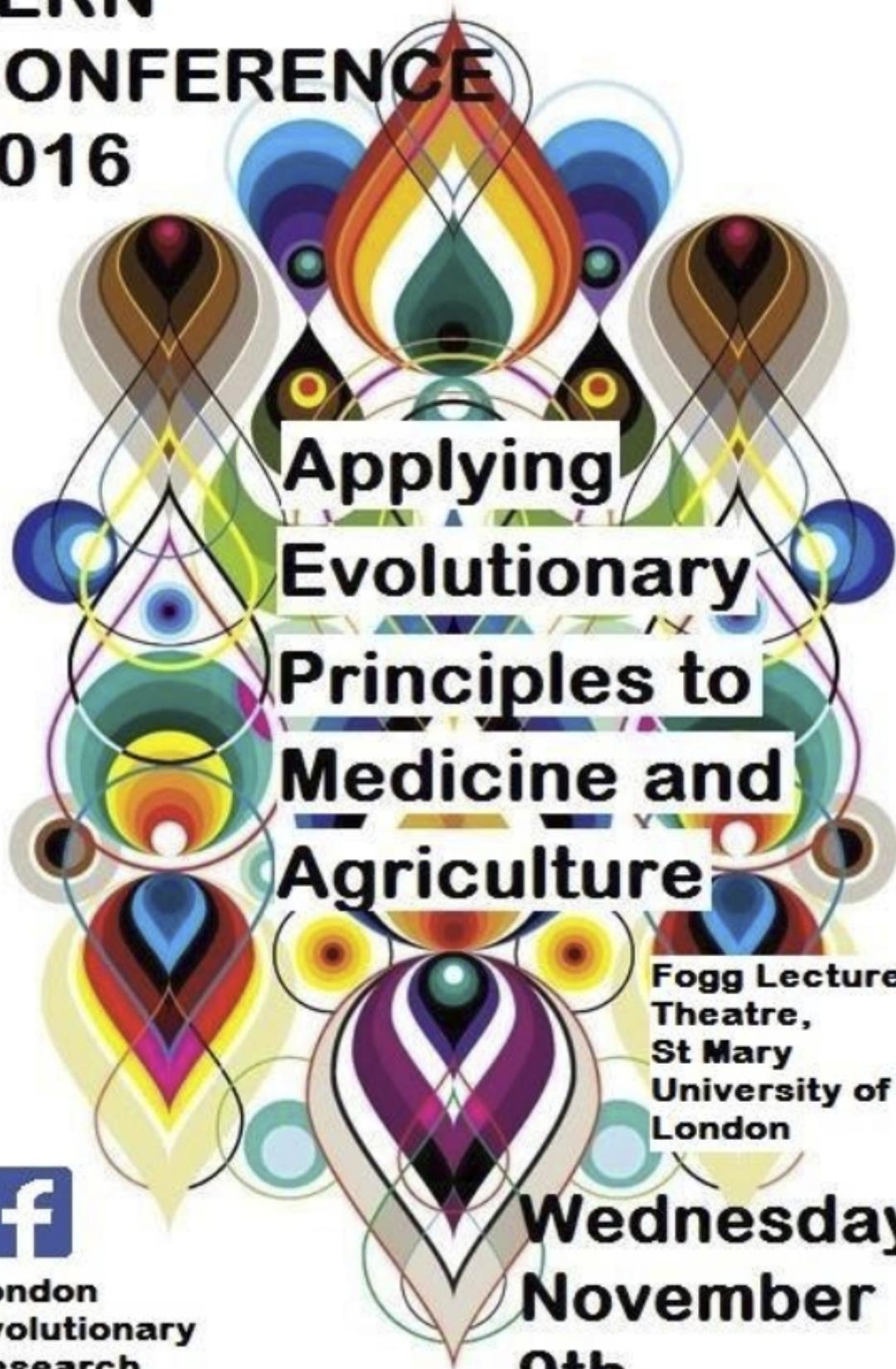


# LERN CONFERENCE 2016



## Applying Evolutionary Principles to Medicine and Agriculture

Fogg Lecture  
Theatre,  
St Mary  
University of  
London



London  
Evolutionary  
Research  
Network

Wednesday  
November  
9th

The **London Evolutionary Research Network (LERN)** annual conference has come up! Join us for a great day of discovering the great evolutionary research being done by fellow students and PostDocs from around London and beyond!

