Origins of antibiotic resistance genes reported in bacteriophage

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Background to topic

- **Origins knowledge about the effects of antibiotics go back to work of Fleming in 1928**

- **Full effects of the potential use of penicillin date from the early 1940s when it was used to treat a patient with streptococcal meningitis**

- **However soon afterwards microbes started to show resistance to penicillin**

Background to topic

- In general genes for antibiotic resistance have been found on bacterial plasmids

- Therefore the normal mode of transmission of antibiotic resistance genes between organisms is by plasmid conjugation

- However some resistance genes can also be acquired by transformation from DNA environmental samples

Background to topic

- More recently antibiotic resistance genes have been shown to have association with mobile elements

- This has been hypothesised as being the reason that they have been reported in bacteriophages

Purposes of investigation

- **Study the taxonomic relationship between antibiotic resistance genes in bacteriophages and those in other organisms**

- **Use codon usage patterns to compare the antibiotic resistance gene with other genes within the bacteriophages**

Methodology

- **Bacteriophage genomes which contained one or more antibiotic resistance genes were identified in GenBank**
- **Full gene DNA sequences were downloaded from GenBank**
- **Related antibiotic genes, from bacterial sources, were downloaded**

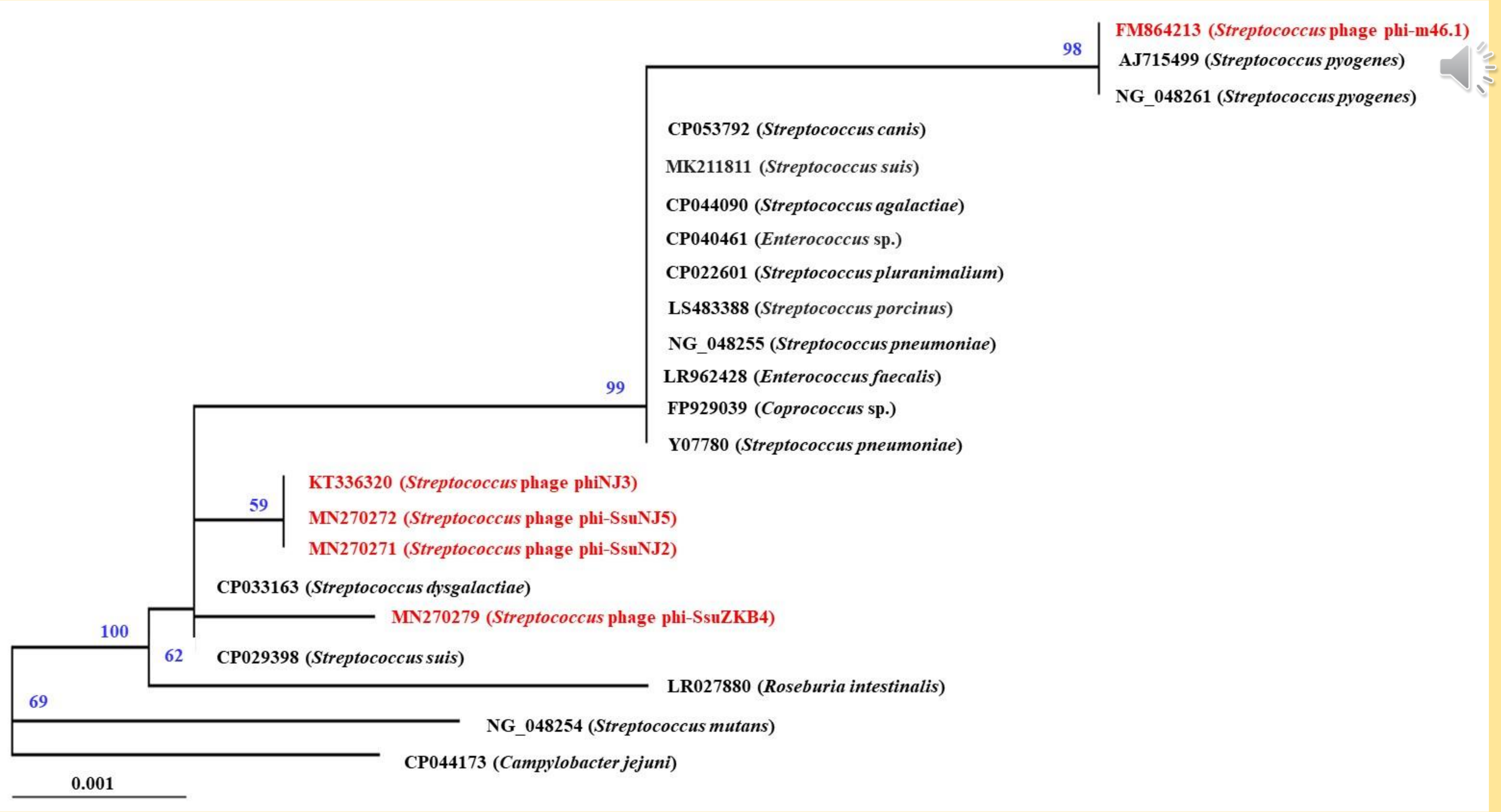
Methodology

- DNA sequences were aligned using Clustal Omega compared by use of Neighbor-Joining analysis with use of bootstrapping in PHYLIP
- Codon usage evaluated by mutational response index and effective codon number

