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IDENTIFICATION AND CHARACTERIZATION OF RNA-BINDING PROTEINS IN STAPHYLOCOCCUS AUREUS

A. Catalán-Moreno[1], *C. Caballero*[1], *A. Toledo-Arana*[1]
[1]*Instituto de Agrobiotecnología, Laboratory of Bacterial Gene Regulation, Mutilva, Spain*

Backgrounds

In bacteria, post-transcriptional regulatory elements, such as small RNAs (sRNAs), riboswitches and RNA-binding proteins (RBP) control RNA decay, transcription elongation and translation efficiency in response to environmental changes. Although sRNAs-mediated regulation has been extensively studied, post-transcriptional regulatory mechanisms involving RBPs remain to be deciphered. RBPs are present in all kingdoms of life and can be divided in different groups depending on their protein domains: ribosomal proteins, ribonucleases or RNA chaperones.

Objectives

In order to have a better understanding of RBPs-mediated regulation, we aimed to identify and characterize the RNA chaperones and their targets using as a bacterial model *Staphylococcus aureus*, one of the most important human pathogens.

Methods

First, we performed an *in silico* analysis to identify the potential RNA chaperones present in the staphylococcal genome. Subsequently, relevant RBPs were chromosomally flagged with a 3xFLAG tag and their expression patterns analyzed by Western Blot. Finally, to identify the RNA targets recognized by RBPs *in vivo*, we performed Cross-Linking Immuno-Precipitation assays (CLIP).

Conclusions

The expression analyses revealed that the RNA chaperones, CspA, CspB, CspC, CvfB and SA_00892 are highly expressed in all the analyzed points of the growth curve of *S. aureus*. In contrast, we could not detect Hfq expression in these conditions. CLIP experiments demonstrated that the selected RBPs bind RNA *in vivo*. Preliminary results on the targets recognized by these RNA chaperones will be discussed at the meeting.