

**Graduate Schools
Infection Immunity and Cancer, UniGe & UniL: CUS
Biology & Medicine, CMU**

Seminars in Microbiology

Monday, 8th December, 2014

Salle de séminaire 7172, CMU

11:00 – 12:00

Dr. Martha Clokie

Department of Infection, Immunity and
Inflammation, University of Leicester, UK



The ecology, evolution and applications of *Clostridium difficile* bacteriophages

Clostridia are Gram positive, anaerobic, sporulating bacteria of which some are important human pathogens. *Clostridium difficile* is present in the gut and is known to cause antibiotic treatment associated diarrhea. Bacteria have a core genome that is complemented by many genes that contribute to strain specific behavior and possibility to adapt to different environments. Some of these genes, which may encode virulence factors in pathogenic bacteria, are encoded by bacteriophages. The group of Martha Clokie has recently shown that a *Clostridium* phage encodes an *agr*-type quorum sensing system (QS), in which a secreted peptide represents the signaling molecule. It is suggested that the phage encoded *agr* system, which is missing the transcriptional activator AgrA, was taken from a bacterium and is transferred horizontally between Clostridia strains, thereby influencing the behavior of the lysogenic bacteria, though the interaction with resident *agr* quorum sensing systems in *Clostridium*.

Hargreaves et al., Abundant and diverse clustered regularly interspaced short palindromic repeat spacers in *Clostridium difficile* strains and prophages target multiple phage types within this pathogen. MBio. 2014;5:e01045-13.

Hargreaves et al., Bacteriophage behavioral ecology: How phages alter their bacterial host's habits. Bacteriophage. 2014 8;4:e29866.

Hargreaves et al. What does the talking?: quorum sensing signalling genes discovered in a bacteriophage genome. PLoS One. 2014;9:e85131.

Malik et al., On the difficulties of isolating *Clostridium difficile* from hospital environments. J Hosp Infect. 2013;84:181-3.

Shan et al. Prophage carriage and diversity within clinically relevant strains of *Clostridium difficile*. Appl Environ Microbiol. 2012 ;78:6027-34.

Contact: P. Linder