When: **9th November 2016**

Location: Fogg Lecture Theatre, **Queen Mary University**

Cost: Free!

Accessibility: The Fogg Lecture Theatre is wheelchair-accessible. There is easy access to a wheelchair-accessible toilet.

**The LERN conference is organized by a Committee of volunteers:**

Viola Walther (Barts Cancer Institute)

Saioa López (University College London)

Ivana Pilizota (University College London)

Rodrigo Pracana (Queen Mary, University of London)

Carlos Martínez Ruiz (Queen Mary, University of London)

Kevin Carolan (Rothamsted)

Naomi Cauchi (Brunel University London)

All abstracts are available online on the LERN's website: <https://londonevolution.org/lern2016/>

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**Don't forget to live tweet using #LERN2016!**

# Programme

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9:30 Registration

10:00 Welcome

## Session I

10:10 **Keynote lecture:**

**Prof. Dallas Swallow (UCL)** What can we learn from milk drinking? Life style changes and selection for adult lactase persistence.

11:00 **Lucy van Dorp (UCL)** Exploring the origins of farming using ancient DNA.

11:20 **Carlos Martinez Ruiz (QMUL)** Understanding the evolution of a social chromosome: a gene expression approach.

11:40 Coffee/Tea

## Session II

12:00 **Abrar Hussain (Rothamsted)** Impact of evolutionary changes on nutritional value of wheat grain.

12:20 **Kevin Carolan (Rothamsted)** Strategies for integrated deployment of host resistance and fungicides to sustain effective crop protection.

12:40 **Saioa López (UCL)** Genetic diversity and structure in human populations from Ethiopia and Sudan.

13.00 Lunch

## Session III

14:00 **Keynote lecture:**

**Dr. Paul Neve (Rothamsted)** '*Running to stand still*': The evolution of resistance to pesticides and drugs in agriculture and medicine.

14:50 **Katherine Brown (UCL)** Past, present and future implications of amylase gene copy number variation.

15:10 **Nicola Hawkins (Rothamsted)** Fungicide resistance in saprophytes: unintentional selection in agriculture.

15:30 Coffee/Tea

## Session IV

16:00 **Charlotte Bickler (Royal Botanic Gardens)** Adapting agriculture to climate change: characterising diversity in conservation collections of crop wild relatives.

16:13 **Bruno Vieira (QMUL)** Dealing with big genomic data using Bionode.io.

16:26 **Liam Shaw (UCL)** Perturbation and stability in the gut microbiome.

16:39 **Guilherme Rossato (Rothamsted)** Investigating the current status and predicting further evolution of azole fungicide resistance in the wheat pathogen *Zymoseptoria tritici*.

## **ABSTRACTS**

## Keynote speakers

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### **What can we learn from milk drinking? Life style changes and selection for adult lactase persistence**

