Evolutionary training: how bacteriophages adapt to multiple strains of Salmonella enterica

Amandine Maurin*[1]

[1]CNRS – UMR 224 MIVEGEC (IRD, UM, CNRS), Montpellier – France

Résumé

The efficacy of phage therapy depends not only on the ability of bacteriophages to infect pathogenic bacteria but also to limit the emergence of new resistant bacterial genotypes nor to select rare resident resistant genotypes. We performed in vitro evolutionary training of one isolated and purified Tequintavirus bacteriophages (four independent lineages) by performing 6 to 7 consecutive passages against 8 not co-evolving bacterial genotypes *of* Salmonella enterica serotype Tenessee. While the ancestral bacteriophage was able to infect 3 out of 8 bacterial genotypes, evolved populations expanded their host range (8/8 infected bacterial genotypes). Moreover, bacterial growth inhibition of adapted bacteriophage populations was maintained without appearance of resistant bacteria for more than 20 hours despite a 3-4 log dilution of the bacteriophages. After sequencing DNA from both ancestral and evolved populations, we observed parallel evolution toward modification of several genes such as the long tail fiber protein gene (potentially involved in host range expansion) and exo- and endonuclease as well as hydrolase (potentially involved in increase of virulence). For the sake of successful phage therapy, our results demonstrate the importance of in vitro evolutionary training taking into account the diversity of bacteria isolated in situ prior to the use of therapeutical bacteriophages.

Mots-Clés: daptation, biocontrol, Bacteriophage evolution, coevolution, experimental evolution, host range, Phage Therapy, Salmonella enterica, Sequencing

*Intervenant