Optimising Microbial Communities for the Removal of Priority Micropollutants from Water

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Introduction

Widespread and constant release of organic micropollutants (OMPs), including pharmaceuticals, personal care products and pesticides into aquatic environments occurs primarily due to incomplete OMP removal during wastewater treatment (WWT)[1,2].

In surface and groundwater, OMPs persist in ng.L^{-1} to µg.L$^{-1.}$ concentrations with **unknown toxicity risks to aquatic organisms and the wider ecosystem**[3].

The toxicity of individual OMPs depends on complex abiotic and biotic factors[4].

A promising **green, inexpensive OMP degradation method is to utilise aerobic microorganisms as biofilters to degrade OMPs**[5].

Methods

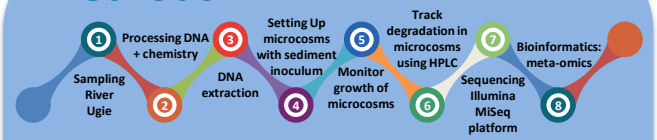

Figure 2 |Schematic diagram of research plan including sampling, processing and experiments.

To test their efficacy as biofilters, microbial communities from River Ugie sediments (**Fig. 1; Fig 3.**) were aerobically spiked with diclofenac (DCF, a non-steroidal anti-inflammatory drug) in lab-scale microcosms (**Fig. 4**) and the degradation was tracked over time. DCF was selected due to its ecotoxicity, resistance to breakdown in WWT and widespread aquatic presence[5].

Results

- Microcosms spiked with DCF have been sampled, HPLC samples are in queue for analysis. Expected result is partial to complete aerobic degradation of DCF.
- Pending analysis on HPLC, sequencing to be achieved in April 2020.

Future

Research Objectives: 1) Test whether taxa which are exposed to OMPs are degrading them. Using sediments from River Ugie, a priority Scottish catchment (**Fig. 1**).

2) Characterise the microbial community, enzymatic reactions and how the community composition changes following OMP exposure.

- Future experiments to be completed in line with **Fig. 2**. First of which is DNA extraction, PCR, Illumina sequencing and analysis to understand microbial community composition.
- Future work is to optimise microcosms for DCF removal, test degradation of other high priority OMPs, increase bioreactor scale and isolate and characterise OMP degrading taxa.

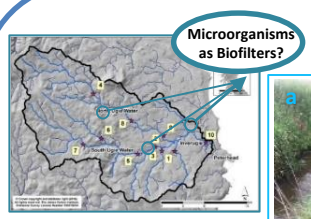

Figure 1 | Map of the River Ugie area from Zhang et al., 2018[6].

Figure 3 | Photographs of sampling sites along the River Ugie. **a,** Site 1. **b,** site 8. **c,** site 10.

Figure 4 | **a,** Photographs of microcosms with bacteria which putatively degrade OMPs. **b,** custom-built packed bed bioreactor.

References: 1) Breton, R., & Boxall, A. (2003). QSAR & Combinatorial Science, 22(3), 399-409. **2)** Kümmerer, K. (2009). Journal of Environmental Management, 90(8), 2354-2366. **3)** Kraigher, B., Kosjek, T., Heath, E., Kompare, B., & Mandic-Mulec, I. (2008). Water Res, 42(17), 4578-4588. **4)** Ferrari, B. t., Paxéus, N., Giudice, R. L., Pollio, A., & Garric, J. (2003). Ecotoxicology and Environmental Safety, 55(3), 359-370. **5)** Groning, J., Held, C., Garten, C., Claussnitzer, U., Kaschabek, S. R., & Schlomann, M. (2007). Chemosphere, 69(4), 509-516. **6)** *Zhang, Z., Lebleu, M., Osprey, M., Kerr, C., & Courtot, E. (2018). Environ Geochem Health, 40(5), 1987-2005.*

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