**¿Desea presentar comunicación oral? SI**

**The different roles of TasA and CalY in the biofilm formation of B. cereus**

Ana Álvarez-Mena1, Luis Díaz-Martínez1, Joaquín Caro-Astorga1, Oscar P. Kuipers2, Antonio de Vicente1, Diego Romero1

1Institute for Mediterranean and Subtropical Horticulture "La Mayora", Spanish National Research Council–University of Malaga, Boulevard Louis Pasteur 31 (Campus Universitario de Teatinos), 29071, Málaga, Spain; 2 Department of Molecular Genetics, Groningen Biomolecular Sciences and Biotechnology Institute, Centre for Synthetic Biology, University of Groningen, Nijenborgh 7, 9747 AG Groningen, The Netherlands

alvarezmena@uma.es

The human pathogen *Bacillus cereus* is responsible of many food poisoning due to the ingestion of contaminated vegetables or processed foods. For the survival and colonization, the bacteria form a biofilm on biotic and abiotic surfaces in which a specific subpopulation differentiates to produce a multifunctional extracellular matrix (ECM), mainly composed by exopolysaccharides, proteins and extracellular DNA. One of the most attractive components of the ECM are the amyloid proteins due to its high tendency to fibrillate and the multifunctional role in the bacterial physiology.

In the *B. cereus* genome there is a specific genomic region that contains two orthologues genes to the *tasA* gene in *Bacillus subtilis*, initially described as essential in the assembly of amyloid fibers, named *tasA* and *calY* respectively. The deletion of these genes gives a different phenotype related with a deficient biofilm formation in both cases. In the *tasA* mutant, the biofilm finally detaches at 72 hours, and the *calY* mutant shows a thinner ring phenotype in comparison with the wild type strain. The gene expression dynamic during the biofilm development reveals that there are three different subpopulations: both genes are expressed, only *calY* or none of them. Furthermore, transcriptomic analysis by RNA-Seq show that the mutants have different changes in the gene regulation and the *calY* mutant is the most affected, with 227 genes deregulated that affect to several important pathways such as the synthesis of extracellular DNA, an important component of the ECM.

The results mentioned above indicate that TasA and CalY might have complementary roles in the biopellicle development but also evidence that this physiological process is more complex in *B. cereus* in comparison with the model described in *B. subtilis*.

This work was supported by grants from the National Plan I+D+I of the Ministerio de Ciencia e Innovación (AGL2016-78662-R and PID2019-107724GB-I00) and by the European Research Council Starting Grant (BacBio 637971). Ana Álvarez is supported by a PhD fellowship (BES-2017-081275) from the FPI program of the same Ministry.