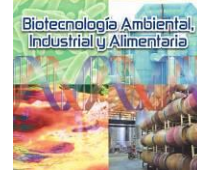

Talk

¿Qué puede hacer la bioinformática para responder preguntas microbiológicas?



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ABSTRACT

Motivation: Bioinformatics now makes it possible to analyze thousands of bacterial genomes and answer biological questions such as how many different genes we can associate with a species and how to discover gene markers linked to resistance and other bacterial defense systems.

Methods: In this talk I showed how to perform bacterial pangenomes using several public and home-made bioinformatics tools, including the Sma3s gene annotator, or the Roary pangenome software.

Results: With this methodology, we have analyzed groups of genomes of human pathogenic bacteria with CRISPR-Cas-acquired immunity systems and have discovered that they are highly specialized in phages, especially in variants called phagoplasmids. In addition, we have found that some of the genomes carrying these systems may have been forced to acquire them because they have genes that encode possible receptors for entry of specific phages.

Conclusions: With all this, we have reduced the so-called dark matter of CRISPRs, proposing a new theory about their acquisition in bacteria.

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