UNIVERSIDAD DE GRANADA

Máster Universitario en Investigación y Avances en Microbiología

# Seminarios y conferencias curso 2013/2014

## Dr. Álvaro Peix

Instituto de recursos naturales y agrobiología de Salamanca (IRNASA-CSIC)

### Diversidad genética y simbiótica en rhizobia: Especies, simbiovariedades y promiscuidad en la simbiosis rhizobia-leguminosa

- **Fecha**: 18 de julio de 2014
- **Hora**: 12:30 h
- **Lugar**: Salón de Actos de la Estación Experimental del Zaidín (EEZ-CSIC).
- **Contenido**: Las leguminosas constituyen la tercera familia más amplia de angiospermas, con 20000 especies repartidas en 750 géneros. La mayoría de ellas establecen simbiosis asociativas con bacterias diazotróficas que reciben conjuntamente el nombre de rhizobia, induciendo nódulos en las raíces donde se lleva a cabo la fijación biológica de nitrógeno. Este grupo de bacterias que durante años se pensaba constituido por un número limitado de especies de la clase alfa-proteobacteria, incluye en la actualidad una gran diversidad de especies filogenéticamente divergentes tanto en el fondo cromosómico como en sus genes simbióticos. En este seminario se abordará la evolución de la clasificación de los rhizobia desde su descubrimiento en el siglo XIX hasta la actualidad, así como los conceptos de simbiovariedad y promiscuidad en la simbiosis rhizobia-leguminosa y las características simbióticas que se utilizan para definir las diferentes simbiovariedades en rhizobia.

## Dr. Ramiro Vílchez Vargas

Laboratory of Microbial Ecology and Technology, Ghent University, Belgium

### Taxonomic and catabolic bacterial profiles in contaminated soils:A high-resolution analysis shows the same players with different scripts

- **Fecha**: 30 de mayo de 2014
- **Hora**: 12:00 h
- **Lugar**: Seminario - Centro de Instrumentación Científica. Campus de Fuentenueva.
- **Contenido**: The adaptation of microbial communities to stress factors generated by pollutants was assessed in one area where non-contaminated sites coexisted with sites contaminated with alkanes, toluene-xylene-ethylbenzene, or alkanes-toluene-xylene-ethylbenzene. Phylogenetical diversity and catabolic gene potential were analysed in parallel. Taxonomical characterizations were carried out using the Illumina deep sequencing technology obtaining 200335 OTUs, while catabolic gene potential was evaluated by a novel systematic methodology comprising four steps. Screening for catabolic potential was performed initially by using a targeted microarray containing 1426 probes for catabolic genes detection. Subsequently, a set of 56 primers was designed based on the positive signals detected. Finally, 134 clone libraries were constructed, and 1638 gene fragments related to key catabolic genes were sequenced using Sanger technology. As a result of these analyses, it was found that the relative abundance of Xanthomonadaceae was strongly correlated with the incidence of -Proteobacteria-related alkane hydroxylase genes at site contaminated with alkanes. Rhodocyclaceae were enriched at toluene-xylene contaminated areas, and correlated to the incidence of extradiol dioxygenases EXDOD and EXDODbt types and diiron monooxygenases evolutively related to -Proteobacteria. However, when both contaminants were present, an enrichment of both taxa was observed, but microarray profiles as well as clone libraries results showed a drastic shift of the prevalent pathways, suggesting that the catabolic organization was a function of the number of pollutants present in the environment.

## Dr. Hugo Roume

Laboratory of Microbial Ecology and Technology, Ghent University, Belgium

### A Biomolecular isolation framework for eco-systems biology

- **Fecha**: 29 de mayo de 2014
- **Hora**: 11:30 h
- **Lugar**: Seminario - Centro de Instrumentación Científica. Campus de

Fuentenueva.

- **Contenido**: Mixed microbial communities are complex, dynamic and heterogeneous. It is therefore essential thatbiomolecular fractions obtained for high-throughput omic analyses are representative of single samples to facilitate meaningful data integration, analysis and modeling. We have developed a new methodological framework for the reproducible isolation of high-quality genomic DNA, large and small RNA, proteins, and polar and non-polar metabolites from single unique mixed microbial community samples. The methodology is based around reproducible cryogenic sample preservation and cell lysis. Metabolites are extracted first using organic solvents, followed by the sequential isolation of nucleic acids and proteins using chromatographic spin columns. The methodology was validated by comparison to traditional dedicated and simultaneous biomolecular isolation methods. To prove the broad applicability of the methodology, we applied it to microbial consortia of biotechnological, environmental and biomedical research interest. The developed methodological framework lays the foundation for standardized molecular eco-systematic studies on a range of different microbial communities in the future.

## Dra. María Romero González

Department of Civil and Structural Engineering, University of Sheffield, UK

### Introducción a la espectroscopia Infrarrojo y sus aplicaciones en Biología

- **Fecha:** 22 de mayo de 2014
- **Hora**: 16:00 h
- **Lugar**: Aula A11, Facultad de Ciencias

## Dra. Sonja Selenska-Pobell

Helmholtz-Zentrum Dresden Rossendorf Dresden, Germany

### Microorganisms from extreme environments as templates for metallic nanoparticles: “bio-nano-catalysts and bio-nano-magnets”

- **Fecha:** 29 de abril de 2014
- **Hora:** 12:15 h
- **Lugar:** Seminario - Centro de Instrumentación Científica Campus de

Fuentenueva

## Dña. Marta Torres Béjar

Alumna egresada del máster en Investigación y Avances en Microbiología|

### Presentación escrita y oral de un Trabajo Fin de Máster

- **Fecha**: 6 de febrero de 2014
- **Hora**: 17:00 h
- **Lugar**: Aula 16, Facultad de Medicina