Bacteriophage | Acinetobacter | capsule degrading depolymerase

## Understanding the complete reservoir of bacteriophage depolymerases against *A. baumannii* capsules

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*A. baumannii* is an important nosocomial and drug-resistant pathogen. The capsule is a major virulence factor that helps bacteria to avoid host immunity and viral predation. *Acinetobacter* phages can bind and degrade host capsules through capsular depolymerases with proven anti-virulence activity (1-3). Understanding the full reservoir of phage depolymerases against *A. baumannii* capsules, as well as relevant capsular types in clinical isolates, is crucial for developing depolymerase-based treatments.

In this work, we 1) characterized 94 carbapenem-resistant *A. baumannii* Portuguese isolates; 2) isolated phages for relevant capsular types and characterized their depolymerases and 3) developed bioinformatic tools to collect the diversity of phage depolymerases.

We show clonal shifts of *A. baumannii* KL2, KL7, KL9 and KL120 serotypes over time, with different virulence assessed in *G. mellonella*. *Acinetobacter* phages specific for particular k-types were isolated and several depolymerases (for KL1, KL2/KL19, KL9, KL30/KL45, KL32, KL38, KL44, KL67 types) characterized. We also demonstrate that most *Acinetobacter* phages encode capsular depolymerases (from 134 deposited in 2021, 73 contain capsular depolymerases), exclusively located in small viruses (<90 kb).

To disclose the full genetic diversity, we developed PhageDPO (available in Galaxy uminho.pt server), a machine learning tool that identifies depolymerases in phages and bacteria genomes (prophages). We also present PhageKDB, a database that compiles available information of capsular depolymerases, retrieved through both manually and text-mining approaches, serving as an open portal to phage community.

Overall, we present novel insights into *A. baumannii* isolates and phage depolymerase diversity and a collaborative tool to advance research in the field.

(1) Oliveira *et al* (2017). EM. PMID: 34185951

(2) Oliveira *et al* (2019). JV. PMID: 30463964