I'm happy to supervise a project in the area of cultivated meat, specifically on sustainable media formulations or cell sources.	Ruth Wonfor <u>rec21@aber.ac.uk</u>
I would be happy to discuss potential projects with applicants in the area of sports performance or human health, as long as there is a physical activity / exercise focus.	Rhys Thatcher <u>ryt@aber.ac.uk</u>
I am willing to discuss project ideas which use bioinformatics approaches to explore datasets comprising glacier microbiomes and/or microbial genomes/metagenomes	Arwyn Edwards <u>aye@aber.ac.uk</u>
Broadly equine projects (toxins in feeds/general feeds/hoof structure and diseases/stress testing) and agriculture and the environment.	Elizabeth Hart <u>elh18@aber.ac.uk</u>

The following pages have some more specific project ideas

## jhd2@aber.ac.uk

#### Summary

Verification of potential genetic regulators of seedpod size in model plants and crops identified by machine learning (ML) programme DeepCanola.

#### Background

Seed pod size has a critical relationship with yield in the UK's largest oil crop, *Brassica napus*, but is affected by temperature – and therefore climate change. The Lu and Doonan labs at Aberystwyth have developed the deep-learning program DeepCanola to automatically measure pod characteristics from images, which we have used on a GWAS experiment treated with different winter temperatures, and for which we have both genetic and transcriptomic data. This data presents several candidate genes for the control of this key trait: but are they real? To assess the accuracy of DeepCanola, we will analyse a selection of mutants in Arabidopsis and *Brassica rapa* – both identified from the GWAS experiment, and *a priori* targets known to modulate pod size and shape. These will be tested with DeepCanola, and for new targets, their molecular function characterised via standard molecular biology techniques, including transgenesis, qPCR, and protein work where appropriate.



Figure 1. DeepCanola generalisation capability - Examples test images showing samples from varying domains from the target and novel species. From van Vliet, Atkins et al.

#### Aims

To identify candidate genes from GWAS, and assess their role in Arabidopsis and Brassica via analysis of mutants and transgenic analysis and comparison with known mutants with DeepCanola imaging. To molecularly characterise the function of identified targets.

#### Methodology, techniques and training

**Transferrable:** cloning (expression construct production), genotyping techniques (PCR and KASP), RNA extraction and high quality qPCR, fluorescent protein (confocal) microscopy, image analysis with DeepCanola. Depending on project progress, could include transcriptomics.

**Plant specific:** plant growth, genetics and mutant analysis of Arabidopsis models and *Brassica* crops. Production of transgenic Arabidopsis, phenotyping.

#### References

- DeepPod: a convolutional neural network based quantification of fruit number in Arabidopsis. Hamidinekoo *et al.* 2020. Gigascience. https://doi.org/10.1093/gigascience/giaa012
- Integrated Phenomics and Genomics reveals genetic loci associated with inflorescence growth in *Brassica napus*. *Williams* et al. 2023 BioRXiv. doi: <u>https://doi.org/10.1101/2023.03.31.535149</u>
- DeepCanola: Phenotyping Brassica Pods Using Semi-Synthetic Data and Active Learning. *Van Vliet, Atkins* et al., under revision to Computers and Electronics in Agriculture.

## anl50@aber.ac.uk / jhd2@aber.ac.uk (with Chuan Lu, Computer Sci)

#### Summary

Why is fruit formation sensitive to ambient cold/heat.

#### Background

Fruit development is profoundly affected by temperature – and therefore climate change. GWAS allows us to survey *and ultimately understand* natural variation for how plants respond to environmental variables such as ambient cold and heat. Using Arabidopsis as a model system, the project will explore variation in fertility and fruit development as a function of ambient temperature. Several variants of this project are possible, with different collections or mapping populations, and different defined stresses. The student will be trained in both genetics/genomics and computer vision/Al.







### Aims

To screen genetically defined populations (Arabidopsis accessions collected from across the world, or biparental mapping populations) for fruit formation at 2 different but ambient temperatures. 22 and 32 C are illustrated but other combinations such as 4 / 8 / 15 and 22 are possible. Fruiting stems will be imaged and computer vision/AI approaches used to extract trait information.