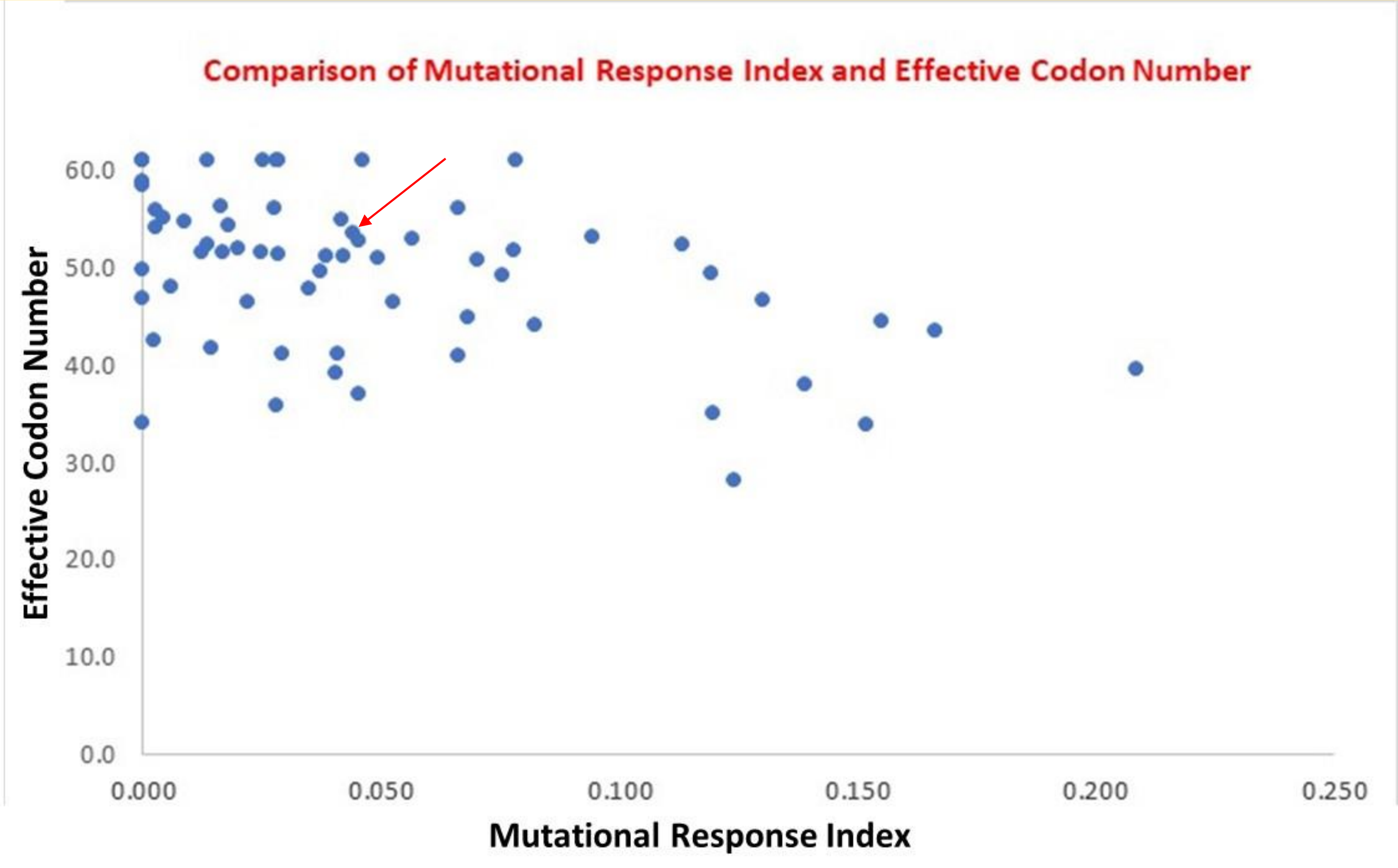
Results

- **First dataset examined was for *tetO***
- **5 genes from bacteriophage identified**
- **Based on BLASTn searches they appear to be most similar to sequences previously described in *Streptococcus* species**

