

Tracking the “Ghost” of the Genome: The epigenetics of pollution adaptation in an environmental sentinel

Supervisors:

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Project description: It has been shown that “epigenetic” changes in the composition and physical structure of DNA (e.g. DNA methylation, histone modification and non coding RNA production) can affect the activity of genes to produce long-lasting changes in expression. In this way, epigenetic mechanisms are thought to influence many important aspects of biology. The aim of this PhD project will be to investigate how epigenetic DNA modifications are involved in the adaptation to pollution. The work will focus on the responses of earthworms, because these organisms are a very common and ecologically important group that are often intimately exposed to soil pollution. The species to be studied, *Lumbricus rubellus*, also has a small and sequenced genome with a high degree of DNA methylation. It can also be used for long term multi-generational environmental genomics studies.

To understand the contribution of the epigenome to pollutant adaptation in *L. rubellus* earthworms, the candidate will undertake laboratory and field work related to the following tasks.

- i. Identify the epigenetic (cytosine methylation, histone modification and microRNAs) modifications cause by within generational and multigenerational exposure to pollutants and relate these to profiles for drugs known to effect DNA methylation and histone modification.
- ii. Determine the spatial association of epigenetic modification with loci of genes displaying altered expression levels.
- iii. Characterise the specificity, dose dependency and timing of epigenetic changes in field populations living at clean and polluted field sites.
- iv. Derive the functional relationship between epigenetic change and adaptation responses.

To complete the work, the candidate will work learn a range of laboratory methods to assess behavioural and ecological response to pollution. Additionally the student will also learn a range of cutting edge genetic analysis methods such as bisulphide DNA sequencing, Q-RT-PCR and DNA methylation mapping under the guidance of expert staff. Fieldwork mainly in the UK and also potentially overseas (the Azores, and continental Europe) will be a vital part of the project.