

TRANSCRIPTIONAL RESPONSES OF *Posidonia oceanica* UNDER MULTIPLE

STRESSES: THE INFLUENCE OF THE NATIVE ENVIRONMENT

JESSICA PAZZAGLIA, Alex Santillán-Sarmiento, Miriam Ruocco, Emanuela Dattolo, Antonio Terlizzi, Lazaro Marín-Guirao, Gabriele Procaccini

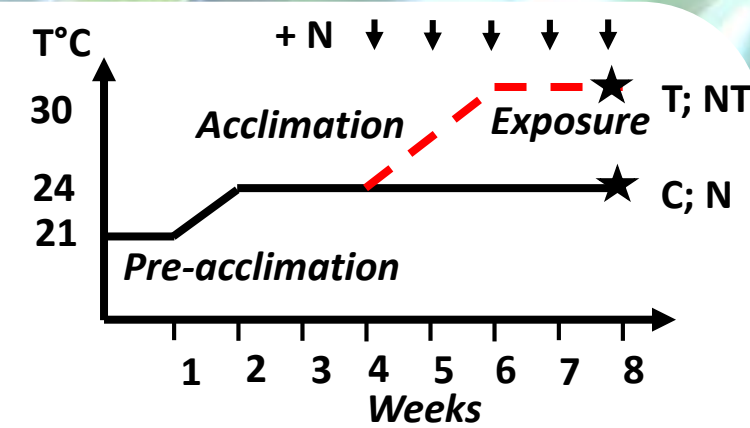
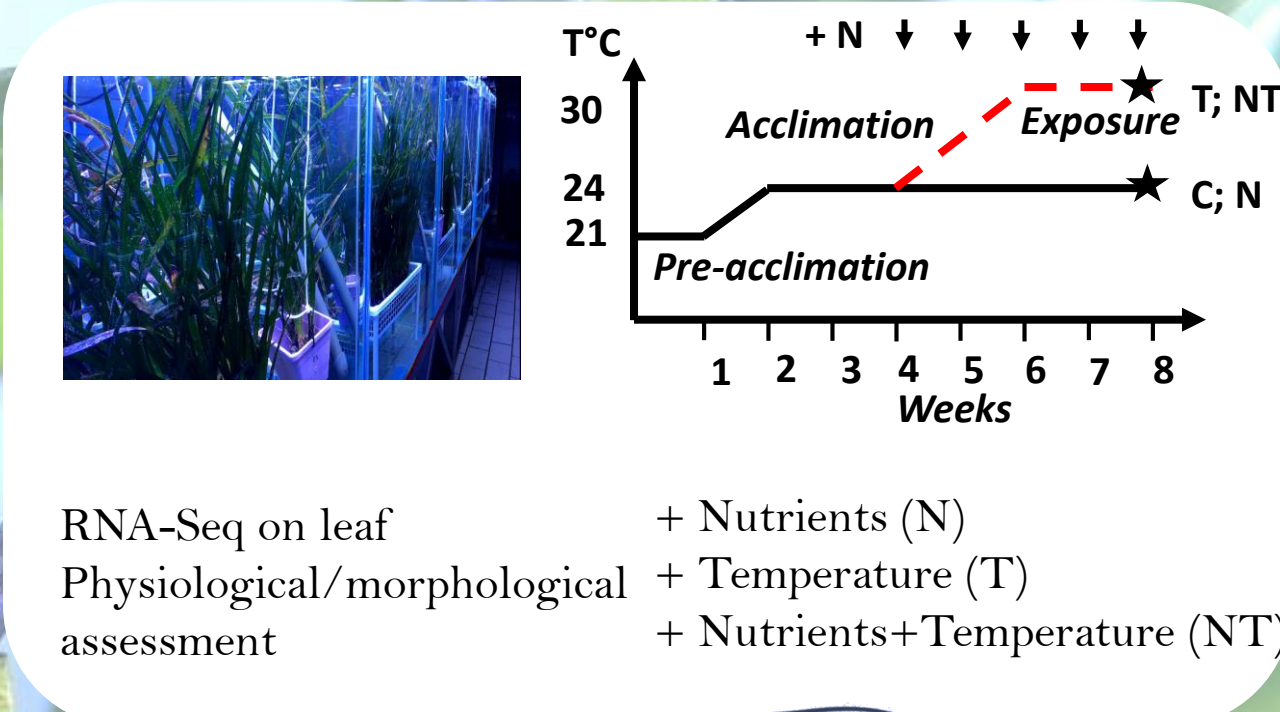
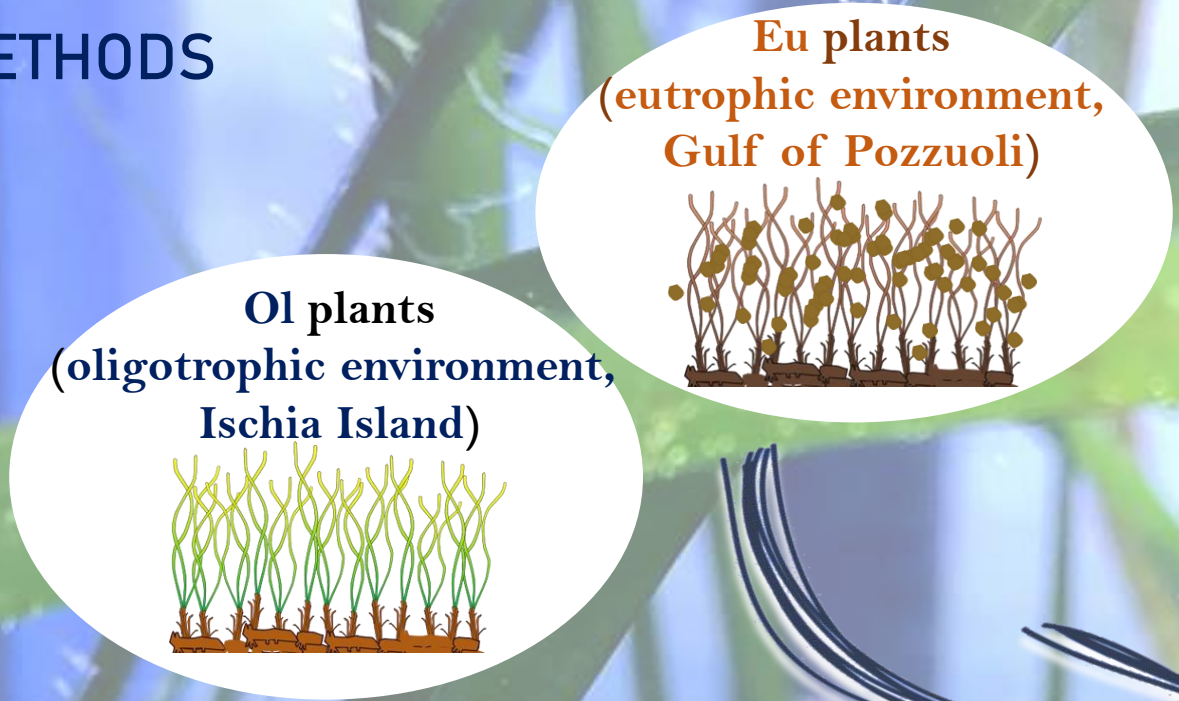
University of Trieste, Piazzale Europa Trieste, 34127, Trieste, Stazione Zoologica Anton Dohrn, Villa Comunale, 80121, Napoli, (Italy)



