Identification of host receptors for bacteriophages which infect *Clostridium difficile*

Application deadline: Applications accepted all year round

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**Summary (max 200 words)**

*Clostridium difficile* is a significant health care problem as it causes severe infectious diarrhea in hospitals. Resistance is developing to the only two antibiotics that can be used to treat it and there is an urgent need for alternative treatments. Bacteriophages offer an exciting new avenue to explore for the treatment of *C. difficile* either being administered as whole bacteriophages, or by using products derived from their genomes. Before they can be developed for therapeutic use however we need to understand their basic biology. One important facet of this is the biology behind their host ranges, in other words what receptors in *C. difficile* are bacteriophages are attaching to. This work may also identify novel targets that are suitable for non-phage based antimicrobials. We have isolated *C. difficile* from clinical and environmental samples and now have a collection of ~500 hundred of strains *C. difficile*. We have also isolated eight bacteriophages with overlapping host ranges. Several of these bacteriophages have had their genomes sequenced so we have a full genetic background from which to identify their tail fibers this will help us identify their corresponding receptor targets. The project will use a range of biochemical and biophysical techniques to identify the receptors that the bacteriophages use to gain entry into their hosts.