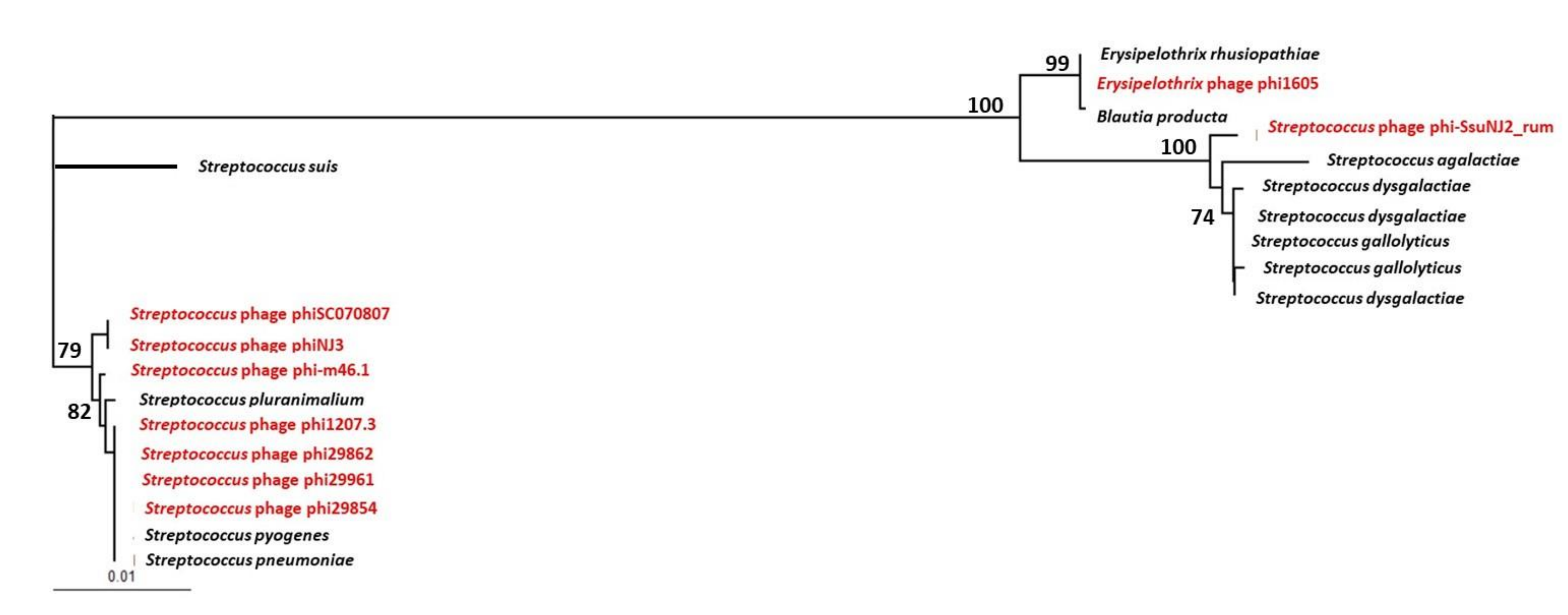
Results


FM864213 (*Streptococcus* phage phi-m46.1)
AJ715499 (*Streptococcus pyogenes*)
NG_048261 (*Streptococcus pyogenes*)
98
CP053792 (*Streptococcus canis*)
MK211811 (*Streptococcus suis*)
CP044090 (*Streptococcus agalactiae*)
CP040461 (*Enterococcus* sp.)
CP022601 (*Streptococcus pluranimalium*)
LS483388 (*Streptococcus porcinus*)
NG_048255 (*Streptococcus pneumoniae*)
LR962428 (*Enterococcus faecalis*)
FP929039 (*Coprococcus* sp.)
Y07780 (*Streptococcus pneumoniae*)
99
KT336320 (*Streptococcus* phage phiNJ3)
MN270272 (*Streptococcus* phage phi-SsuNJ5)
MN270271 (*Streptococcus* phage phi-SsuNJ2)
59
CP033163 (*Streptococcus dysgalactiae*)
MN270279 (*Streptococcus* phage phi-SsuZKB4)
CP029398 (*Streptococcus suis*)
62
100
LR027880 (*Roseburia intestinalis*)
69
NG_048254 (*Streptococcus mutans*)
CP044173 (*Campylobacter jejuni*)
0.001

Results


Comparison of Mutational Response Index and Effective Codon Number
Effective Codon Number
Mutational Response Index
60.0
50.0
40.0
30.0
20.0
10.0
0.0
0.000
0.050
0.100
0.150
0.200
0.250

Results – *msrD* (macrolide resistance)



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Discussion

- **The data presented here are only a small component of antibiotic resistance genes reported in bacteriophage**

- **Results suggest that antibiotic resistance genes in the phages are most similar to the organism which they are associated with**

- **Codon usage patterns are in keeping with other genes**

Discussion

- This suggests that the genes for antibiotic resistance have been transferred into the phages from the bacterium

- In the unlikely event that they came into the bacterium from elsewhere, they have rapidly ameliorated their codon usage pattern to conform to that of the bacteriophage

Questions?