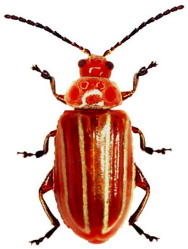

Peterhouse Biology Symposium 2022 Abstracts

Saturday 12th March 2022, Peterhouse Theatre

Justin Gerlach (Fellow) – **Ecology projects from rewilding to Darwin's beetles**

Last year I started supervising 1B Ecology projects, initially as a way of ensuring that there were field-projects for Ecologists during the pandemic restrictions. This year I supervised three different projects. Two of these related to restoring ecosystems: a survey of woodland invertebrates at the Ken Hill rewilding project in Norfolk, and a study of the ecology of the European pond turtle to determine its past role in British wetlands and whether it could be reintroduced. The third was a study of 'Darwin's beetle box', a collection of beetles thought to have been made by Charles Darwin during his undergraduate years in Cambridge. Whether this is really Darwin's collection has been questions. His copy of the 1829 'British Insects' has his annotations which enabled us to show that at least some of the specimens were indeed collected by Darwin, some on study trips to Wales but many from Cambridgeshire in 1828.

Danai Kontou (PhD student) – **Evolution in the wild: the predictability of adaptation to global change**

Focusing on zooplankton communities from Canadian Shield lakes and integrating genetics with resurrection ecology, my research investigates the nature and repeatability of rapid adaptation in the wild. Learning how keystone species in lakes respond to environmental change and the introduction of invasive predators, is key to our understanding how global change will affect vulnerable freshwater ecosystems and how we can best manage and protect them in the future.

Sabrina Guzen (II Plant Sciences) – **Investigating the effects of arbuscular mycorrhizal colonisation on barley**

Excessive fertiliser usage in agriculture has led to shortages in global phosphorus reserves and has caused extensive pollution of water systems. By investigating the effects of arbuscular mycorrhizal fungi on barley biomass, chlorophyll content and root colonisation, we attempt to see if such symbioses can enhance nutrient capture, increase yields, and show promise in helping reduce our reliance on fertilisers to feed the planet.

Wes Robertson (Research Associate) – **Sense codon reassignment in a recorded bacterium enables viral resistance and encodes polymer synthesis**

We created cells with a compressed genetic code that removes two sense codons and one stop codon, thus allowing us to delete their corresponding tRNAs and release factor. The resulting recoded cells could not read the canonical genetic code and were completely resistant to a cocktail of viruses. We then reassigned these 'blank codons' to non-canonical amino acids (ncAAs) to enable the synthesis of proteins containing three distinct ncAAs. This provides a platform for the sequence-defined synthesis of novel classes of unnatural polymers for materials and medicines.

Louis Fisher (II Zoology) – **Ecophenotypic response to microhabitat in freshwater mussels**

Bivalves can display significant phenotypic variability due to environmental conditions ("ecophenotypes"). This ecophenotypic variation can make some bivalve morphologies particularly suited to specific habitats, so understanding this variability is important for determining where individual bivalves should be reintroduced within ecological restoration programmes. Additionally, understanding ecophenotypic variability can improve species identification and palaeoenvironmental reconstructions. However, there has, to-date, been an absence of literature examining morphological variability within a single habitat. Accordingly, this project investigates microhabitat effects on mussel morphology, comparing phenotypes found in deep and shallow water for three Unionid mussel species (*Unio tumidus*, *Unio pictorum* and *Anodonta anatina*) at two sample sites within the River Cam and the River Great Ouse, Cambridgeshire. Bivalve morphology was analysed with traditional (measurement and comparison of the relative length-width-height ratios) and modern (Fourier analysis) morphometrics to identify trends across microhabitats and between species.

Lloyd Fung (Research Fellow) – **From choanoflagellate to choanocyte chamber: lessons learnt from the fluid dynamics of *Choanoeca flexa***

Sponges are widely regarded as the basalmost animal and one of the early examples of multicellularity, with a body plan that is specialised for filter feeding. A sponge body is highly porous. Water enters through the pore and through a system of canals to eventually reach the choanocyte chamber, the main site where pumping and filtering occurs. A chamber is formed by multiple choanocytes sitting on a spheroidal surface with their collars and flagellae on the inside. On the other hand, choanoflagellates, a sister taxon of animals, are single-cell organisms that share many similarities with individual choanocytes. Because of the similarities, many simply assume the two taxa are homologous, although this assumption is challenged by recent studies.

