**University of Leicester**

**BBSRC MIBTP Studentship Project 2025-6 entry.**

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**Section 2 – *Project Information***

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| **Project Title** | Transgenerational epigenetic consequences of pollution exposure. |
| **Project Summary** | |
| Environmental insults such as pollution can cause transgenerational negative health outcomes in both wild animal populations and humans. These outcomes can be mediated by epigenetic changes, such as changes in DNA methylation. However, transgenerational epigenetic inheritance is difficult to study in mammals/humans due to their long generation times and need for ethical practices. We therefore use New Approach Methodologies, such as ecologically responsive invertebrates, to identify the molecular mechanisms underpinning transgenerational health outcomes.  This project has two related aims which will be carried out in the marine amphipod, *Parhyale hawaiensis*. The first is to determine if pollution-induced DNA methylation changes in an individual can act as biomarkers, predicting the health of offspring. The second is to determine if these DNA methylation changes play a causative role in offspring health.  Objectives and methods:   * Identify pollution-induced phenotypic changes in adult and offspring *P. hawaiensis*: you will use ecotoxicology techniques to carry out chemical exposures, measuring fitness (growth, fecundity) and health (wound healing – ability to regenerate limbs).      * Identify pollution-induced DNA methylation changes in adult and offspring *P. hawaiensis*: using Nanopore Sequencing you will identify pollution-induced DNA methylation changes via bioinformatic analysis.      * Determine if pollution-induced DNA methylation changes predict offspring health: using machine learning you will integrate the above datasets to identify potential multigenerational biomarkers of health.      * Optional: depending on your interests, you can either pursue further machine learning models with additional ecotoxicology data or you can carry out CRISPR/Cas9 DNA methylation editing to see if epigenetic changes play a causative role in health outcomes.   Project Environment  This is a multidisciplinary project which will provide you with skills in ecotoxicology, bioinformatics and molecular epigenetics – opening doors for a career in a wide variety of sectors. You will also be part of the Centre for Environmental Health and Sustainability at Leicester and a member of both the Neurogenetics group and Applied Population Genetics group. These groups consist of >20 group leaders, >15 postdocs and >30 PhD students, meaning you will have a wide network of support and the ability to learn from a variety of labs.  Techniques that will be undertaken during the project  - Ecotoxicology using New Approach Methodologies (*Parhyale hawaiensis*)  - Molecular biology: DNA/RNA extraction etc.  - Whole Genome Bisulfite Sequencing / Nanopore / RNA-Seq  - Bioinformatic analysis (R / Bash / Python / Machine Learning)  - Gene editing using CRISPR/Cas9 | |
| **References** | |
| Averof (2022) The crustacean *Parhyale*. *Nature Methods.* 19, 1014-1016.    Chaturvedi et al. (2023) The hologenome of *Daphnia magna* reveals possible DNA methylation and microbiome-mediated evolution of the host genome. *Nucleic Acids Research*. 51, 9785-9803.  Saunderson, et al. (2023) CRISPR/dCas9 DNA methylation editing is heritable during human hematopoiesis and shapes immune progeny. *PNAS*. 120, e2300224120    Takahashi et al. (2023) Transgenerational inheritance of acquired epigenetic signatures at CpG islands in mice. *Cell*. 186, 1-17. | |