SCIENTIFIC PROGRAM

Wednesday, October 19

PLENARY SESSION 3: Beneficial Microbes for Soil and Environment

Chairs: Helena Machado and Nuria Ferrol

9.00-9.30 **CONFERENCE S3-L-01**

Jessica Purswani
(Universidad de Granada, Spain)

"Social PGPMs for future biofertilizers"

9.30-10.00 **ORAL COMMUNICATIONS**

- **S3-O-01:** Civantos C, Murillo-Torres M, Velasco-Amo M P, Adrián R, Filloux A, Mavridou D, Landa B, **Bernal P**
  "Type VI Secretion System: a bacterial killing machine and biocontrol weapon"
- **S3-O-02:** Vicente CSL, Espinosa-Saiz D, Curto M, Faria JMS, Velázquez E, Inácio L, Mateos PF, **Menéndez E**
  "Exploring soil Plant Growth Promoting Rhizobacteria potential to control Plant-Parasitic Nematodes: the case of *Phyllobacterium* and *Paenibacillus* against the pinewood nematode *Bursaphelenchus xylophilus"*
- **S3-O-03**: **Reyes Pérez P**, Jiménez-Guerrero I, Sánchez-Reina A, Moreno-de Castro N, Civantos C, Ollero FJ, López-Baena FJ, Bernal P, Pérez-Montaño F
  "Antibiosis or symbiosis? Characterizing the *Sinorhizobium fredii* USDA257 type VI secretion system"

PLENARY SESSION 6: Genetics and "Omics" of Plants and Associated Microbes

Chairs: Margarida Oliveira and Socorro Mesa

10.00-10.30 **CONFERENCE S6-L-01**

Estíbaliz Larrainzar
(Universidad Pública de Navarra, Pamplona, Spain)

"Is ethylene required for an active nitrogen fixation and nodule development in Medicago truncatula?"

10.30-11.00 **COFFEE BREAK** - *CAP Building (1st Floor)*

11.00-11.30 **CONFERENCE S6-L-02**

Jose I. Jiménez Zurdo
(EEZ-CSIC, Granada, Spain)

"Structure and function of the α-rhizobia non-coding transcriptome investigated by RNAseq"

11.30-12.30 **ORAL COMMUNICATIONS**

- **S6-O-01**: **del Cerro P**, Cook NM, Huisman R, Dangeville P, Grubb LE, Marchal C, Ho Ching Lam A, Charpentier M
  "Engineered Calmodulin modulates nuclear calcium oscillation and enhances legume root nodule simbiosis"
- **S6-O-02**: Torres DP, Alexandre A, Menéndez E, **Brígido C**
  "Genomic characteristics and comparative genomics analyses of non-rhizobial endophytic bacteria isolated from legumes"
- **S6-O-03**: Fernandes I, Paulo OS, Sarjkar I, Sem A, Marques I, Graça I, Pawlowski K, Ramalho JC, **Ribeiro-Barros AI**
  "Salt stress tolerance in *Casuarina glauca*: insights from the branchlets transcriptome"
- **S6-O-04**: Ayala García, P, Moreno de Castro N, Jiménez Guerrero I, Pérez Montaño F, **Borrero de Acuña JM**
  "Engineering membrane vesicles for fine-tuned modulation of rhizobia species interactions for enhanced nodulation and plant growth"
- **S6-O-05**: De Sousa BFS, Tighilt L, Arrabal A, Domingo-Serrano L, Gómez-Pellicer R, Albareda M, Boulila F, Palacios JM, **Rey L**
  "Relevance of rhizobial T6SS for the interaction with some legumes"
- **S6-O-06**: **Casas-Román A,** Lorite MJ, Muñoz S, Gallegos MT, Sanjuán J.
  "Characterization of the Glyceraldehyde-3-phosphate dehydrogenase protein in *Rhizobium etli"*

S6-L-02

Structure and function of the α-rhizobia non-coding transcriptome investigated by RNAseq

