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Recombination, phage therapy and bacterial infections

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Decades ago, bacteriophages have been used to treat various bacterial infections which for many years now are known as phage therapy. The ability of these phages to multiply *in vivo*, requiring very low initial dosage, their unharmed nature to most human host cells and the high level of specificity has made them an ideal choice in treating various bacterial infections in humans. This poster explores the mechanisms and the factors involved in recombination in a phage and the potential advantages of the concept recombination in the world of phage therapy for bacterial infections.

This study based on recombination in the Φ X174 shows the effect of number of mutants co-infecting the *Escherichia coli* C (C122- wildtype and BAF8- amber suppressor) at a particular multiplicity of infection on the frequency of recombinants obtained.

Approach and Result: Genes F and H amber mutants of the Φ X174 bacteriophage were generated through mutagenic PCR (Polymerase Chain Reaction) in addition to an E cistron amber mutant already in stock. Genetic crosses of two amber mutants (gpF and gpH) and all three amber mutants were carried out and the frequency of recombination were obtained from the two crosses. The crosses were in the absence of recombination promoting genes. It was found that the frequency of distribution was higher in the 2-mutant cross than in the 3-mutant cross.

Conclusion: The data obtained suggests that the number of co-infecting mutants phages affects the frequency of rearrangement/reassortment between the infecting phages. It also suggests that the more the number of mutants present, the lower the frequency of recombination. Also, the specificity of the phage makes it advantageous in that human host cells are unaffected. Since recombination helps preserve specific genes and widen the host susceptibility range, a particular phage mix can be used for a wider range of bacterial infections and resistance can be ruled out. Hypothetically, the susceptibility range of a particular phage mix should be determinable by the recombinants frame obtainable from the phage mix. Also, the presence of fewer mutants optimizing recombination reduces the risk of virulence evolving with more infecting mutants.

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