*Prof. Dallas Swallow, Emeritus Professor of Human Genetics, UCL*

The ability to digest milk as an adult is a recent evolutionary adaptation brought about by the 'parallel' positive selection of several different single nucleotide changes in an enhancer sequence upstream of the lactase gene. These substitutions affect lactase gene expression, but only in adults, and do so via different molecular routes to the same phenotypic outcome. The mechanism is not yet fully understood, but is now known to include age-related epigenetic changes that, in the enhancer region, behave in an allele-specific way. The mutations apparently arose in the last few thousand years in several different locations (probably Europe, the Near East and Africa) and the European allele shows one of the strongest signals of selection described in humans. Archaeological and ancient DNA evidence show that the spread of lactase persistence (from 5000 years BP) followed on after the spread of animal milking which can be traced to some 9000 years BP. Although it is clear that lactase persistence enabled the more efficient use of fresh milk as a food source, how this selection operated is not totally clear, particularly since fermentation of milk reduces the lactose, allowing a 'cultural' adaptation to milk consumption. However epidemiological evidence does suggest that there is a nutritional benefit from being lactase persistent, and milk as a source of water was undoubtedly important. Fresh milk was clearly a very nutritious dietary source for many, but in some of those people in whom lactase does not persist into adult life there can be severe adverse symptoms of diarrhea and flatulence, even on consumption of small amounts. This illustrates how policy makers should be aware that one size does not fit all, when giving dietary advice. But more broadly, this lactase example also tells us a great deal about the kinds of variants that we might expect to be functionally relevant in relation to susceptibility to multifactorial disease; namely that regulatory mutations are much more likely to become polymorphic, since they are more flexible to continued function than coding sequence changes. Positive selection at some disease susceptibility loci may be followed by life-style changes which then make those same variants disadvantageous.

**‘Running to stand still’: The evolution of resistance to pesticides and drugs in agriculture and medicine.**

*Dr. Paul Neve, Senior Research Scientist, Rothamsted Research*

The adequate provision of safe and nutritious food in agriculture and the control of infectious disease are two of the greatest challenges facing human civilisation. Both endeavours are threatened by evolutionary forces which make pathogens and pests ever harder to control. In particular, the evolution of pesticide and drug resistance impacts the control of insect pests, weeds and pathogens in agriculture, and compromises the efficacy of antimicrobial and anti-cancer drugs. A good deal of research has resolved the physiological and molecular genetic mechanisms that enable organisms to resist these toxophores. As understanding of resistance mechanisms increases, there is now an opportunity to integrate across disciplines to unravel the eco-evolutionary drivers of pesticide and drug resistance, to move towards identification of general principles for resistance management. In this talk, using my own research to explore the ecological and evolutionary dimensions of evolution of resistance to herbicides, I will explore how an understanding of genetic architecture, fitness costs and co-variation in resistance traits can inform the design of rational resistance management strategies. In particular, I will consider how herbicide dose can impact evolutionary dynamics and how herbicide cycling (rotations), mixtures and sequences may be employed to delay the evolution of resistance. Integration of chemical, genetic, biological and cultural will be investigated as a means to slow evolution of resistance. This work is informed by a range of experimental evolutionary studies, using higher plants and model organisms and by modelling and simulation approaches. I will conclude with a consideration of the potential to identify common principles that can be applied for the management of pesticide and drug resistance across diverse ecological contexts and treatment settings. This latter analysis is an outcome from an international workshop held in 2016 to bring together researchers working on eco-evolutionary dynamics and management of evolved resistance to pesticides and drugs across a range of diverse disciplines in agriculture and healthcare.

## Exploring the Origins of Farming using ancient DNA

*Lucy van Dorp, Saïoa López, Farnaz Broushaki, Zuzana Hofmanova, Susanne Kreutzer, Daniel Wegmann, Joachim Burger, Mark G Thomas, Garrett Hellenthal*

