



## XIII REUNIÓN DEL GRUPO DE MICROBIOLOGÍA MOLECULAR DE LA SEM

Granada, 7-9 de septiembre de 2022



UNIVERSIDAD  
DE GRANADA



- 10:00 Type III secretion system effectors form robust and flexible intracellular virulence networks.  
David Ruano-Gallego, Julia Sánchez-Garrido, Elena Núñez-Berruero, Massiel Cepeda-Molero, Luis Ángel Fernández, Alfonso, Rodríguez-Paton, Gad Frankel – P106
- 10:15 La pérdida de la proteína fijadora de penicilina 3 (PBP3) en respuesta a señales propias del fagosoma y su contribución a la evolución de *Salmonella* como patógeno intracelular.  
David López-Escarpa, Sónia Castanheira, Francisco García-del Portillo – P107
- 10:30 *In vivo* genome-wide fitness analysis uncovers *Haemophilus influenzae* metabolic network requirements during airway infection: study of the tryptophan-serine metabolic axis.  
Javier Asensio-López, Begoña Euba, Celia Gil-Campillo, Beatriz Rapún-Araiz, Goizeder Almagro, Nahikari López-López, Irene Rodríguez-Arce, María Lázaro, Mariette Barbier, Jeroen Langereis, Alejandro Toledo-Arana, Saioa Burgui, Junkal Garmendia – P108
- 10:45 La interacción hospedador-patógeno en el complejo *Mycobacterium tuberculosis* reinterpretada en base a un metabolito presente en sus hospedadores.  
Elena Campos-Pardos, Santiago Uranga, Ana Picó, Jesús Gonzalo-Asensio – P109

## 11:00 Café y sesión de pósteres

### Sesión VII: Biotecnología

Moderadores: Junkal Garmendia, Instituto de Agrobiotecnología, CSIC - Gobierno de Navarra; y Centro de Investigación Biomédica en Red de Enfermedades Respiratorias, Madrid  
Alejandro Toledo Arana, Instituto de Agrobiotecnología, CSIC - Gobierno de Navarra

- 11:30 Response of *Pseudomonas putida* to noxious compounds susceptible of synthesis by *Pseudomonas putida*.  
Ana García Franco, Patricia Godoy Alba, Rocío Palacios Ferrer, Estrella Duque Martín de Oliva, Juan Luis Ramos Martín – P116
- 11:45 Improved colonization of human tumor spheroids by *E. coli* bacteria with synthetic adhesins binding cell-surface receptors of tumor cells.  
Alba Cabrera Fisaç, Carmen Mañas-Torres, Eva Pico-González, Elena M. Seco, Luis Ángel Fernández – P117
- 12:00 El papel de los metales en la deprecación bacteriana.  
Francisco Javier Contreras-Moreno, Juana Pérez, María José Soto, Aurelio Moraleda-Muñoz, José Muñoz-Dorado – P118
- 12:15 Optimization of bacterial recombineering by *in vivo* production of single-stranded DNA.  
Alejandro González-Delgado, Alfonso Matías Rojas-Montero, Seth L. Shipman – P119
- 12:30 The genetic basis of fast-growth adaptation in cyanobacteria, revealed by long term evolution.  
Alfonso Mendaña, María del Mar Santos-Merino, Raquel Gutiérrez-Lanza, Carlos Díaz, Ana González-Guerra, Víctor Campa, Rocío López-Igual, Daniel Volke, Pablo I Nikel, Didier Mazel, Fernando de la Cruz, Raúl Fernández-López – P120
- 12:45 Diseño de nuevas herramientas moleculares útiles en la prevención de la diseminación de genes de resistencia a antibióticos en plantas de tratamiento de aguas residuales.  
David Correa Galeote, Lizandra Pérez Bou, Belén Rodetas, Alejandro González Martínez, Jesús González López – P121
- 13:00 Producción de nanocelulosa bacteriana por *Starkeya* sp. STN1A.  
Inés Castillo-Rodríguez, Rocío Fernández-González, Sophie-Marie Martirani-von Abercron, Patricia Marín, Jaccoline Zegers, Daniel Pacheco, Silvia Marqués – P122



