Haven; Alison P. Galvani, Yale University, New Haven; Alex Dornburg, University of North Carolina, Charlotte.	The durability of immunity and time to likely reinfection was among the most consequential unknowns of the COVID-19 pandemic. For much of the pandemic, there was limited to no direct data on SARS-CoV-2 long-term immune responses and reinfection. We performed a comparative evolutionary analysis of antibody optical density levels following infection by SARS-CoV-1, MERS-CoV, HCoV-229E, HCoV-OC43, and HCoV-NL63 coronaviruses to estimate times to reinfection by SARS-CoV-2. Paired with coronavirus reinfection data, we performed ancestral and descendent states analyses to estimate the expected waning of antibody levels, the probabilities of reinfection given antibody level, and the anticipated times to reinfection after recovery under conditions of endemic transmission. Prior to substantial reinfection (and consistent with later reinfection and breakthrough infection studies), we predicted reinfection by SARS-CoV-2 under endemic conditions would likely occur between 3 and 63 months, with a median of 16 months. This protection is less than half the duration revealed for the endemic coronaviruses circulating among humans, and is a key component of public health decision-making. This comparative evolutionary approach can also be applied to diverse traits, such as predicted seasonality for SARS-CoV-2, and to other viral clades that are likely to present zoonotic threats to public health
The Evolutionary Role of MicroRNAs in Cardiovascular Disease	Angelle Bradford, Tulane University School of Medicine	What are the evolutionary benefits of CVD, if there are any at all? In what ways do biomedical researchers and respective research overlook the importance of integrating evolutionary principles and approaches in order to explain and treat cardiovascular disease? I will present a review of the literature and gaps that substantiate and challenge our assumptions around cardiovascular disease and metabolic syndrome.
The social environment alters how the brain responds to an immune challenge	Patricia C. Lopes, Chapman University, CA, USA	The social environment can affect animal physiology, with important health implications. For example, in humans, social isolation is a risk factor for worsened health outcomes. Zebra finches, Taeniopygia guttata, undergoing an immune challenge and presented with females show reduced behavioral symptoms of sickness, indicating that the social environment influences how these birds respond to an infection. How the social environment changes brain responses to an infection is not known. Using RNA-seq, we studied male zebra finch neural molecular responses to an immune challenge under four social environments. Finches in each social environment showed distinct transcriptomic profiles in response to an endotoxin challenge. Out of the four treatments, males paired with a novel female had the smallest number of differentially expressed genes as a response to endotoxin. Thus, acute changes to the social environment have major implications for how the brain responds to an infection.
Evolutionary mismatch induced by high fat diet reveals sex-specific metabolic alterations in C57BL/6J obese mice	Jian Han, North Carolina A&T State University, Greensboro, USA; Bo Wang, North Carolina A&T State University, Greensboro, USA; Vidya Jadhav, North Carolina A&T State University, Greensboro, USA; Scott H. Harrison, North Carolina A&T State University, Greensboro, USA; Antoinette M. Maldonado-Devincci, North Carolina A&T State University, Greensboro, USA; Joseph J. Graves, North Carolina A&T State University, Greensboro, USA,	The availability of food in excess is an evolutionary mismatch that has contributed to a dramatic increase in diseases of homeostasis in industrialized nations. This food excess has resulted in a higher proportion of individuals considered overweight or obese. Obesity poses a risk for many diseases, including diabetes, cardiovascular disease, and cancer. Evidence suggests that prevalence of these diseases differs by biological sex. This study utilizes a mouse (C57BL/6J) model of obesity to analyze metabolites in key organs (e.g. the liver) at various time points of dietary treatments: 5, 9, and 12 months of control or high fat diet treatment (HFD). Our study discovered that the female HFD group has a more discernable perturbation and set of significant changes in metabolites than the male HFD group in the C57BL/6J mouse model. A high glutathione and lactate levels in the liver samples of the female HFD group was observed and such result further indicates a potential staving off of oxidative stress. These metabolite-based findings for a diet-induced effect of obesity may help guide future pioneering discoveries relating to the analysis and prevention of obesity in people, especially for females.