#### Methodology, techniques and training

**Transferrable:** genotyping techniques (GWAS/QTL mapping), microscopy, image analysis with AI. Depending on interests, could focus on AI and computer programming.

**Plant specific:** plant developmental analysis, genetics and mutant analysis of Arabidopsis models. Production of transgenic Arabidopsis, phenotyping.

#### Lab References

32°C

- DeepPod: a convolutional neural network based quantification of fruit number in Arabidopsis. Hamidinekoo *et al.* 2020. Gigascience. <u>https://doi.org/10.1093/gigascience/giaa012</u>
- Uncovering the genetic basis of competitiveness and the potential for cooperation in plant groups B <u>Biernaskie</u> et al 2025 <u>Proceedings of the Royal</u> <u>Society B</u> 292(2042):20241984 DOI: <u>10.1098/rspb.2024.1984</u>
- Unlocking the power of AI for phenotyping fruit morphology in Arabidopsis
  Atkins et al (2025) GigaScience 14, giae123

#### Summary

Water holding capacity is fundamental to the ecology of and carbon storage in temperate peat bogs. The mechanisms are very poorly understood. The moss Sphagnum contributes to water holding, both during its life time and as it decomposes. Projects associated with the biology of moss water responses , water transport and the role of diverse pore size could be designed to fit student interest and learning requirements



Figure 1. DeepBog – a deep learning pipeline being developed to estimate sphagnum moss density and health from smart phone images. From van Vliet, et al in prep

#### Aims

To identify characteristics of the moss that contribute to water holding and movement within the upper "biocrust" of the bog. Experiments could be designed to suit lab or field.

#### Methodology, techniques and training

**Transferrable:** microscopy, microCT scanning, EM and associated image analysis.

Plant specific: plant growth, phenotyping.

#### Lab References

- Variation in Water-Holding Capacity in Sphagnum Species Depends on Both Plant and Colony Structure van de Koot et al (2024) <u>Plants</u> 13(8):1061 DOI: <u>10.3390/plants13081061</u>
- Molecular and physiological responses to desiccation indicate the ABA pathway is conserved in the peat moss, Sphagnum Nibau et al (2022) Journal of Experimental Botany <u>10.1093/jxb/erac133</u>
- Development of an Image Analysis Pipeline to Estimate Sphagnum Colony Density in the Field van de Koot et al (2021) Plants 10(5):840 <u>10.3390/plants10050840</u>

## jkb@aber.ac.uk / jhd2@aber.ac.uk

#### Summary

Drone-based surveys of vegetation important for both ecology and agronomy. High resolution camera's mounted on drones can in theory provide detailed image data on plant health and species composition, that could replace labour intensive botanical surveys. However, the use of these approaches remains challenging so this project will evaluate approaches to improve the reliability of image-based composition on commercial and species-rich grassland swards.







*Figure. Estimating species composition from drone: example plots with known grass-clover mixtures* 

#### Aims

To test image based methods for grassland analysis.

#### Methodology, techniques and training

**Transferrable:** drone image analysis, computional image analysis, AI. Potential advanced UAV training for students with previous drone experience and CAA licence holders

Plant specific: species identification.

#### References

- Semi-Automated Field Plot Segmentation From UAS Imagery for Experimental Agriculture Robb et al., (2020) <u>Frontiers in Plant Science</u> 11 DOI: <u>10.3389/fpls.2020.591886</u>
- UAV Remote Sensing for High-Throughput Phenotyping and for Yield Prediction of Miscanthus by Machine Learning Techniques. Impollina et al., (2022) <u>Remote Sensing</u> 14(12):2927 DOI: <u>10.3390/rs14122927</u>

## dae51@aber.ac.uk / jhd2@aber.ac.uk (with Candida Nibau, Chuan

### Lu, Computer Sci)

Summary

MicroCT scanning and seed biology

Background CT scanning can provide internal information on 3D biological (and other) structures without the need to destructively dissect or section them. CT therefore has the potential for streamlining much biological analyses, allowing us to scale investigations to include (a) very large numbers or (b) a wide diversity of different species. The application of CT to seed biology can open up new avenues of enquiry, from evolution of diversity to domestication and breeding



Figure microCT scanning of wheat grain within its floral organs. A deeplearning CNN was trained to recognise different parts of the structure and to measure them

#### Aims

To explore the potential of CT scanning in illuminating a question in seed biology. Although the lab focuses on domesticated crops such as cereals and oilseeds, there is the potential to apply this technology to plant diversity, seed pests, etc and student interests can be accomodated

#### Methodology, techniques and training

Transferrable: microscopy, image analysis

Plant specific: plant development, particularly of seeds.

