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Impact of filamentous bacteriophage on *Neisseria gonorrhoeae* biology

Author(s)

Daniel Stein, PhD

Professor

Department of Cell Biology and Molecular Genetics, University of Maryland, College Park

Jessica Kopew, BS

Graduate Student

University of Maryland

Wenxia Song, PhD

Professor

Department of Cell Biology and Molecular Genetics, University of Maryland, College Park

Background

All *Neisseria gonorrhoeae* (GC) strains that have been sequenced possess four highly conserved genomic regions associated with filamentous bacteriophage; little is known of their impact on gonococcal biology. We hypothesize that filamentous phages increase GC pathogenicity by enhancing their fitness.

Aim/Methods

To test this hypothesis, we generated an isogenic derivative of strain FA1090 (FA1090 Δ fil) that lacked the four phage genomes using a PCR/ spot transformation protocol. The correct deletions of the various phage encoding regions were verified by DNA sequencing.

Results

We found that the FA1090 Δ fil grew poorly at 37°C in both broth and on agar, as compared to FA1090: there was no difference when the strains were grown at 34°C. No apparent differences in growth were observed when the bacteria were grown anaerobically. In the absence of pili, FA1090 Δ fil formed larger bacterial aggregates than FA1090. When these strains were analyzed for their ability to produce biofilms, no differences were seen in the overall biofilm's biomass, yet the overall structure of the biofilm was different. FA1090 Δ fil producing taller and rougher biofilms. One of the phage-encoded proteins disrupted polarized T84 monolayers, induced significant T84 cell death, and promoted rapid epithelial exfoliation of human cervical tissue explants, when added to these cells in a purified form.

Conclusions

Taken en toto, these data suggest that filamentous phages provide the gonococcus with a growth advantage, and that phage proteins can lead to loss of the integrity of the epithelium, providing the gonococcus with a mechanism for disrupting host tissues and causing disseminated gonococcal disease.