Title	Authors	Abstract
Serving Two Masters: Evolution of Dual Resistance in Escherichia coli	Olusola Jeje, North Carolina Agricultural and Technical State University, Greensboro; Akamu J Ewunkem, Winston Salem State University, Winston Salem; Joseph L Graves Jr, North Carolina Agricultural and Technical State University, Greensboro; Liesl K Jeffers-Francis, North Carolina Agricultural and Technical State University, Greensboro.	In bacteria, common fitness related tradeoffs exist between various components of survival including anti-phage and antibiotic resistance. We utilized experimental evolution to test for the existence of potential tradeoffs between iron (III) resistance and T7 phage resistance in Escherichia coli. Dual-resistant (iron (III)/phage) populations were compared to their controls (iron (III) resistant, phage resistant, no resistance to either) for their performance against excess iron (III) and phage; and correlated resistances to iron (II), gallium (III), silver (I) and conventional antibiotics. Iron (III)/phage resistant populations demonstrated superior 24-hour growth compared to all other populations when exposed to increasing concentrations of iron (II, III), gallium, ampicillin, and tetracycline. No differences in 24-hour growth was shown between iron (III)/phage resistant and iron (III)-resistant populations in excess chloramphenicol, sulfonamide, and silver. Genomic analysis identified selective sweeps in phage resistant variants (iron (III)/phage and phage-resistant) including mutations in envelope stress genes. E. coli selected for resistance to both excess iron (III) and T7 phage showed no evidence of a trade-off between these resistances. The selection resulted in correlated resistances to ionic metals (iron (II), gallium and silver) and antibiotics. There is a likelihood that combination antimicrobial therapy may result in bacterial variants with multiple resistances.
Quantitative approaches to antibiotic resistance evolution	Tobias Bollenbach, University of Cologne	Genetic perturbations that affect resistance have been characterized genome-wide, but how do such perturbations interact with subsequent evolutionary adaptation to antibiotics? We have recently developed a high-throughput platform for the automated evolution of antibiotic resistance under tightly controlled selection pressure. Using this technique, we systematically investigate how different perturbations alter evolutionary dynamics in Escherichia coli K-12. Our results show that strong epistasis between resistance mutations and specific genes can be exploited to control spontaneous resistance evolution. We further identified a global pattern of diminishing-returns epistasis: Strains that are initially more sensitive generally experience greater resistance gains. We are currently investigating the extent to which these phenomena apply more generally to different antibiotic classes. Our preliminary results suggest that certain targeted perturbations, such as disruption of drug efflux pumps, are a promising strategy to slow the emergence of resistance to various antibiotics.
Switching from commensal to pathogen: experimental evolution to understand microbial adaptation to host environment	Angharad E Green, University of Liverpool, UK; Thomas E Barton, University of Liverpool, UK; Marie Phelan, University of Liverpool, UK; Daniel R Neill, University of Liverpool, UK	Streptococcus pneumoniae is a major human pathogen, adept at colonising various host-niches. Asymptomatic upper airway colonisation is the predominant infection outcome, but disease manifestations including pneumonia and septicaemia can result when the pathogen gains a foothold in other niches. The ability of bacteria to alter metabolite acquisition and utilisation, virulence factor expression and cell surface structures, in the face of a changing environment, is key to pathogenesis. In recent years, our lab has undertaken large-scale in vivo experimental evolution studies with pneumococcus, using pneumonia and nasopharyngeal carriage mouse models. This work yielded bacterial lineages adapted to lower or upper airway environments, respectively. These have enabled us to characterise the genetic and phenotypic basis of niche adaptation, uncovering novel pneumococcal virulence factors. In parallel, we have aimed at determining the host factors providing the selective pressures that drive niche adaptation in pneumococci. Metabolomic profiling of murine nasopharynx and lungs, in the presence and absence of pneumococcal infection, has identified key nutritional differences between airway microenvironments and highlighted the impact that infection has on sugar and amino acid bioavailability. Combining experimental evolution data, host metabolomics, microbial transcriptomics and carbon-source utilisation data, we aim to link niche-evolved adaptations in pneumococci to the respiratory tract metabolite-profile, identifying key pathogen metabolic gene pathways that might be targeted by therapeutic intervention.

Title	Authors	Abstract
Is codon usage orienting horizontal gene propagation?	Stéphanie Bedhomme, CEFE, Montpellier, France; Léa Pradier, CEFE, Montpellier, France; Michael Finnegan, CEFE, Montpellier, France.	Previous experiments in E. coli have revealed that (1) codon usage of an antibiotic resistance gene can strongly affect the level of resistance it confers and (2) antibiotic selection pressure led to the recovery of high resistance levels independently of the codon usage, through compensatory evolution. Based on these results, we formulated the hypothesis that codon usage is a factor determining the success of horizontal gene transfer (HGT) and set out to test this hypothesis by comparative and experimental approaches. In the comparative approach, oriented networks of horizontal transfers of aminoglycoside resistance genes were reconstructed across Eubacteria. They revealed that phylogenetic and ecological distances as well as dissimilarity in codon usage act as barriers to HGT but also that carriage by certain mobile genetic elements allows to jump over these barriers. In the experimental approach, HGT of synonymous versions of a resistance gene was mimicked across four species. The synonymous version effect seen earlier in E. coli exists in other species and is species-dependent: highly resistant versions are not the same in all species. We are currently investigating the mechanistic explanations behind these patterns and the mode of compensatory evolution in each species.