CENTRE OF ENGINEERING

# A novel Helicobacter pylori phage to combat gastric infections: first characterizations 

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Helicobacter pylori, a Gram-negative microaerophilic bacterium in a spiral shape, is recognized as an etiological agent of active chronic gastritis and contributes to peptic ulceration ${ }^{1}$. Furthermore, some studies associate it to development of gastric carcinoma ${ }^{2}$. Currently, treatment of H. pylori is performed with conventional antibiotics that in addition to the several side effects, increase the appearance of antibiotic-resistant strains, which, consequently, increase their inefficiency ${ }^{3}$. Thus, novel strategies targeting $H$. pylori are a serious challenge. Bacterio(phages) have emerged in recent years as an effective alternative to fight bacterial infections ${ }^{4}$, but very little is known about H. pylori phages ${ }^{5}$. In this study, we described a novel H. pylori phage named HPy1R, induced by UV radiation from a Portuguese clinical strain, and characterized in terms of morphology, host range, stability, and efficacy against a H. pylori cultures. Moreover, the phage HPy1R was characterized in an in vitro gastric model with simulated salivary fluid and simulated gastric fluid ${ }^{6}$. Overall, the developed research allowed the isolation of a new $H$. pylori podovirus, that forms small uniform plaques ( 1 mm diameter) in five of the 76 H . pylori strains tested. Additionally, in terms of genomic characterization, HPy1R has a genome length of 31162 bp , and $37.1 \% G+C$ content. HPy1R shares $80 \%$ query coverage and 88.64 \% identity with phage Helicobacter phage COL 23-PUJ. Moreover, using OrthoVenn2 software, we noticed that the COL 23-PUJ, Pt5771G, SwA626G and pHiHP33 phage genomes share between 66.67 \% and 97.22 \% orthologous proteins with HPyR1. Interestingly, HPy1R was stable from pH 3 to 11, and in in vitro gastric model small loss in the phage titer was observed in the gastric phase, suggesting that this phage could be adapted to the human stomach environment. Farther, this phage demonstrated to be capable of maintaining the $H$. pylori population at low levels for up to 24 h post-infection with MOIs of $0.01,0.1$ and 1 . In conclusion, in this work we present the first complete characterization of an $H$. pylori phage, which has features that envisage a great therapeutic potential against $H$. pylori gastric infections, if safety measures are guaranteed.


Keywords: Helicobacter pylori, Phage, Phage therapy, Genomic analysis

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