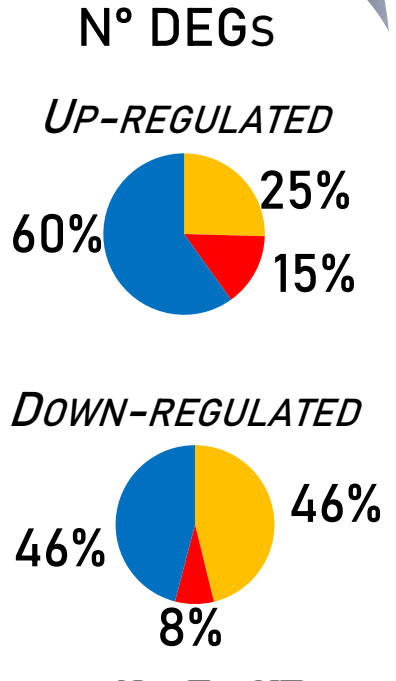
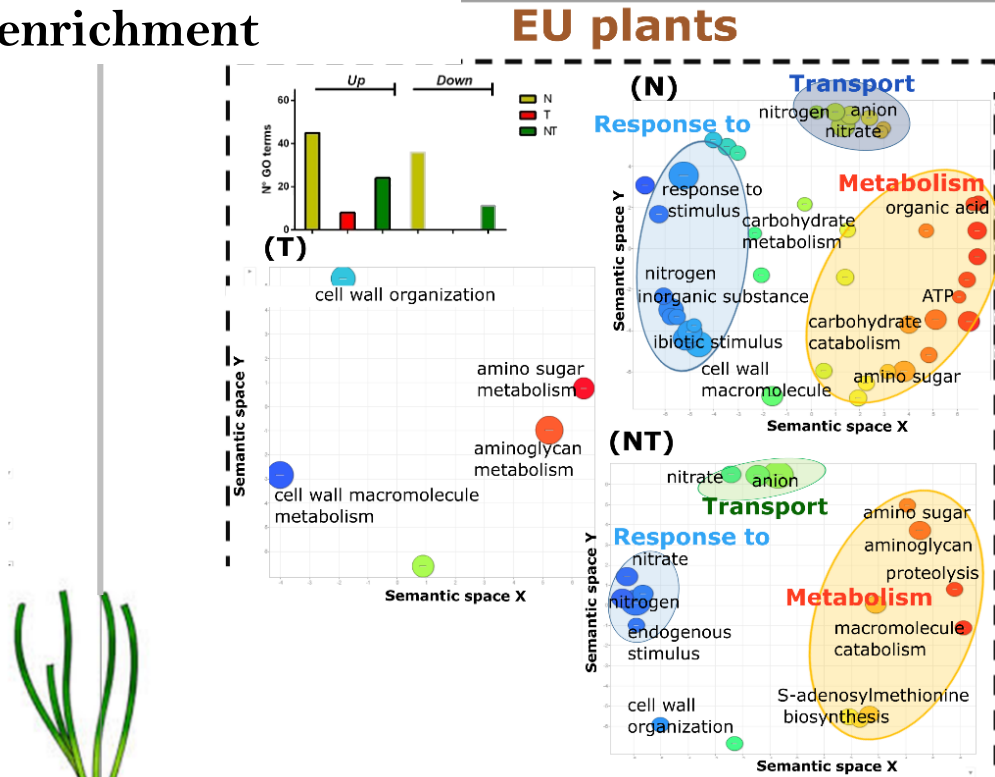
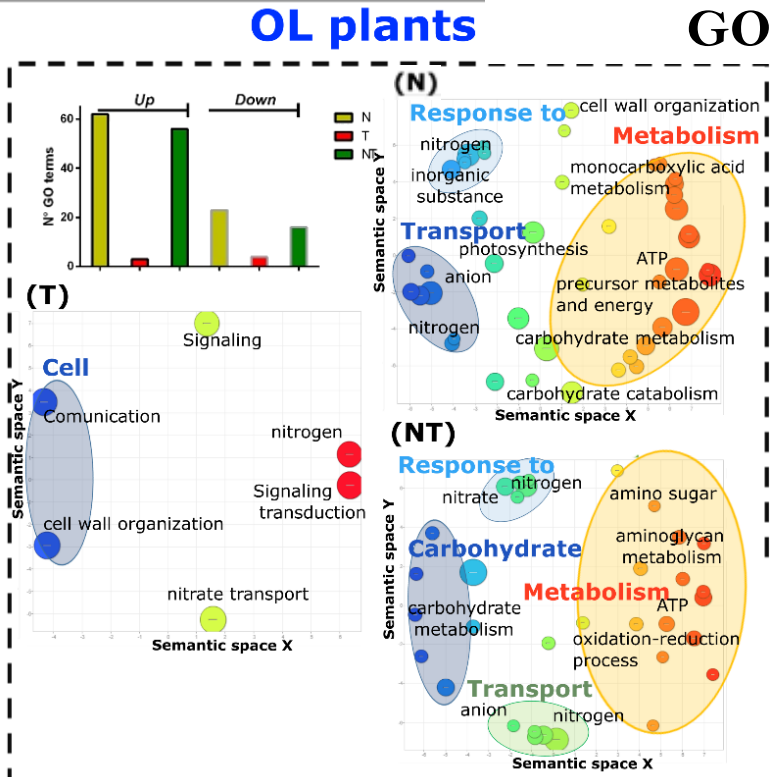
