*Poster*

# Histidine Kinases: A World to Discover in the Stress Response of Sphingopyxis granuli TFA


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## ABSTRACT

**Motivation:** In nature, there is a correlation between the diversity of habitats and the organisms that live in them. In such a way that different and changing environments can sometimes be observed, which causes stressful conditions for the organisms that inhabit them [1].

Alphaproteobacteria (α-proteobacteria) are a specific case of microorganisms that present a great diversity of metabolisms and distinct ecological environments. As a survival response to these different habitats, they have developed a stress response system called the General Stress Response (GSR), which allows them to survive in changing environments with stressful conditions [2].

The core of the alphaproteobacterial GSR system encompasses three main proteins: an extracytoplasmic function (ECF) sigma factor (σ factor) EcfG; an anti-sigma factor (anti-σ factor), NepR; and an anti-anti-sigma factor (anti-anti-σ), PhyR [3]. PhyR, consists of a unique multidomain protein that links signal transduction, acting as a phosphorylation-dependent protein-associated "switch" that also regulates the bacterial GSR system. In the case of Sphingopyxis granuli TFA, these regulatory proteins are duplicated in two different clusters, and whose functions within the GSR system have been accurately characterized.

In the case of TFA, there are four histidine kinases of the HWE and HisKA2 subfamily that could be involved in the regulation of PhyR (SGRAN_1165, SGRAN_1773, SGRAN_2544 and SGRAN_3483). In this work we have constructed single, double and triple mutants to study the involvement of these histidine kinases in the regulation of GSR in TFA and its role in protection against environmental stresses.

**Methods:** The experimental approach consists in constructing in frame deletion mutants of the genes encoding the histidine kinases.The aim is to observe the response to different environmental stresses (desiccation, osmotic, heavy metal and oxidative stress) and thus examine their involvement in the regulatory cascade.

**Results:** As a result, the successful construction of one single mutant in ΔSGRAN_3483, two double mutants in ΔSGRAN_1773_ΔSGRAN_3483 and ΔSGRAN_2544_ΔSGRAN_3483, and one triple mutant in ΔSGRAN_1773_ΔSGRAN_2544_ΔSGRAN_3483 was achieved. Additionally, the phenotypic characterization of their stress response was carried out, obtaining some clear evidence of its involvement in the GSR in TFA.

## REFERENCES

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