H. pylori phages: from genome release to hope for use as therapy

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Background

The increasing antibiotic-resistant *Helicobacter pylori* infections worldwide and the ineffectiveness of treatments led the World Health Organization to designate clarithromycin-resistant *H. pylori* as a high-priority bacterium for antibiotic research and development. (Bacterio)phages, viruses that infect bacteria, showing effectiveness in the treatment of pathogenic bacteria, could be a promising alternative strategy in the fight against *H. pylori* infections.

Material and methods

In this work, a collection of 74 Portuguese *H. pylori*-clinical strains was used to screen for the presence of phage genes, using a new PCR-based method. Selected strains were subsequently sequenced and prophage isolation was attempted using UV radiation. Three phages were isolated, one of which was further characterized genetically and biologically.

Results

PCR-based detection indicated the presence of target phage sequences in 14 strains, and the induction strategies resulted in the release of a new phage. It presents a genome length of 31,162 bp with a G+C content of 37.1 %. This podovirus showed capability to form phage plaques in five strains, was stable under an *in vitro* gastric digestion model, and was able to maintain a *H. pylori* population at low levels for up to 24 h post-infection.

Conclusion

The new PCR screening method proved to be very effective in the selection of strains carrying prophages, resulting in the isolation of a new *H. pylori* phage. This phage presented very promising characteristics in terms of stability and efficacy, being therefore a small step towards the future use of phage therapy in the fight against *H. pylori* infections.