### Lab References

- Ectopic Expression of Triticum polonicum VRT-A2 Underlies Elongated Glumes and Grains in Hexaploid Wheat in a Dosage-Dependent Manner Adamski et al., (2021) <u>The Plant Cell</u> 33(7) DOI: <u>10.1093/plcell/koab119</u>
- μCT trait analysis reveals morphometric differences between domesticated temperate small grain cereals and their wild relatives Hughes et al (2019) <u>The</u> <u>Plant Journal</u> 99(1):98-111 DOI: <u>10.1111/tpj.14312</u>
- Barley lys3 mutants are unique amongst shrunken-endosperm mutants in having abnormally large embryos Cook et al., (2018) <u>Journal of Cereal Science</u> 82 DOI: <u>10.1016/j.jcs.2018.04.013</u>
- Non-Destructive, high-Content analysis of wheat grain traits using X-ray micro computed tomography Hughes et al., (2017) <u>Plant Methods</u> 13(1) DOI: <u>10.1186/s13007-017-0229-8</u>

## jhd2@aber.ac.uk (with Sarah Higgins, Information studies)

### Summary Herbarium Al

Background Herbarium vouchers have been collected since the 1600's, documenting botanical diversity through time in a physical format. Globally, they amount to several 100 million samples and many have been digitised. Local collections in Aberystwyth include a large crop herbarium (gogerddan campus) that focuses on core crops such as forages and oats and a more general diversity collection on Penglais.



Aims: to develop and evaluate computer vision methods to extract useful information from Herbarium vouchers. The crop herbarium (1919-1970) spans the core years of the Green Revolution, particularly the introduction of artificial fertilizers so could be used to ask whether new farming methods led to differences in elemental composition

#### Methodology, techniques and training

**Transferrable:** photography/digitialisation, image analysis, Computer Vision/AI, XRF elemental analysis

Plant specific: plant development, herbarium voucher creation and curation

#### Lab References

• No specific reference – this is a new project but uses imaging and Al techniques developed for others (see above)

Figure Local collection of vouchers

## Manfred Beckmann, David Warren Walker and Amanda Lloyd Advanced Methods for Innovation in Nutritional and Optimised Tea Extraction Applications

A project focusing on developing bioactive-rich tea extracts using advanced, sustainable processing methods. This project aims to optimise extraction techniques to retain bioactive compounds, creating high-value functional ingredients for the food and nutraceutical sectors.

## Aims:

- To develop novel extraction methods that maximise the retention of bioactives in tea.
- To characterise the bioactive profile of tea using advanced metabolomic techniques.
- To create scalable, sustainable processes for producing functional tea extracts.
- To explore market applications in functional foods and nutraceuticals.

## Manfred Beckmann, Alun Hughes and Amanda Lloyd

## Valorisation of Spent Mushroom Substrate: Sustainable Bioactive Discovery

Spent mushroom substrate (SMS), a by-product of mushroom cultivation, is typically discarded despite its rich lignocellulosic and biochemical content. This project aims to transform SMS into valuable bioethanol and bioactive compounds using simultaneous saccharification and fermentation (SSF) and advanced analytical techniques. This project supports circular economy principles and contributes to renewable energy and sustainable agriculture goals.

## Aims:

- To optimise SSF processes for converting SMS into bioethanol.
- To identify and extract bioactive compounds such as polysaccharides and sterols from SMS.
- To evaluate the commercial potential of SMS-derived products in energy and health sectors.
- To support sustainable waste management and resource efficiency in mushroom farming.