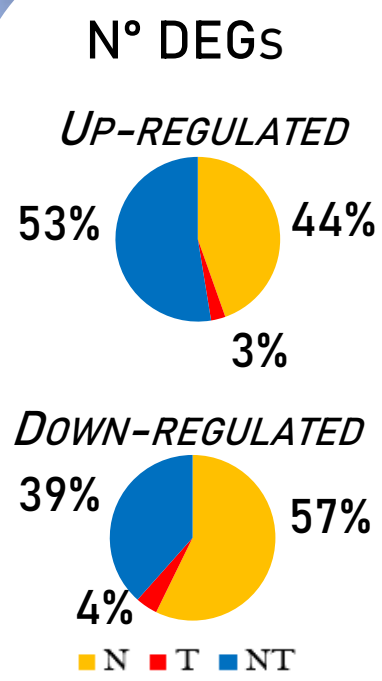
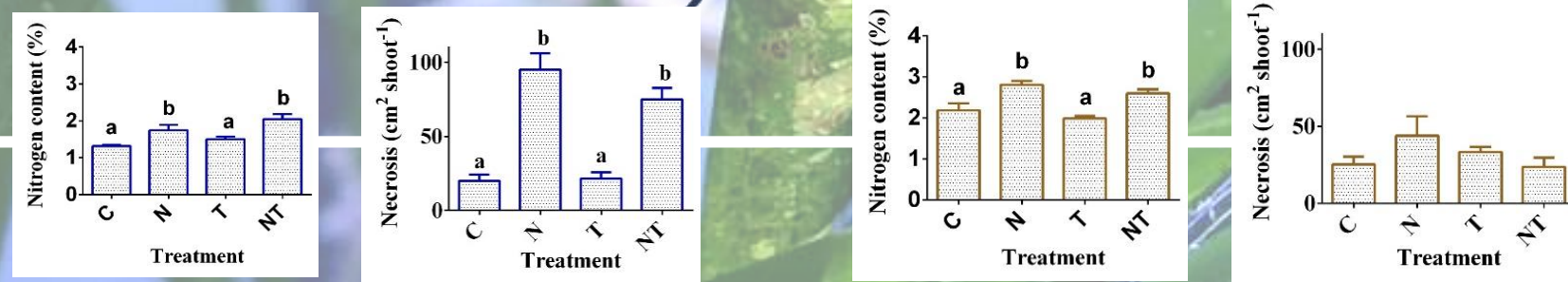
INTRODUCTION