A key process in the history of modern humans is the transition from a hunter-gatherer way of life to agro-pastoralism. This process began in the so-called "Fertile Crescent" that stretches west to modern-day Egypt, north to southeast Turkey and east into Iran, after which farming technology spread into Europe and elsewhere. Whether the spread of farming across the world was mediated by the exchange of ideas or the large-scale movement of peoples has been highly debated, and little is known about the genetic structure of the first farmers. We present a novel Bayesian mixture modelling approach based on chromosome painting designed to elucidate patterns of shared ancestry between modern human populations and aDNA from early Neolithic farmers. Specifically we infer proportions of shared ancestry among present-day world-wide groups and ancient farmer genomes from Greece, Anatolia, Germany, Hungary and Iran, including several sequenced to high coverage (>7X). We present strong evidence that the spread of farming from Anatolia into Europe was accompanied by extensive migration of peoples, and that modern groups in Europe descend in part from these early farmers. In contrast, we show that the early farmers of Iran share surprisingly little genetic affinity with the early farmers that spread into Europe, and also appear to be ancestors of modern day groups in Pakistan, India and Iran. By resolving these patterns of ancestry we provide evidence for strong genetic structure in the first farmers, suggesting that multiple hunter-gatherer groups adopted farming in SW-Asia.

## **Understanding the evolution of a social chromosome: a gene expression approach**

*Carlos Martinez-Ruiz, Richard A. Nichols and Yannick Wurm*

Supergenes may play a key role in the evolution and maintenance of complex phenotypes such as social behaviour, by reducing the recombination which would break up haplotypes having beneficial epistatic interactions. A recently characterised example is the supergene that controls a polymorphism in the social structure of red fire ant (*Solenopsis invicta*) colonies. This species displays two social phenotypes: colonies can either have single or multiple queens. A suite of phenotypic differences between the social forms is perfectly correlated with the presence of an inversion in a region referred to as the 'social chromosome'. The effect of the inversion is dominant, and homozygotes appear not to be viable; hence the inversion is effectively non recombining, which means its evolutionary history has similarities with Y and W sex chromosomes. However, there are also some differences to sex chromosomes, so this system provides an interesting test for theories describing the evolution of sex chromosomes and of supergenes. I use transcription patterns in workers and queens of both social forms in *S.invicta* to understand the nature of the selection that has shaped the evolution of the social chromosome. These results will help understand whether social chromosomes have evolved under a scenario of evolutionary conflict, in a similar way to sexual chromosomes.

## **Impact of Evolutionary Changes on Nutritional Value of Wheat Grain**

*Abrar Hussain*

Wheat is most important cereal crops grown all over the world with a production of more than seven hundred million tons. It can grow in a wide range of climates. Health benefits wheat grain are related with a number of nutritional compounds such as dietary fibre, minerals, vitamins and phytochemicals. Evolutionary changes in genetics are known to have significant effect on nutritional components of wheat. The present study was planned to screen variation among diverse wheat genotypes from six genotype groups i.e. selections, old landraces, primitive wheat, spelt, old cultivars and cultivars for different nutritionally relevant compounds such as proteins, minerals, tocopherols (Vitamin E) and heavy metals (HMs) under different set of climates. Minerals and heavy metals were analyzed by ICP-MS and ICP-OES. SE-HPLC was used to quantify different protein fractions in the wheat flour. Results showed significant variations in nutritional profile of wheat genotypes from diverse genetic background. Genetics and climatic location also found to have significant interaction. Primitive wheat showed higher amounts of minerals as compared to other genotype groups. It can also be concluded from the results that nutritional quality of wheat grain can be enhanced by selecting wheat genotypes for a particular climatic conditions. Further, the wheat genotypes with higher amount of nutritional compounds can be used in future breeding programs to produce wheat higher nutritional contents.

## **Strategies for integrated deployment of host resistance & fungicides to sustain effective crop protection**

*Kevin Carolan*

Pathogens evolve virulence against the genetic resistance in crops. This results in loss of disease control. Simultaneously, they evolve insensitivity to the fungicides we deploy against them. However, population genetics theory would predict that application of a fungicide should reduce selection for virulence, and use of genetic resistance in a crop should reduce selection for insensitivity – so integration of the two strategies should result in more durable disease control.