Jiménez-Zurdo JI[1], García-Tomsig NI[1], Acosta-Jurado S[2], Guedes-García SK[1], Fuentes Romero F[3], Navarro-Gómez P[3], Ayala-García P[3], Robledo M[4], Pérez-Montaño F[3], Ollero FJ[3], Vinardell JM[3]

[1] Estación Experimental del Zaidín, CSIC, Granada (Spain); [2] Centro Andaluz de Biología del Desarrollo, CSIC; Departamento de Biología Molecular e Ingeniería Bioquímica, Universidad Pablo de Olavide, Sevilla (Spain); [3] Departamento de Microbiología, Universidad de Sevilla, Sevilla (Spain); [4] Instituto de Biomedicina y Biotecnología de Cantabria, CSIC-Universidad de Cantabria-Sodercan, Santander, Spain.

Deep sequencing of strand-specific cDNA libraries (RNAseq) has unveiled unexpectedly complex transcriptional outputs from prokaryotic genomes, adding large and heterogeneous inventories of small non-coding transcripts (sRNAs) to the classical translation-related ribosomal (rRNA), transfer (tRNA) and messenger (mRNA) RNA species (Hör *et al*. 2018). Most sRNAs regulate extensive post-transcriptional networks underlying virtually any adaptive trait in bacteria. Therefore, it is increasingly evident that no microbial process can be understood in its full dimension without assessing regulation of gene expression by RNA (riboregulation). Yet inconceivably, sRNAs are systematically overlooked in the annotation of bacterial genomes and riboregulation remains largely unexplored in most bacterial species.

We have used cutting-edge RNAseq protocols such as Differential RNAseq (dRNAseq), Cappable-seq or Term-seq to determine transcripts boundaries genome-wide in three α-rhizobial species, *Sinorhizobium meliloti, S. fredii and Rhizobium tropici*, as the model symbionts of the agronomically relevant legumes, alfalfa, soybean, and common bean, respectively. These approaches enabled the accurate annotation of protein-coding sequences, untranslated mRNA regions, and sRNAs in all three genomes. The latter were further catalogued as sense, antisense or *trans* according to the location of their *loci* with respect to the annotated ORFs. Classical RNAseq was then used to explore the symbiotic-dependent alterations of the non-coding transcriptomes, which identified differentially expressed sRNAs with putative symbiotic functions.

The so-called *trans*-sRNAs are expressed from transcriptionally regulated promoters within intergenic regions and rely on protein-assisted short and discontinuous base-pairing to regulate translation and stability of multiple *trans*-encoded mRNA targets. Accordingly, we also used RNAseq to profile the RNA ligands of the major bacterial RNA matchmaker Hfq, and the mRNA interactomes of well-characterized *trans*-sRNAs in *S. meliloti* (Torres-Quesada *et al.*, 2014; García-Tomsig *et al.*, 2022). In the communication, we will provide insights into these RNAseq-based approaches to identify and unravel the function of sRNAs in α-rhizobia.

References

Hör, J., Gorski, S.A., Vogel, J. (2018) Bacterial RNA biology on a genome scale. Mol Cell 70, 785–799.

Torres-Quesada O., Reinkensmeier J., Schlüter J.P., Robledo M., Peregrina A., Giegerich R., Toro N., Becker A., Jiménez-Zurdo J.I. (2014) Genome-wide profiling of Hfq-binding RNAs uncovers extensive post-transcriptional rewiring of major stress response and symbiotic regulons in *Sinorhizobium meliloti*. RNA Biol 11, 563-579.

García-Tomsig N.I., Robledo M., diCenzo G.C., Mengoni A., Millán V., Peregrina A., Uceta A., Jiménez-Zurdo J.I. (2022) Pervasive RNA regulation of metabolism enhances the root colonization ability of nitrogen-fixing symbiotic α-rhizobia. mBio 8, 384.

Acknowledgements

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Beneficial Plant-Microbe Interactions

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BOOK OF ABSTRACTS

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