Metagenomic functional analysis as a tool to detect bacterial genes conferring resistance to clinical antibiotics in soils

Amando Flores (Universidad Pablo de Olavide)

The spread of antibiotic resistance genes has become a global health concern identified by the World Health Organization as one of the greatest threats to health. Many of antimicrobial resistance determinants found in bacterial pathogens originate from environmental bacteria, so identifying the genes that confer resistance to antibiotics in different habitats is mandatory to better understand resistance mechanisms. Soil is one of the most diverse environments considered reservoir of antimicrobial resistance genes. The aim of this work is to study the presence of genes that provide resistance to antibiotics used in clinical settings in two oil contaminated soils by metagenomic functional analysis. Using fosmid vectors that efficiently transcribe metagenomic DNA, we have selected 12 fosmids coding for two class A β-lactamases, two subclass B1 and two subclass B3 metallo-β-lactamases, one class D β-lactamase and three efflux pumps that confer resistance to cefexime, ceftriaxone, meropenem and/or imipenem. In some of them, detection of the resistance required heterologous expression from the fosmid promoter. Although initially, these environmental genes only provide resistance to low concentrations of antibiotics, we have obtained, by experimental evolution, fosmid derivatives containing β-lactamase ORFs with a single base substitution, which substantially increase their β-lactamase activity and resistance level. None of the mutations affect β-lactamase coding sequences and are all located upstream of them. These results demonstrate the presence of enzymes that confer resistance to relevant β-lactams in these soils and their capacity to rapidly adapt to provide higher resistance levels.

3 de Octubre de 2022 a las 11:30 en SO5