## **Genetic diversity and structure in human populations from Ethiopia and Sudan.**

*Saïoa López*

Ethiopia and Sudan have some of the highest levels of cultural, ethnic and genetic diversity in the world. In this work we analyse novel genome-wide data from 1,157 Ethiopian individuals (belonging to 77 different ethnic groups) and 355 individuals from Sudan (from 37 ethnic groups). We use a "chromosome painting" approach that exploits linkage among neighbouring SNPs, and has been shown to be more powerful than commonly-used algorithms (like PCA, STRUCTURE or ADMIXTURE) to identify population structure and infer and date admixture events among populations. We provide a comprehensive picture of the genetic diversity across these regions, and use this information to investigate the topographical and/or sociological features that promote interactions leading to genetic exchange or imposing barriers to genetic intermixing. We also identify which modern groups are most related genetically to a previously described 4500-year-old Ethiopian genome, and how those modern groups' genomes have changed due to drift, admixture and selection effects.

## **Past, present and future implications of amylase gene copy number variation.**

*Katherine Brown*

The amylase gene region exhibits greatest variability of copy number of any large-structural variation in the human genome (Iafate et al., 2004). Humans produce salivary and pancreatic amylase, which are encoded by five different, but highly similar genes. Both salivary (AMY1) and pancreatic (AMY2) amylase contribute to the digestion of dietary starch.

It has been hypothesised that increased copy number of AMY1 genes may have been an evolutionary adaptation to increased starch consumption either with the advent of cooking (Hardy et al., 2015) or more recently following the Neolithic transition (Perry et al., 2007). Both of these hypotheses are based on the assumption that increased copies of AMY1 increases the rate or capacity of starch digestion, which would have been advantageous during human evolution.

I will present data from a clinical investigation that provides evidence that AMY1 copy number affects starch digestion, impacting postprandial glycaemic and insulinaemic response, BMI and blood pressure in a healthy British cohort.

## **Fungicide resistance in saprophytes: unintentional selection in agriculture**

*Nichola Hawkins*

Ever since the first crops and livestock were domesticated, the deliberate artificial selection of desired traits has been accompanied by unintentional selection of other traits and in other species. In the first instance, the very acts of gathering and planting seeds for cultivation resulted in unconscious selection for traits such as non-shattering seed-heads, rapid germination and simultaneous ripening. Furthermore, growing whole fields or rearing large herds of a single species, and reducing intraspecific genetic diversity through artificial selection, selects for virulent pathogens and pests able to exploit these high-density, genetically-uniform hosts. The “Green Revolution” in the mid-20th Century produced increases in crop yields vital to feeding a growing population, but in many cases the new high-yielding crop varieties also carried increased disease susceptibility, whether due to pleiotropic effects or genetic linkage. Unfortunately, any measure to control pests and diseases will also exert selective pressure for individuals able to resist control. The use of single-site-inhibitor pesticides has led to the evolution of resistant pathogens, weeds, and insects and other animal pests, and the deployment of disease-resistant plant varieties has also led to the emergence of new virulent strains of diseases such as wheat rusts. However, application of pest control measures will also exert selective pressure on other organisms in the agricultural environment which were not even the intended target for control. *Cladosporium allicinum* is a saprophytic fungus, growing on leaf tissue that is senescing or that has already been killed by pathogenic fungi. We report strains of *C. allicinum* resistant to agricultural fungicides, showing parallel evolution of the same resistance mechanisms found in the fungicides’ intended target pathogens.

## **Adapting Agriculture to Climate Change: Characterising Diversity in Conservation Collections of Crop Wild Relatives**

*Charlotte Bickler*

The Adapting Agriculture to Climate Change Project is a global initiative to collect, conserve and use the crop wild relatives of 29 priority crop species. The project objectives are to identify the wild plant species that are closely related to crops and collect and protect the genetic diversity held within these species. This diversity is being made available in a form that plant breeders can readily use to produce varieties adapted to future climatic conditions. Such adaptation is a key component of securing the world's future food production. However, knowledge of variability in phenotypic traits, their genetic basis, and potential for use in breeding remains limited for many crop wild relative species. Current research aims to characterise the genetic diversity harboured within wild relatives of the carrot *Daucus carota*. In order to improve our knowledge of the genetic potential contained within wild carrot seed collections, our research aims to assay the phenotypic and genetic variation of selected accessions and identify adaptive differences in relation to environmental stress.