***In vivo* genome-wide fitness analysis uncovers *Haemophilus influenzae* metabolic network requirements during airway infection: study of the tryptophan-serine metabolic axis**

Javier Asensio-López<sup>1,2</sup>, Begoña Euba<sup>1</sup>, Celia Gil-Campillo<sup>1,3</sup>, Beatriz Rapún-Araiz<sup>1</sup>, Gozeder Almagro<sup>1</sup>, Nahikari López-López<sup>1,3</sup>, Irene Rodríguez-Arce<sup>1</sup>, María Lázaro<sup>1</sup>, Mariette Barbier<sup>4,5</sup>, Jeroen Langereis<sup>6</sup> Alejandro Toledo-Arana<sup>1</sup>, Saioa Burgui<sup>2</sup>, Junkal Garmentia<sup>1,3</sup>

<sup>1</sup>Instituto de Agrobiotecnología, Consejo Superior de Investigaciones Científicas (IdAB-CSIC)-Gobierno de Navarra, Mutilva, Spain;

<sup>2</sup>Asociación de la Industria Navarra (AIN)-Gobierno de Navarra, Cordova, Spain;

<sup>3</sup>Centro de Investigación Biomédica en Red de Enfermedades Respiratorias (CIBERES), Madrid, Spain; <sup>4</sup>Vaccine Development Center, West Virginia University Health Sciences Center, Morgantown, West Virginia, USA;

<sup>5</sup>Department of Microbiology, Immunology, and Cell Biology, West Virginia University School of Medicine, Morgantown, West Virginia, USA;

<sup>6</sup>Section Pediatric Infectious Diseases, Laboratory of Medical Immunology, Radboud Institute for Molecular Life Sciences and Radboud Center for Infectious diseases, Radboudumc, Nijmegen, The Netherlands

[javier12695@gmail.com](mailto:javier12695@gmail.com)

Nontypeable *Haemophilus influenzae* (NTHi) is a human-adapted bacterial pathogen causing airway infections in immunocompromised patients. Bacteria and host elements dictating the complexity and fitness of NTHi within the lung are not well understood. Here, we exploited the strength of *in vivo* systems multi-omics analyses to study this host-microbe complex. We used transcriptome profiling (RNAseq) and high-throughput transposon mutant library sequencing (Tnseq) to profile NTHi genome-wide gene expression and mutant fitness during lung infection. Integration of these two data sets drew a comprehensive landscape in terms of bacterial metabolic requirements during infection. Genes involved in tryptophan biosynthesis were identified upon screening bacterial mutants underrepresented in lung samples. Tryptophan auxotrophy dampened *in vivo* bacterial fitness upon impaired tryptophan transport, and tryptophan uptake/synthesis relative contribution to bacterial fitness and metabolic end product excretion was established. Also, we considered that: (i) Our Tnseq was performed with the RdKW20 strain as it is highly transformable. However, it lacks the accessory *tnaCAB* genes, encoding the TnaA tryptophanase that catalyses the conversion of Trp to indole, and the TnaB Trp transporter, otherwise present in ~80 % of WGS NTHi isolates. Indole may be an immunometabolite and together with serine, a substrate for TrpB-catalyzed tryptophan synthesis. The *serA* and *serB* genes, involved in L-serine synthesis, were also Tnseq hits. (ii) Visualization of mapped read distribution in the NTHi375 genome by using our previously generated RNAseq data showed a long 3'UTR overlapping event among convergent genes in the *mtr-sdaCA* region, where *mtr* encodes a tryptophan transporter, *sdaC* a L-serine transporter, and *sdaA* a L-serine desaminase catalyzing the conversion of L-serine to pyruvate. Biological significance and contribution of this tryptophan-serine metabolic axis to NTHi airway infection is being studied by generation and phenotyping of a panel of tryptophan and serine transport/metabolism mutant strains, analysis of regulatory elements in the *mtr-sdaCA* region, and analysis of tryptophan-related immunomodulatory events during NTHi infection.

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**E. KAMYR**

