Reed Bed Use Within Scotch Whisky Distilleries to treat Wastewater: A New Toolkit to Help Maximise Performance

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Introduction

Natural (Fig. 1) and constructed wetlands/reed bed systems can act as 'filtration' systems to clean water, including treating whisky distillery byproducts. Among distilleries in Scotland (Fig. 2), while constructed versions of these systems are in use at some sites, there is significant scope to better understand and optimise their performance (Fig. 3).

Fig 1: Natural reed bed systems and eDNA sampling.

Fig 2: Whisky Distilleries in Scotland.

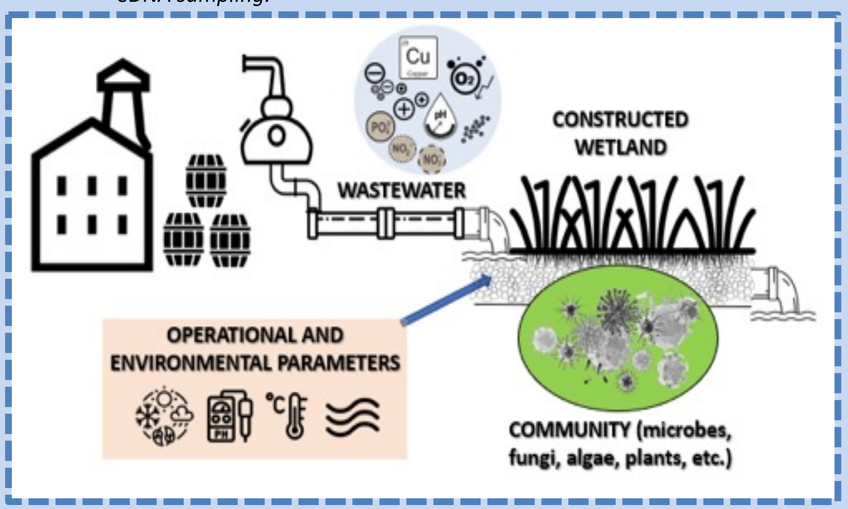

Fig 3: Physical, chemical and biological parameters that can affect reed bed treatment performance in combination.

Aim

To establish relationships between treatment performance, eDNA community and operational and environmental parameters – and in so doing, design a new 'toolkit' to help maximise the performance of constructed wetlands/reed bed systems.

Approach

- Commercial eDNA isolation kits (i.e., Qiagen DNeasy Powermax, etc.) are mainly used for eDNA extraction from water, soil, clay or fine sediment substrates. Since many constructed reed beds contain a gravel substrate, a new method is needed to optimise biota detachment and extraction protocols to attain maximal eDNA information (regarding community biodiversity) from gravels as part of the new toolkit (Fig. 4).
- In continuation, we will also compare biodiversity analysis between the third-generation MinION sequencing platform (Oxford Nanopore) and second-generation MiSeq (Illumina) platform to help us understand the performance efficiency of each system/bioinformatics pipeline for the sequencing-reading-annotation of eDNA extracted from gravel.

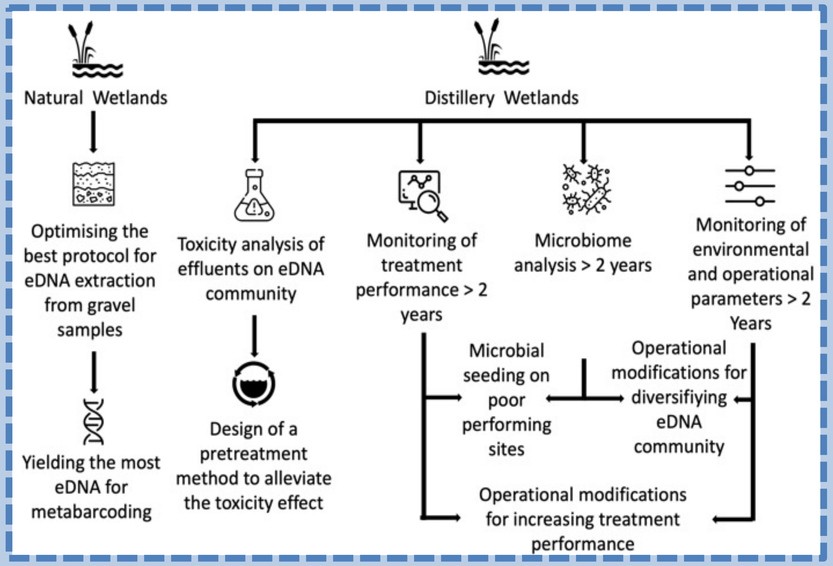

Fig 4: Key steps for the project.

Current Method Development

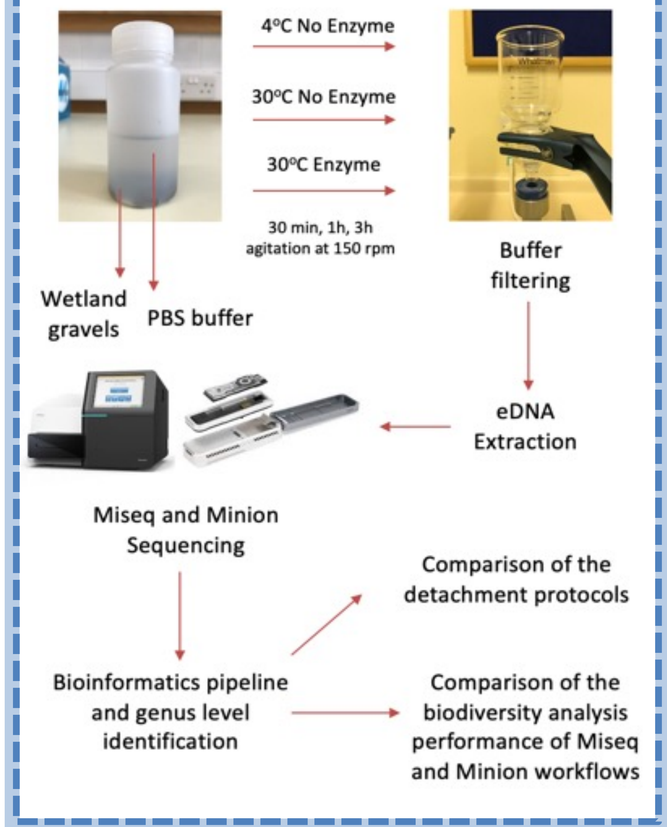

Fig. 5: Workflow for eDNA detachment and sequencing performance experiments.

Weber & Legge (2010) defined a method for the detachment of culturable bacteria from wetland gravel. However, this protocol was defined for community level physiological profiling (CLPP), not for eDNA isolation and metabarcoding. Here, we will evaluate the effect of temperature, agitation time, and enzymes (Lipase, Alpha Glucosidase, Beta Galactosidase) to elucidate which protocol works better in obtaining the best eDNA yield.

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