## **Dealing with big genomic data using Bionode.io**

*Bruno Vieira*

The volume of data generated by genomics is predicted to surpass the amount coming from other fields like astronomy or even big data companies like YouTube. Simultaneously, many analysis tools and interfaces are moving to the Web and the Cloud. We need new approaches to address these challenges. Bionode.io is an Open Source project to build Bioinformatic tools that can process Streams of genomic data on any machine or web browser. Bionode started three years ago at [WurmLab.github.io](https://github.com/WurmLab) during Bruno's PhD, when he faced the challenge of obtaining and processing data needed for his research on the effective population size of eusocial insects.

## **Perturbation and stability in the gut microbiome**

*Liam Shaw, Francois Balloux*

The gut microbiome is a complex ecosystem of interacting bacterial species. While it can be variable in composition between human hosts, it seems relatively stable around an equilibrium state within them (David et al., 2014, *Genome Biology*). This has led to talk of the gut microbiome as being positioned within a 'stability landscape', analogous to a fitness landscape in evolutionary biology (Relman, 2012, *Nutr Rev*). However, it's not quite clear how this should be taken from a conceptual schematic to a preliminary mathematical model. One possibility is considering microbiome time-series as trajectories in multidimensional space. Strong perturbations like broad-spectrum antibiotics then offer an opportunity to see how a disruption of stability changes the resulting trajectories. Using previously published data (Zaura et al., 2015, *mBio*) we look at the effect of a week-long course of antibiotics on the gut microbiome in this manner, compared to placebo. We find that the microbiome seems to continue along a disrupted trajectory for up to a month after administration of clindamycin, suggesting the disruption of the bacterial community is strongly affected and mediated by ecological interactions in addition to the effect of the antibiotic itself.

## **Investigating the current status and predicting further evolution of azole fungicide resistance in the wheat pathogen *Zymoseptoria tritici***

*Guilherme Rossato Augusti, Bart A. Fraaije, Nichola J. Hawkins, Michael W. Shaw*

Plant pathogens are a major challenge to maintaining crop production and food security around the world. *Septoria tritici* blotch (STB), caused by *Zymoseptoria tritici* (formerly known as *Mycosphaerella graminicola*), is one of the most important diseases in wheat-growing countries. Although there are wheat varieties with resistance to STB, the pathogen can overcome plant resistance.

*Septoria tritici* blotch is managed mainly through fungicide applications, although the pathogen can adapt resulting in fungicide resistance. Resistance to the Methyl Benzimidazole Carbamate fungicides (MBCs) occurred by 1984. The G143A mutation in cytochrome b, resulting in resistance to the QoI fungicides, emerged in the UK and Ireland in 2002 and is now widespread throughout the UK. A large number of mutations in the gene that encodes the azole fungicides target site protein have been identified, resulting in populations of *Z. tritici* less sensitive to most azole fungicides. Some field isolates with mutations conferring reduced sensitivity to the SDHI fungicides have already been detected. On the other hand, the multi-site inhibitors have not been affected by resistance in *Z. tritici*, due to their low risk resistance status. It is important to keep monitoring *Z. tritici* populations to design management programs to reduce risk of establishment of fungicide resistance.

The fungicide resistance status of *Z. tritici* populations from South America is not known. This research will establish if fungicide resistance has evolved in *Z. tritici* populations from Argentina, Brazil, Chile and Uruguay. In addition, the mechanisms of fungicide adaptation in the South American populations will also be compared with those found in North America and European populations, with a well-known history of fungicide resistance evolution.

## **Sponsors**

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