## Metabolomic pathways involved in kombucha's health effects

## **Background:**

Kombucha, a fermented tea beverage, has gained popularity for its potential health benefits, including anti-inflammatory, antioxidant, and gut microbiome-enhancing properties. We have pre-existing data where we investigated the physiological and psychological effects of daily kombucha consumption over 8 weeks in healthy adults and where we collected biofluids (bloods and urines) over the intervention. The research explored kombucha's impact on metabolism, stress, inflammation, and overall well-being using both self-report and biological measures.

## Aims:

To characterise longitudinal changes in urinary and plasma metabolomics, particularly short chain fatty acids (SCFAs), in response to kombucha consumption. To identify metabolomic signatures associated with improved quality of life and psychological well-being.

To correlate metabolomic changes with stress biomarkers (salivary cortisol) and physiological responses to the Maastricht Acute Stress Test (MAST).

## Metabolomic changes as biomarkers of gut-brain axis modulation

## **Background:**

This study explores the effects of a postbiotic and a green tea nutraceutical supplementation on cognitive function, gut health, and overall well-being in adults aged 55 and over. The project will use pre-existing data from two trials using EEG and behavioural tasks to assess cognitive changes and biological sample data including inflammation markers, short chain fatty acids and metabolomic markers to evaluate gut-brain axis changes.

## Aims:

To analyse metabolomic shifts, including SCFAs and other gut-derived metabolites, following supplementation in older adults.

To investigate associations between metabolomic profiles and cognitive performance, sleep quality, and mental well-being.

To integrate EEG and metabolomics data to explore biochemical correlates of gut-brain axis activity.

### **Optimising CRISPR-based genome editing in plants.**

CRISPR/CAS9 gene editing is an extremely powerful tool in life sciences, allowing precise and targeted editing of plant and animal genomes. This technology has the potential to help deliver stress or disease tolerant crops, remove allergens, and increase the nutritional value of foods. We are developing next-generation transgene-free gene editing approaches that are applicable across a wide range of plants. This project will use an *Arabidopsis thaliana* reporter line to compare gene editing efficiency in plants with different growth regimes. This project is lab based and will involve molecular genetics (DNA extraction, PCR, gel electrophoresis, Sanger sequencing) and scoring of gene editing efficiency (fluorescence microscopy, image analysis).

### Is The Synaptonemal Complex Required for Meiotic Stability in Polyploid Arabidopsis

This project explores the role of the synaptonemal complex in a polyploid plant species using targeted genome editing. In diploid *Arabidopsis thaliana*, the synaptonemal complex protein ZYP1 is known to be dispensable for successful meiosis and fertility. However, in the allopolyploid *Arabidopsis suecica*—a species formed by hybridisation and whole-genome duplication—we hypothesise that ZYP1 may be essential for stabilising homologous pairing and ensuring fertility. The student will use CRISPR-Cas9 to target ZYP1 homologs in *A. suecica*, and will begin by screening already established transgenic lines for induced mutations using PCR and sequencing. Mutants will then be assessed for defects in meiosis and fertility through phenotypic analysis, including pollen viability and seed set. This project combines molecular genetics and cytological techniques to address a fundamental question in polyploid biology, and is ideal for students interested in genome editing, plant reproduction, and evolutionary genetics.

#### Unravelling Meiotic Gene Expression Dynamics with Single-Cell RNA Sequencing in Arabidopsis

This project offers an opportunity to apply cutting-edge single-cell RNA sequencing (scRNA-seq) to study the dynamic transcriptional landscape of plant meiosis. The student will work with a newly generated scRNA-seq dataset derived from *Arabidopsis thaliana* meiotic-stage floral tissue. The project will focus on using computational tools to process, cluster, and analyze single-cell transcriptomes, with the goal of reconstructing a pseudo-time developmental trajectory of meiosis. This will allow the student to identify stage-specific gene expression patterns and uncover regulatory programs that are obscured in bulk RNA-seq data. Through this project, the student will gain valuable experience in bioinformatics, developmental biology, and plant reproductive genetics, contributing to a better understanding of how gene expression is orchestrated during one of the most critical phases of plant reproduction.

