Talk

Searching for gene markers related to CRISPR-Cas systems in Klebsiella pneumoniae

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ABSTRACT

Motivation: Strains from the ESKAPE bacterial group are resistant against current antibiotic compounds and discovering new ones is too slow to catch up the evolution rate of these bacteria. So, there's a need to find new targets to develop new antibiotics and therapies against them.

Mangas et al [1] discovered a correlation between the presence of CRISPR-Cas systems and biofilm formation genes in Acinetobacter baumanii using large amount of assembled genomes from public databases. These latter could help in the protection from antibiotics. In here, the goal is to find out correlations between CRISPR-Cas systems and virulence genes in Klebsiella pneumoniae since both species belong to the ESKAPE group, have big pangenomes, a lot of plasmids and carry out similar CRISPR-Cas systems.

Methods: A pangenome has been built from 14016 different assembled complete and draft genomes of K. pneumoniae from the NCBI Genome database along with metadata information, finding around 80000 different genes. Then it was processed through association rules to find GO terms and genes associated with CRISPR-Cas and virulence, and it was confirmed by sequence similarity searches using BLASTp.

Results: Functional enrichment analysis showed that there is a strong correlation between CRISPR-Cas type IV-A3 and tellurium resistance genes as both are held in the same plasmid. Tracking the IV-A3 helicase dinG showed it is duplicated in a highly virulent plasmid presents in both negative CRISPR strains and some positive CRISPR strains different from IV-A3 type.

Conclusions: The CRISPR-Cas IV-A3 present in K. pneumoniae is encoding in a great plasmid that always includes an operon of resistance to tellurium. Although this operon is also present in other virulent plasmids the presence of CRISPR-Cas could protect it from other plasmids carrying antibiotic resistance genes.This study supports the relevance of CRISPR-Cas systems on virulence and suggests new gene targets that will help develop new types of antibiotics and contribute to develop alternative therapies such as phage-therapy.

REFERENCES

(1) Mangas, E. L., Rubio, A., Alvarez-Marin, R., Labrador-Herrera, G., Pachon, J., Pachon-Ibanez, M. E., et al. (2019). Pangenome of Acinetobacter baumannii uncovers two groups of genomes, one of them with genes involved in CRISPR/Cas defence systems associated with the absence of plasmids and exclusive genes for biofilm formation. Microb. Genom. 5:e000309. doi: 10.1099/mgen.0.000309