Some species of choanoflagellates also form colonies. This talk dives into the fluid dynamics of a newly discovered colonial choanoflagellates known as *Choanoeca flexa.* Unlike other colonial choanoflagellates, *C. flexa* forms a hemispherical sheet that strongly resembles a choanocyte chamber. Moreover, it is found that *C. flexa* sheet can invert inside-out in response to stimuli such as light. Using a simply fluid dynamical model, we investigate how the inversion affects their filtering rate and motility. We also study the effect of the sheet curvature and the effect of the spacing between each cell. Lastly, we compare the colony's filtering rate and motility with that of a single cell. From these results, we reflect on the evolutionary advantages of forming a colony/chamber and the implication on the homology between choanoflagellates and sponges.

Juliana Nacita (II Biochemistry student) – **Engineering novel polysaccharides: investigating GT61s in vitro**

Accounting for 80% of all biomass carbon on Earth, vascular land plants are the largest renewable carbon source with the potential to replace fossil fuel carbon. Most of this originates from secondary cell wall polysaccharides, the second most abundant of which is the hemicellulose xylan. Engineering and manipulating the cell wall to have desirable properties is important if we are to effectively use cell wall polysaccharides as renewable feedstock. The aim of the project is to characterise the activity of GT61 family of enzymes, responsible for substituting decorations onto the xylan backbone and to determine if GT61s can be engineered to change their function.

Hana Godfrey (II BBS student) – **A mouthful of calcium signalling: a plant's response to herbivory**

A plant which is unaware that it is under attack is unable to respond appropriately. Plants have evolved a diverse range of responses to herbivory, from the initial detection through to the subsequent defence pathways. While there is a lot of converging, the plant's ability to initiate specific responses in response to different herbivores though pathways which all rely on calcium ions to some extent suggests a complex network which this presentation has attempted to begin detangling.

Sebastian Ljung (1B student) – **Applying RNA velocity to human embryonic genome activation**

Jasmin Stowers recently discovered the first in vitro totipotent human 8C-like cells (8CLCs). In humans embryonic/zygotic genome activation (ZGA), where the embryo kickstarts transcription of genes, occurs at the 8C stage. The discovery of 8C-like cells occurring naturally in in vitro pluripotent naive embryonic stem cell (ESC) cultures lead to the question of whether 8CLCs arise and differentiate from and to naive ESCs. In my summer project I applied RNA velocity, which compares unspliced vs spliced mRNA levels in each cell for each gene to predict the differentiation trajectories of cells. RNA velocity results indicate that 8CLCs arise from and re-differentiate into naive ESCs in tissue culture.

Graham Christie (Fellow) – **Bugs delivering drugs (delivering bugs)**

Bacterial endospores represent natures toughest cells. These morphologically distinct survival structures are endowed with a series of structural and biochemical features that render them dormant but durable and viable for perhaps millennia. They germinate in response to appropriate environmental signals, rapidly forming new planktonic cells that can go on and cause disease, food poisoning, and a host of other nefarious activities. Despite these negative aspects, the unique properties of spores can be tailored and engineered for beneficial purposes. Here we examine applications in the biopharmaceutical sector, including spore analytes as excipients, and the synthesis and delivery of biologics.