#### Endosymbiosis and horizontal gene transfer: following the ongoing contribution of organelle DNA to nuclear genomes.

This project investigates the ongoing genomic legacy of endosymbiosis by characterising how organelle DNA continues to shape nuclear genomes. Organelle-derived DNA insertions—often overlooked in traditional genome assemblies due to the exclusion of chloroplast and mitochondrial reads—are now more readily detectable thanks to long-read sequencing technologies. In this project, the student will survey over 70 *Arabidopsis thaliana* long-read genome assemblies to identify and compare nuclear insertions of organelle DNA (NUPTs and NUMTs). Using a combination of bioinformatic tools and comparative genomics, the student will assess the frequency, size, divergence, and genomic context of these insertions—for example, whether they occur near genes, in repetitive regions, or in specific chromosomal domains. A key aim is to understand their evolutionary dynamics: are insertions conserved across accessions? Do large insertions break down over time via deletion and fragmentation? This project offers a rich blend of computational and evolutionary genomics, shedding light on how nuclear genomes incorporate and remodel organellar DNA over time.

# Understanding the perception of pest insects to improve control devices (<u>rds5@aber.ac.uk</u>)

Pest insects cause damage to crops, livestock, and human health, directly by their feeding activities, and indirectly by spreading disease. To mitigate this damage, devices are needed to monitor or control pest insects, and these often work by providing attractive stimuli (e.g. colours, lights, odours) to lure the insects. However, insects perceive the world quite differently to humans, and only by understanding their perceptions of such stimuli can we devise or improve effective control devices (https://doi.org/10.1002/ps.7790). A variety of projects are available investigating pest flies, or pest wood-boring beetles. Projects range from theoretical modelling of insect perception, through to practical studies of trap effectiveness. Please contact me to discuss possibilities.

## **Computing for microbiology**

mts11@aber.ac.uk

A variety of projects could be available using bioinformatics and computational methods to explore large microbial genomic data sets. They can involve genome, transcriptome or metagenome analysis depending on data sets currently available. Microbes of medical, veterinary, or agricultural importance can be studied. These are most suitable for students possessing good statistical, numerical, or computing skills, or at least very keen to learn such computational skills. The projects will usually involve scripting with Python or R, and the use of Linux and High-Performance Computing clusters. Possible topics covered may include horizontal gene transfer, genome architecture of plant endophytes, insertion and mobile elements, anti-microbial resistance, the functional prediction of proteins, comparative genomics, and microbiomes. Projects involving modelling or computer simulations are also possible.

## Balancing the Bowl: Unlocking Nutrition and Tackling Antinutrients in Seeds aig15@aber.ac.uk



This MRes project investigates the nutritional and antinutritional components of major cereals, and legumes. It aims to quantify essential nutrients such as proteins, vitamins, and minerals, alongside antinutritional factors like phytic acid and tannins. The study employs biochemical assays and analytical techniques to evaluate nutrient bioavailability and identify limiting factors in human absorption. Variations among cereal species and cultivars are analyzed to determine genetic and environmental influences on grain quality. Strategies for improving nutritional value, such as breeding, fermentation, or biofortification, are also explored. The findings will contribute to cereal crop improvement efforts and inform nutritional guidelines for food security and public health.

# Investigating heat stress-induced breakdown of self-incompatibility in plants <u>mub@aber.ac.uk</u>

Self-incompatibility (SI) is a key mechanism that prevents self-fertilization in many flowering plants, maintaining genetic diversity and reproductive success. However, environmental factors like heat stress can weaken SI, leading to unexpected selffertilization. This project aims to investigate how elevated temperatures disrupt the SI response, focusing on the well-characterized *Papaver rhoeas* SI system. Specifically, it will examine how heat stress affects the interaction between the PrpS receptor and PrsS ligand, as well as key downstream signalling events, including Ca<sup>2+</sup> signalling, reactive oxygen species (ROS) production, and programmed cell death (PCD) in pollen. Understanding these mechanisms is essential for predicting how climate change may impact plant reproduction and hybrid breeding strategies. The student will gain experience in controlled pollination experiments to determine the contributions of pollen and pistil to SI breakdown. The student will also carry out some cell biology studies to start evaluate the impact of increased temperatures to Ca<sup>2+</sup> and ROS dynamics in pollen tubes. This research has important applications in crop breeding, fertility control, and climate resilience, providing insights into how SI breakdown could be managed to support sustainable agriculture.

