Applying eDNA/Metabarcoding for the Biomonitoring and Assessment of **Environmental Land Management** schemes (ELMs)



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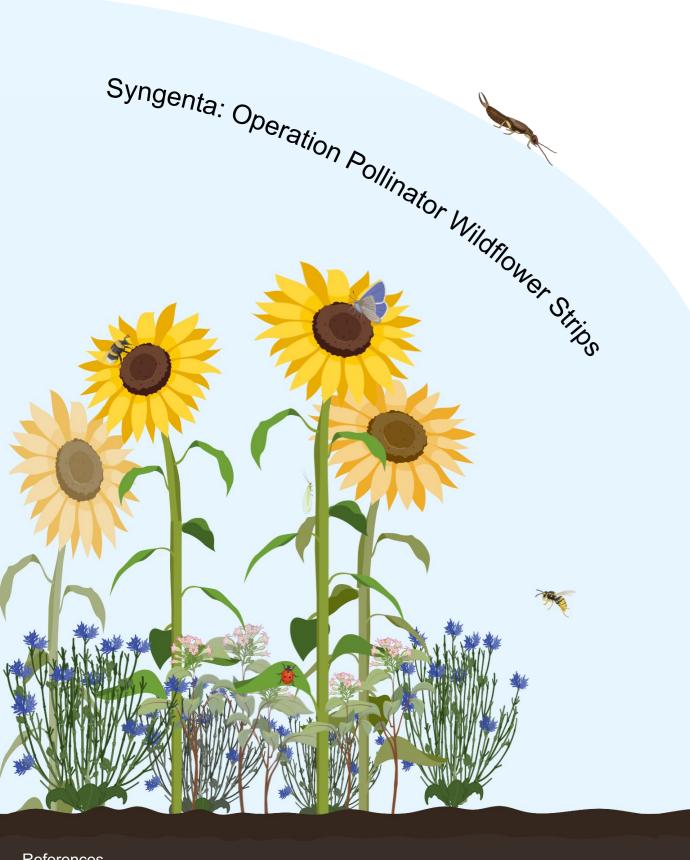
Background

- The biodiversity crisis is a great threat to agriculture, due to the ecosystem services species deliver [1].
- ELMs are a UK Government scheme which aim to boost biodiversity, improve water quality and combat climate change [2].
- Metabarcoding has developed rapidly over recent years, making it a viable tool for identifying species in bulk samples [3]
- Assessing ELMs using metabarcoding could be a more efficient method for measuring biodiversity, with emphasis on pollinators, natural pest predators and crop pests.

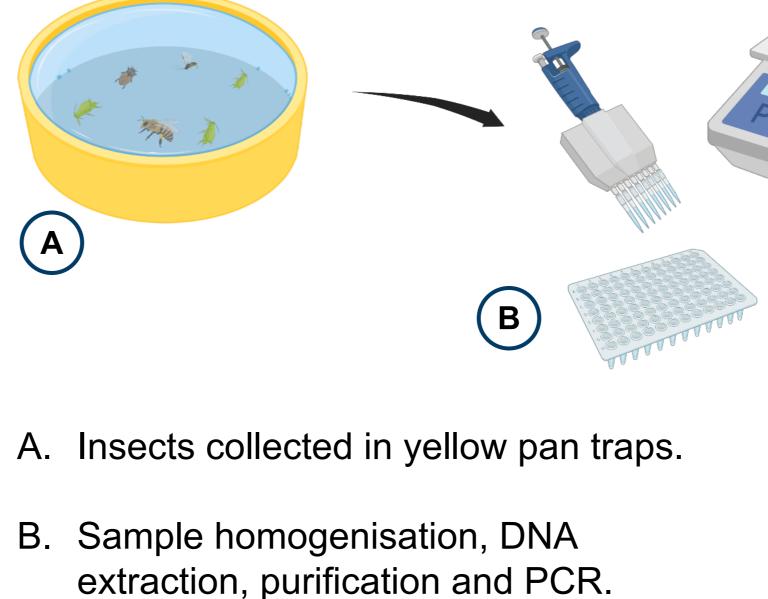
Examples of ELMs: Buffering in-field ponds Hedgerow management Beetle banks

Aims

- How does insect biodiversity (pest and beneficial insects in particular) differ between managed crop and non-crop habitats?
- To what extent can eDNA metabarcoding be used as an agronomy tool for the biomonitoring and surveillance of pests and diseases?
- What are the spatial and temporal effects on insect natural capital?



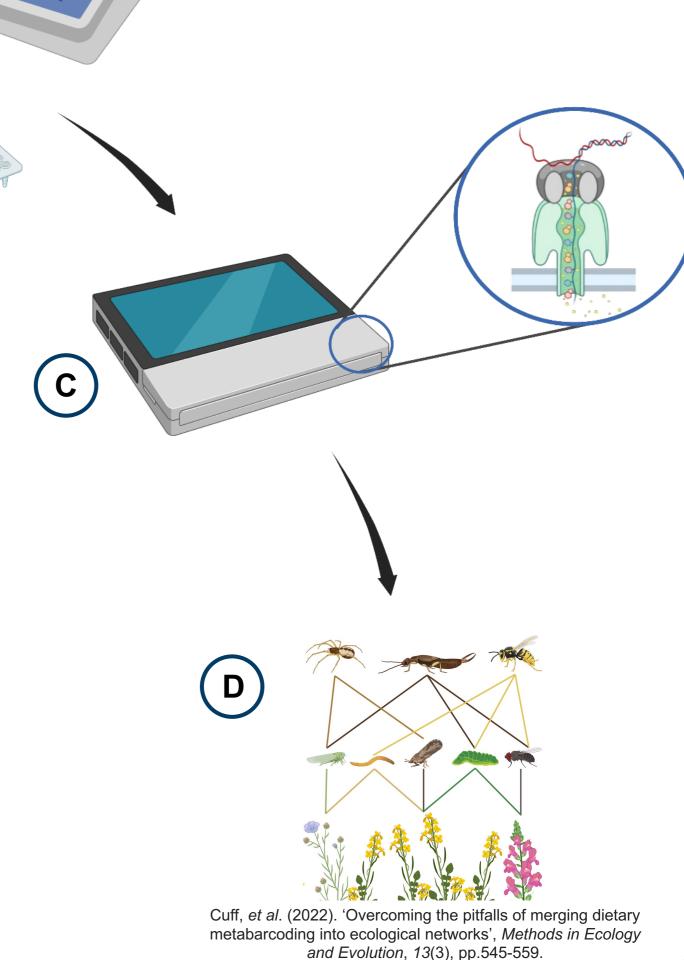
Methodology



C. DNA sequencing, for example with Nanopore:

- As strands of DNA feed through protein pores, the charge associated with each base is recorded and the bases (ATCG) are assigned.

Bioinformatics to identify species based on DNA fragments, and producing ecological networks.





2. Department for Environment, Food & Rural Affairs (2021). Environmental Land Management schemes: overview. 3. Petsopoulos, et al. (2021) 'Using network ecology to understand and mitigate long-term insect declines', Ecological Entomology, 46(4), pp. 693–698.