Charlotte Wright (PhD student) – **Painted ladies and painted chromosomes: Merian element evolution in the Lepidoptera**

Chromosomes are a major unit of genome organisation and of inheritance. While chromosomes and their contents are usually evolutionarily stable, major karyotypic changes sometimes occur that have consequences for speciation, population divergence, and adaptation. Lepidoptera, butterflies and moths, are a diverse order of insects, with a largely conserved karyotype of 31 chromosomes. However, a subset of species display dramatic variation in patterns of genome and chromosome organisation. The growing number of high-quality, chromosomal assemblies means that we can begin to ask fundamental questions surrounding the processes that drive chromosome structure in Lepidoptera. Here, we draw upon 90 chromosomally-resolved lepidopteran genomes, generated as part of the Darwin Tree of Life Project, to analyse patterns of chromosome organisation across the group. By clustering genes by co-occurrence, we defined sets of genes that mark ancestral lepidopteran linkage groups, known as Merian elements, and used these to identify chromosomes that have undergone fusions or splits and place these events within a phylogenetic context. We inferred over 100 fusion and fission events, including dramatic karyotypic changes in Lycaenidae and Tortricidae. Moreover, we found that some chromosomes, including the Z, are more likely to fuse than others. Together, these analyses demonstrate how chromosomally-contiguous genomes across Lepidoptera offer an unprecedented opportunity to explore the role of selective constraint in the evolution of genome structure.

Jaruwatana (Sodai) Lotharukpong (MPhil student 2020-1) – **Extensive genic innovations at the origin of modern cephalochordates**

Cephalochordates (also known as amphioxus or lancelets) are a group of marine invertebrates occupying a critical phylogenetic position as the sister group to the remaining members of the chordate phylum (vertebrates and tunicates). This position has been indispensable in detailing the origin and evolution of the vertebrate genome, anatomy and development. However, of the three genera of amphioxus (*Branchiostoma*, *Asymmetron* and *Epigonichthys*), most studies have focused exclusively on *Branchiostoma*. Indeed, only *Branchiostoma* draft genomes have been published to date. This introduces potential biases in our *understanding* of the genomic features present in the ancestral cephalochordates, and consequently in the ancestral chordates, towards features present in *Branchiostoma*. During my MPhil, I assembled and annotated the genomes of Asymmetron and *Epigonichthys*. Multi-locus phylogenetic analyses reveal that, in contrast to previous studies, *Branchiostoma* is the sister group to *Asymmetron* and *Epigonichthys*. I further uncovered surprisingly complex gene histories

between these three genera, with the distribution of gene phylogenies indicative of past hybridisation between *Branchiostoma* and *Epigonichthys*. Lastly, contrary to the depiction of the amphioxus genome as slow evolving, I found that extensive gene births and duplications preceded the origin of modern cephalochordates. These findings emphasise amphioxus' unique biology and caution against viewing the amphioxus as mere proxies for the ancestral chordate.

Fani Memi (Research Associate) – **Using high throughput spatial genomics to construct cellular atlases of the human brain in development and disease**

Jen Lim (II Pathology student) – **A hybridisation-based method for lymphocyte immunoreceptor profiling and lymphoma diagnosis**

T and B-cell neoplasias can give rise to a wide variety of lymphomas and leukaemias, which can be difficult to diagnose despite the use of various histological and imaging techniques. Nonetheless, they all involve the clonal proliferation of a malignant set of lymphocytes as a central feature. This, combined with the unique system of recombination which takes place at genomic loci encoding T and B-cell receptors, allows the DNA-based assessment of biopsy sample clonality. Here, we examine a DNA hybridisation-based method for clonality assessment, which offers several advantages over current multiplex polymerase chain reaction (PCR)-based tests. By applying this method to DNA from biopsy samples of a cohort of 52 patients including 28 with T-cell and B-cell malignancies and 24 healthy controls, we found that addition of a novel subtractive hybridisation step does not improve the retention and enrichment of recombined immunoreceptor sequences. However, focussing on T-cell lymphomas where the utility of this method would be greatest, we also show that sample clonality can be quantified based on clonotype profiles generated by this method, and that it accurately identifies T-cell lymphoma samples as exhibiting significantly higher degrees of clonality than benign controls.

Eleanor Sheekey (PhD student) – **Senescence, cancer and p53**

P53 is a very important protein for a cell. It responds to cellular stress and mediates damage-repair. If the damage is not resolved it may cause a cell to die or to enter a state known as cellular senescence. In this latter case cells stop replicating and develop an inflammatory secretory phenotype. You may not be surprised to hear then that TP53 (gene encoding p53) is the most commonly mutated gene seen in human cancers. But how does mutant p53 alter the response to stress?