Poster

Search of phage-plasmids and analysis of their role in CRISPR-Cas mediated phage-bacteria interaction in Acinetobacter baumannii

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ABSTRACT

Motivation: The emergence of new antibiotic-resistant bacterial strains represents one of the top 10 global health threats, with A. baumannii as a species of special concern. The use of bacteriophages as a treatment for infectious diseases is a potential solution for this issue. Making this therapy a viable alternative requires a deep knowledge of interaction between phages and bacteria. Some special elements in these context are sequences known as phage-plasmids (PPs), wich carry sometimes defense system such as CRISPR-Cas.

Methods: Identification of PPs was carried out by similarity searching between phage and plasmid sequences from two databases. Results obtained in this search were confirmed by using the phage prediction tool PHASTER, and comparison with previous studies. CRISPRCasTyper tool was used to search CRISPR arrays in sequences.

Results: Results obtained from previous PPs studies were confirmed, also providing a larger quantity of new plasmids identified as PPs. It remains clear that PPs show a great diversity throughout a variety of bacteria species, being more represented in gram-negative species rather than gram-positive. Hence, we propose a method of identification of PPs elements. CRISPR-Cas arrays were found in a small quantity of identified PPs, although none were found in PPs from Acinetobacter baumannii. Analysis of protospacers of PPs in A. baumannii show that they are targeted by CRISPR-Cas defence system, finding a higher percentage of protospacers identified as IF-a1 type in PPs, comparing with simple phages or plasmids.

Conclusions: The results obtained confirm the idea that PPs have a prominent presence throughout strains of different bacteria species. The protocol proposed in this work provides a fast way of finding new phage-plasmid when databases information is updated. Previous studies reported the presence of CRISPR-Cas defence systems in a phage-plasmid from A. baumannii. However, no CRISPR arrays were found in the present work in that species. Future searches applying this method with actualized databases may find the presence of CRISPR arrays in A. baumannii PPs. The higher presence of IF-a1 in PPs than in other elements suggest a specialization of this type of CRISPR array on PPs. Given that IF-a1 arrays have been found in phages and PPs, these results show some insight into the process of competition between phages.

REFERENCES

Organización Mundial de la Salud. (2021). Resistencia a los antimicrobianos. https://www.who.int/es/news-room/fact-sheets/detail/antimicrobial-resistance

Camargo, A. P., Nayfach, S., Chen, I. M. A., Palaniappan, K., Ratner, A., Chu, K. Roux, S. (2023). IMG/VR v4: an expanded database of uncultivated virus genomes within a framework of extensive functional, taxonomic, and ecological metadata. Nucleic Acids Research, 51(D1), D733–D743. https://doi.org/10.1093/nar/gkac1037

Pfeifer, E., Moura De Sousa, J. A., Touchon, M., & Rocha, E. P. C. (2021). Bacteria have numerous distinctive groups of phage-plasmids with conserved phage and variable plasmid gene repertoires. Nucleic Acids Research, 49(5), 2655–2673. https://doi.org/10.1093/nar/gkab064

Rubio, A., Garzón, A., & Pérez-Pulido, A. J. (2023). A biological warfare between two bacterial viruses in a particular genomic region using a CRISPR-Cas system as a weapon, (6). Retrieved from https://doi.org/10.1101/2023.09.20.558655