Seagrasses are declining worldwide due to the intensification of warming, eutrophication events and the occurrence of rapid environmental changes. *Posidonia oceanica* is endemic for the Mediterranean Sea and ranks among the slowest-growing and longest-lived plants on earth. Recent evidence revealed that pre adaptation to local environmental conditions play a crucial role in driving seagrass responses to stress. Here we aimed to analyse the physiological and transcriptional responses to multiple stresses of *P. oceanica* plants living in different environmental conditions.

METHODS



RESULTS



OL plants

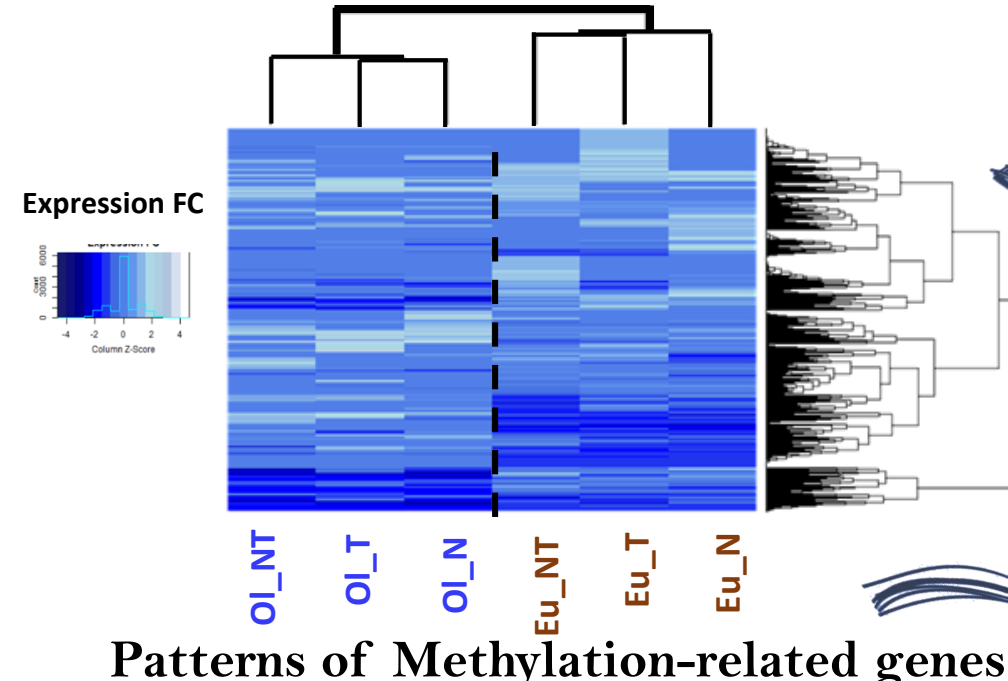
N; NT: Leaf nitrogen content and necrotic area increased; high metabolic activation and transcriptomic responses.

T: Leaf nitrogen content and necrotic area were similar to the control; low metabolic activation and transcriptomic responses

EU plants

N; NT: Leaf nitrogen content increased; Necrotic area was similar to the control; high metabolic activation and transcriptomic responses.

T: Leaf nitrogen content and necrotic area were similar to the control; low metabolic activation and transcriptomic responses



CONCLUSIONS

The different life histories of *Posidonia oceanica* plants are crucial to understand future persistence of this species, especially under rapid environmental changes. Nutrients are the main stressor that trigger physiological and transcriptomic responses. OL plants activated metabolic processes, to overcome nutrients excess, whereas EU plants, showed similar responses with the activation of regulatory mechanisms. This was corroborated by different patterns of methylation related genes. Thus, local environmental conditions seemed to differentiate plants responses to multiple stresses through transcriptional regulation that could have an epigenetic basis.