

Investigation of mechanisms allowing resurgence of infection during *in vivo* evolution of *E. coli* clinical strains

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Zebrafish (*Danio rerio*) has been shown to be a useful model organism for the study of host-pathogen interactions. It is also sensitive and hence applicable for examining pathogenicity and closely related strains of *Escherichia coli* have been shown to display differences in virulence capability in the zebrafish model which correspond with differences in pathogenicity in the human host *E. coli* (Wiles et al, 2009).

During complicating bacterial chronic infections there is a high risk that bacterial populations adaptively evolve, producing novel subpopulations with persistent phenotypes and increased fitness. In this context, we have three couples of clinical *E. coli* strains isolated during human chronic bone infection. Each corresponds to two samples of the same strain following an infection for the first sample, and a resurgence of infection following *in vivo* evolution for the second sample. We intend to test in each couple of strains if the evolved strain exhibit a higher virulence than the ancestral one. The main objective is to evaluate the virulence and its evolution of different strains of *E. coli* in the zebrafish larvae infection model.