# Investigating the impact of environmental stress on forage grass cell walls and digestibility

## mub@aber.ac.uk

Forage grasses form the foundation of UK livestock nutrition, but climate change is increasing the frequency of extreme weather events that can alter their growth and quality. A major factor influencing forage digestibility is the composition and structure of cell walls, which make up ~70% of plant dry weight. This project will examine how environmental stress affects cell wall integrity and digestibility, focusing on the role of reactive oxygen species (ROS) and oxidative cross-linking in stress-induced modifications. Understanding these changes is crucial for developing resilient forage crops that maintain nutritional value under variable climate conditions. The student will use fluorescent probes (DCFH-DA, Amplex Red) and confocal microscopy to track ROS accumulation in stressed plants, alongside spectrophotometric assays to quantify peroxidase activity and oxidative cross-linking. This research will provide valuable insights into how stress impacts forage quality, with implications for livestock productivity, sustainable agriculture, and climate adaptation strategies.

## Use of historical histology collections to investigate to questions of anatomy

## sor24@aber.ac.uk

There are historical collections of microscope slides of whole embryos from different developmental stages. Some species included are rare and/or protected, and therefore the these collections can represent rare, scientifically valuable material that is under-utilised.

It has become routine to create 3D models from 2D datasets, and this allows researchers to unlock a new dimension of quantitative data from specimens. There are also methodologies for applying such an approach to histological datasets, but these variably require pre-sectioning steps (e.g. scanning or marking) to align slices, expensive software and/or hardware, and/or manually intensive processes. I am interested in the development or a methods that requires minimal user-input, using open-source software and standard computing power, that can be applied to existing histological sections.

This project aims to develop a workflow for investigating anatomy via historical histological collections. It would suit a candidate with interest and knowledge of vertebrate histology, and with good computer skills.

# Innovation and cognition of invasive and native crustacea sad31@aber.ac.uk

Innovation and cognitive ability are thought to be key traits associated with successful invasion potential of species, the ability to adapt behaviour to access new resources and new environmental challenges. However, work to date has focused on vertebrates, including birds and mammals. The proposed project will compare these traits in native and invasive crustaceans. The student will gain experience in experimental design, laboratory work, data analysis and presentation in comparative cognition.

# Could snails be sentient?

## sad31@aber.ac.uk

There is a growing interest in the potential for sentience in invertebrates, which may impact on how we treat these animals from a welfare perspective. Cephalopods are currently protected in research under home office regulation, and decapod crustaceans have recently been recognised as sentient by the U.K. government. Gastropods are a very large phylogenetic group, used in both farming and research; however, we lack the evidence needed to determine whether this group could be considered sentient. The student will have the opportunity to explore areas of interest within this general area, for example if we can demonstrate support for 'pain' in gastropods, or whether they are capable of more complex cognitive processes generally assumed to be indicators of sentience.

## Identifying schistosome drug targets from genomic dark matter. <a href="https://www.weighted.ic.ac.uk">krh@aber.ac.uk</a>

Summary:

*Schistosoma mansoni* causes schistosomiasis, a parasitic disease that is primarily controlled by chemotherapy with praziquantel. IN the absence of a vaccine and due to well-documented limitations of praziquantel, new drugs are urgently-needed to sustain schistosomiasis control into the 21<sup>st</sup> century. We propose to identify new schistosome drug candidates from 30% of the parasite's protein coding genome that has limited similarity to the human genome (Schistosome Genomic Dark Matter). Using a variety of bioinformatic and computer science-driven approaches to identify compounds predicted to interact with the schistosome's dark matter, the student will identify and source compounds for validation in ex vivo, whole-organism assays.



