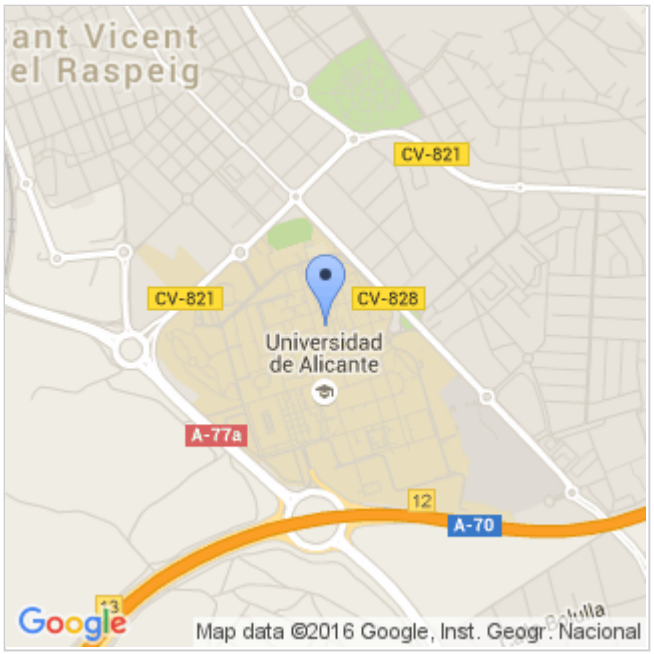
Expression of Interest



Contact Person/Scientist in Charge

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Universidad de Alicante

Department / Institute / Centre

- **Name of institution:** Department of Physiology, Genetics and Microbiology
- **Address:** Carretera Alicante - San Vicente S/N
- **Province:** Alicante

Research Area

- Life Sciences (LIF)

Brief description of the institution:

The University of Alicante (UA) was created in 1979. Today it educates and trains more than 36.000 students -2.500 of them are international students - and offers more than 80 undergraduate and 96 postgraduate programmes: consequently it is proportionally one of the fastest growing universities in Spain. The UA houses 227 research groups in Social and Legal Sciences, Experimental Sciences, Technological Sciences, Human Sciences, Education and Health Sciences and 15 Research Institutes (Water & Environment, Materials, Electrochemistry, Biodiversity, Chemical Processes and Organic Synthesis, and Modern Languages, among others). Thus, the UA employs over 2.400 researchers/ professors and has a complex management /administration structure of 1.300 people, which involves an annual budget of 175 million Euros.

UA is a young and dynamic university with vast experience in implementing EU funded projects in different programmes and areas, with presence in more than 60 countries worldwide. In the last 10 years, UA has successfully acted as coordinator of many Tempus, Alfa, Edulink projects involving Third Countries and Lifelong Learning and Framework Programme (FP, DG Research) Projects. Moreover, the participation in FP has been increasing in the last years, taking part in 25 5th FP, 26 6th FP, 45 7th FP projects (13 of them coordinated by UA), and 6 in H2020.

It is worth underline the big effort performed by UA in order to meet the commitment with the principles set out in the European Charter for Researchers and in the Code of Conduct for the Recruitment of Researcher

Brief description of the Centre/Research Group (including URL if applicable):

Cyanobacteria are a compact group of great ecological and biotechnological interest. We are using the unicellular cyanobacterium Synechococcus elongatus PCC 7942 as a model system in the following research lines:

1. The cyanobacterial nitrogen interaction network

A complex network of protein interactions allows cyanobacteria to control nitrogen metabolism in response to the intracellular nitrogen to carbon balance. PipX, a protein identified by us, is a multifunctional protein that forms complexes with the two nitrogen regulators PII and NtcA according to the 2-oxoglutarate levels. We are studying the molecular details and consequences of the complex protein interaction network in which these protein work

1. Two component systems and signaling mechanisms

Non-diazotrophic cyanobacteria respond to stress conditions by inducing a process termed chlorosis or bleaching, which involves the degradation of photosynthetic pigments and allow them to survive.

NblS (Non bleaching Sensor) the most conserved histidine kinase in cyanobacteria, interacts with SipA (NblS interacting protein A) and the response regulators RpaB and SrrA, forming a branched two-component system. We are working to test our recently proposed model for environmental control of the two phosphorylation pathways.

NblR, the phosphorylation independent response regulator (PIARR), is an atypical response regulator also involved in the response to stress

http://dfgm.ua.es/genetica/investigacion/cyanobacterial_genetics/index.html

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Project description:

Research Project:

Cyanobacteria are photosynthetic prokaryotes of enormous ecological importance and potential for biotechnological applications, but have received comparatively little attention in terms of molecular mechanisms of gene regulation. Our research group is using the model cyanobacterium

Synechococcus elongatus PCC7942 to obtain insights into fundamental regulatory interaction networks. We are particularly interested in signaling mechanisms that influence nitrogen regulation and photosynthesis adaptation.

To modulate the expression of genes involved in nitrogen assimilation, PipX, a unique cyanobacterial protein, interacts with the global transcriptional regulator NtcA and the signal transduction protein PII, which is found in all three domains of life as an integrator of signals of the nitrogen and carbon balance. PipX can form alternate complexes with NtcA and PII and these interactions are respectively stimulated and inhibited by 2-oxoglutarate, providing a mechanistic link between PII signaling and NtcA-regulated gene expression. However, our recent results indicate that PipX also interacts with additional transcription factors to modulate gene expression under conditions of nitrogen sufficiency, when PII-PipX complexes are favored. Understanding the molecular details of these interactions is our main goal.

Amongst the signaling pathways influencing photosynthesis adaptation we are focusing on specific two-component systems: the essential NblS-RpaB system, for which we have just revealed rather complex regulatory interactions with the SasA-RpaA circadian clock output system, and the NblR system, which is independent of phosphorylation. In both cases the molecular details await further investigation.

Applications

Letter of motivation and CVDeadline: 1st July 2016