***STREPTOMYCES* EFFECT ON THE BACTERIAL MICROBIOTA ASSOCIATED TO *CRASSOSTREA SIKAMEA* OYSTER**

Dra. C. Milagro García Bernal. Centro de Bioactivos Químicos. UCLV. Cuba.

\*Dr. C. Ricardo Medina Marrero. Centro de Bioactivos Químicos. UCLV. Cuba. [rpmedina@uclv.edu.cu](mailto:rpmedina@uclv.edu.cu)

Dr. C. José M. Mazón Suástegui. Centro de Investigaciones Biológicas del Noroeste. México.

(\*) Ponente

**Abstract**

Aim: To determine the composition and diversity of the microbiota associated to *Crassostrea sikamea* treated during 30 days with *Streptomyces* strains N7 and RL8. Methods and Results: DNA was extracted from oysters followed by 16S rRNA gene amplification and pyrosequencing. The highest and lowest species diversity richness was observed in the initial and final control group, whereas *Streptomyces*-treated oysters exhibited intermediate values. Proteobacteria was the most abundant phylum (81.4-95.1%), followed by Bacteroidetes, Actinobacteria and Firmicutes. The genera *Anderseniella*, *Oceanicola*, *Roseovarius*, *Ruegeria*, *Sulfitobacter*, *Granulosicoccus* and *Marinicella* encompassed the core microbiota of all experimental groups. The genus *Bacteriovorax* was detected in all groups except in the final control and the depurated N7, whereas *Vibrio* remained undetected in all *Streptomyces*-treated groups. RL8 was the only group that harboured the genus *Streptomyces* in its microbiota. Principal component analysis showed that *Streptomyces* strains significantly changed oyster microbiota with respect to the initial and final control. Conclusions: *Crassostrea sikamea* treated with Streptomyces showed high species diversity and a microbiota composition shift, characterized by keeping the predator genus *Bacteriovorax* and decreasing the pathogenic *Vibrio*.

Palabras clave: *Bacteriovorax,* microbiota, oyster, pyrosequencing*, Streptomyces, Vibrio*