Poster

Metagenomic mining for cold adapted phage enzymes

A. Wiseman[1], E. Pohl[1], A. Wipat[2]

[1]Department of Chemistry, Durham University, South Road, Durham, DH1 3LE, United Kingdom, [2]School of Computing, Urban Sciences Building, Newcastle University, 1 Science Square, Science Central, Newcastle upon Tyne, NE4 5TG, United Kingdom

amy.v.wiseman@durham.ac.uk

Bacteriophages are the most abundant and diverse biological entities, found in all known ecosystems. However, phage genetic material remains largely uncharacterised [1]. With an estimated population of 10^{31}, phages are most prolific natural predators of bacteria, outnumbering bacteria 10-fold and causing up to 50% mortality of bacterial cells produced daily [2]. Phage-encoded lytic enzymes are therefore ideal targets for producing antimicrobial agents. In particular, endolysins target and cleave bonds in the peptidoglycan of bacterial cell walls, leading to bacterial cell lysis and nascent phage escape [3]. With potential uses as antibiotics with low resistance, endolysins can also be utilised in the food, agricultural and cleaning industries, owing to their activities over a range of conditions [4].

Due to the diversity of phage-inhabited environments, phages from extreme environments can be sampled and their gene products characterised to find enzymes with properties useful for biotechnology. As the need for lower temperatures in industrial and domestic processes grows, enzymes that retain catalytic activity at low temperatures are in increasing demand. The molecular mechanisms behind enzyme cold adaptation remain elusive [5]. Phages adapted to extreme cold are a promising source of cold-adapted enzymes. Here, preliminary results on putative endolysins from extreme cold environments will be presented, from initial structure prediction to biochemical characterisation of selected targets, leading to structural characterisation using X-ray crystallography.

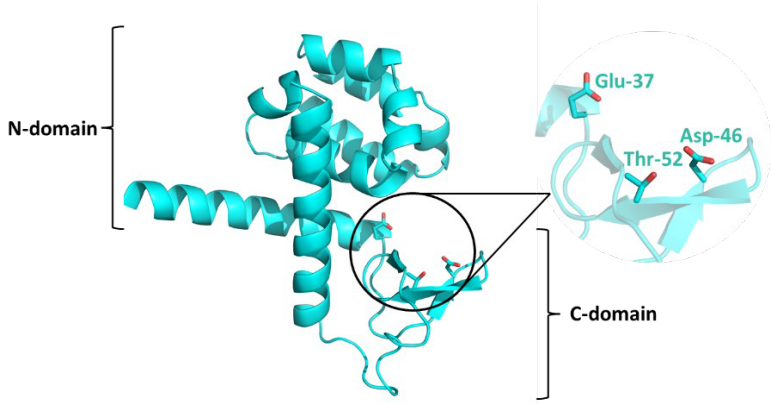

Figure 1. ESMfold predicted structure of a putative endolysin identified from a low temperature environment with potential active site residues highlighted.

[1] Aevarsson, A. *et al.* (2021), *FEMS Microbiol Lett*, **368**.

[2] Noble, R. T. & Fuhrman, J. A. (2000), *Appl Environ Microbiol,* **66,** (9), 790–3797.

[3] Abdelrahman, F. *et al.* (2021), *Antibiotics*, **10,** (2), 124.

[4] Murray, E. *et al.* (2021), *Viruses*, **13,** (4), 680.

[5] Liu, Y. et al. (2023) *Front Microbiol,* **14** 1152847.

We would like to thank the BiSCoP CTP for the funding of this PhD project.