Environmental DNA survey of freshwater snails on farmland to assess the risk of liver fluke transmission in areas where *G*. *truncatula* is absent. <u>raj22@aber.ac.uk</u>

Galba truncatula is the main intermediate snail host of liver fluke (F. hepatica) and it is assumed that if it is absent from an area then liver fluke cannot transmit. Our current research shows that this snail is absent from areas commonly assumed to be fluke transmission sites by farmers which indicates that fluke transmission risk may be lower than anticipated on certain farms. However, other snails, including O. glabra and R. balthica can also transmit fluke, although their presence on farmland is somewhat uncertain. Using an eDNA metagenomic analysis approach, we will aim to identify which other amphibious snails are present on Welsh farmland with focus on those that may transmit fluke.

# Balancing veterinary disease control with biodiversity: Surveying amphibian presence in liver fluke infection sites via environmental DNA metagenomic analysis.

## raj22@aber.ac.uk

As chemical control of liver fluke (*F. hepatica*) becomes increasingly difficult due to drug resistance and climate change, there is growing interest in using land management strategies to limit fluke infection opportunities. However, these strategies which may include draining, fencing, tree planting or avoidance of grazing may impact other wildlife species that also inhabit these sites. However, fluke infection risk areas are poorly defined and there is limited knowledge of their value to wildlife species and overall biodiversity. Using an eDNA metagenomic approach this project will identify which amphibian (or other groups) species are commonly present in such sites which will inform of how these areas should be managed in future.

# Invasive Chinese mitten crabs as food and behavioural enrichment for zoo animals

## jei@aber.ac.uk

The Chinese mitten crab *Eriocheir sinensis* is one of the most damaging invasive non-native species in Europe. In the River Dee, North Wales, efforts are being made to trap mitten crabs as they migrate downstream to breed. This raises the problem of how to dispose of the captured crabs in a sustainable way. As invasive non-native species, they cannot be sold commercially. This project would investigate whether mitten crabs trapped in the River Dee are suitable to feed to zoo animals, in terms of contamination and food quality. It might also be possible to investigate whether whole, dead mitten crabs provide behavioural enrichment to zoo animals who would normally eat crabs (e.g. Asian short-clawed otters). Students would gain experience in laboratory analysis of food quality and behavioural enrichment studies of zoo animals.

# Origins of invasive non-native species

# jei@aber.ac.uk

Discovering the origins of new introductions of invasive species in Wales is a research priority, as it can inform efforts to control the spread of non-native species through biosecurity measures. This project will use population genetic methods to investigate the origins of recently established priority invasive non-native species in Wales. These may include (for example): American slipper limpet in Cardigan Bay Chinese mitten crab in the River Conwy

Carpet sea squirt in Milford Haven

Students will gain experience in molecular laboratory work and may also have opportunities for marine and/or freshwater fieldwork.

# Toxicity of mercury to the fungal symbionts of leaf-cutting ants

# jei@aber.ac.uk

The use of mercury in artisanal gold mining is a major source of pollution in tropical rainforests. Leaf-cutting ants are among the most abundant and ecologically important organisms in neotropical rainforest ecosystems. They depend entirely upon symbiotic fungi which they farm in underground nests and feed with leaves cut in the surrounding rainforest. This project will aim to establish whether the fungi cultivated by leaf-cutting ants are harmed by exposure to the levels of mercury encountered in rainforests adjacent to artisanal gold mines. Students will gain experience in laboratory culture of fungi and ecotoxicological methods

## Understanding helminth extracellular vesicles

## rom@aber.ac.uk

Parasitic helminth extracellular vesicles (EVs) are enriched with pathogen molecules, which could potentially be utilised for improved control of helminths. Helminth EVs are now known to function in numerous ways such as promoting or inhibiting host immunity, transporting molecules to recipient cells and even to detoxifying anthelmintic drugs. Therefore, understanding EVs from helminth parasites will aid our understanding of host parasite interactions whilst potentially leading to novel control options such as vaccinations or improved diagnostics. Projects in this area will develop skills in classical parasitology, EV purification and analysis, and a variety of omic technologies such as proteomics and peptidomics.



# Lignocellulose degrading genes in fungi

# gwg@aber.ac.uk

A large number of fungal genomes have been sequenced in recent years. I have an interest in phenoloxidase genes which are important in the degradation of lignin, and in the defence of fungi against reactive oxygen species. Possible project areas include data-mining of the ca. 35 fungal genomes now available for genes involved in lignin and cellulose degradation.

# **Insect-fungus interactions**

# gwg@aber.ac.uk

Insects are important vectors of fungal spores. We are investigating the way in which insects can mediated the dispersal of yeasts and other fungi in nature. Possible project areas include examination of insect populations on mushrooms, vectoring of yeast and fungal spores by insects, consumption of mushrooms by slugs.

# Can fungal metabolites modify insect behaviour? gwg@aber.ac.uk

Secondary metabolites have very different effects on different animal species (e.g., theobromine in chocolate is toxic to dogs). Secondary metabolites in fungi may be toxic or psychoactive in humans but the effects of these compounds on other animals is less well -understood. this project will explore the effects of fungal metabolites on the behaviour of Drosophila melanogaster.

# DNA barcoding of fungi

## gwg@aber.ac.uk

Many organisms can be difficult to identify based on morphological features alone. This project will use DNA extraction/PCR/DNA sequencing to identify fungi (choice of specific group is flexible). Such approaches can reveal cryptic speciation and sometime discover species new to science.

# Spore survival in soil

## gwg@aber.ac.uk

Fungal spores deposited in soil often need to undergo a period of dormancy before germination and growth. In order to germinate at the appropriate time, fungal spores need to respond to environmental signals, notably external nutrient. The ability of fungal spores to survive in soil and to respond to nutrient stimuli will be examined using soil microcosms.

# **Lichens on Gravestones**

## gwg@aber.ac.uk

Using historic photographs from 1970s, the diameter of lichen thalli (and thus growth rate over 40-year period) will be measured. Project requires car transport to reach field sites near Porthmadog

# Indoor aerobiology

# gwg@aber.ac.uk

Using simple air samplers, air spora in various indoor environments will be quantified and the abundance/diversity of fungal spores quantified. Comparisons will be made between difference room usage and may include farm buildings, horse stables etc.

# **Conservation management of grassland fungi**

## gwg@aber.ac.uk

Waxcaps and other fungi found in nutrient-poor grassland habitats are a valuable and threatened component of European biodiversity, having declined drastically in abundance due to habitat loss. In order to be able to conserve these fungi more information is needed about their ecology, in particular what management regimes are conducive to their growth. This project will investigate the effect of different sward management regimes (e.g., hay cutting etc.) on the diversity of mushroom formation.

# Effect of soil fungi on germination of seeds of invasive plants gwg@aber.ac.uk

Seeds of many species of plant show differences in germination rate according to whether they are placed in sterile compost or native soils. It is believed that the presence of certain fungi are involved in mediating this phenomenon.

## Potential drugs from Seaweeds

## ifp@aber.ac.uk

As many as 40 to 50 % of drugs currently used to treat human maladies are derived from terrestrial organisms. However, there is a requirement to encompass even greater biological biodiversity to tap into novel biochemical variation which will include many new compounds with pharmaceutical potential. The sea represents an almost untapped resource as it contains over 80 % of all life forms on Earth.

Preliminary research on Bladder Wrack (*Fucus vesiculosus*) has identified a range of (poly)phenolics. These often have antioxidant and UV-absorbing properties which are recognised by the pharmaceutical, nutraceutical and cosmetic industries. The novelty of seaweed species opens up the possibility of new IP, process developments and product differentiation. In this project, we propose to begin to assess the pharmaceutical potential of four locally sourced seaweed species; Bladder Wrack (*Fucus vesiculosus*); Knotted wrack (*Ascophyllum nodosum*), Toothed Wrack (*Fucus serratus*) and Gutweed (*Enteromorpha intestinalis*). The student will extract natural products from seaweed and extensively characterise these by HPLC, MS and NMR. The extracts will be assessed for anti-helminthic and anti-inflammatory activities. Extracts will be fractionated and defined anti-helminthic and anti-inflammatory activity related to discrete biochemicals.