Reflecting on the 21st International Sunflower Conference: A Report on My Experience and Insights

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Abstract

The 21st International Sunflower Conference provided an exceptional platform for sharing and discussing advancements in sunflower research. This report reflects on my participation as a PhD student, where I presented my work on "Whole-genome Identification and Expression of Lateral Organ Boundaries Domain Genes under Biotic and Abiotic Stresses in *Helianthus annuus* L." Receiving the Student Conference Award facilitated my involvement and enabled me to engage in meaningful academic exchanges. The conference offered a comprehensive overview of the latest research trends and methodologies, fostering valuable discussions and collaborations. This report highlights the enriching experience of presenting my research, the insights gained from the conference, and the memorable moments captured in an accompanying photo gallery. The support provided by the award was instrumental in enhancing my conference experience and contributing to my professional development.

Introduction

The 21st International Sunflower Conference provided a valuable opportunity to present my research on the "Whole-genome Identification and Expression of Lateral Organ Boundaries Domain Genes under Biotic and Abiotic Stresses in Helianthus annuus L." The study focused on the Lateral Organ Boundaries Domain (LBD) proteins, a plant-specific transcription factor family crucial for plant development, phytohormone regulation, and stress responses. Despite their significance, the *LBD* gene family in sunflowers *(Helianthus annuus* L.) had not been previously explored. My research involved identifying 47 *LBD* genes in the sunflower genome, categorizing them into Class I and Class II clusters, and analyzing their distribution across the 17 chromosomes. Evolutionary and collinearity analyses revealed insights into gene expansion and duplication. Expression profiles indicated organ-specific patterns, with key genes like *HaLBD11* and *HaLBD25* implicated in drought stress and *HaLBD10* in parasitism responses. Structural predictions using AlphaFold3, coupled with network and enrichment analyses, underscored the *LBD* gene family's role in regulating growth and stress responses. Presenting these findings at the conference and receiving the Student Conference Award enabled me to share this groundbreaking work and engage with peers and experts, enriching my research experience and broadening my academic perspective.

Academic Exchange and Insights

During my presentation, I had the opportunity to engage in thought-provoking discussions with esteemed scholars, which significantly enriched my research perspective.

One of the insightful questions came from Dr. Nicolas Langlade from INRAE, University of Toulouse. He inquired about the absence of heat treatment analysis in my WGCNA results, which showed a more significant association of heat treatment with various gene modules. My initial response highlighted that the study focused on *LBD* genes, and thus, I selected the brown module where *LBD* genes played a central role. However, I could not adequately address the specifics of heat treatment conditions at the time. During the field trip on the final day of the conference, I had the opportunity to clarify that the seedlings were exposed to 39°C for 4 hours, 8 hours, 16 hours, and 32 hours (designated as H4, H8, H16, and H32, respectively) for heat stress. Dr. Langlade's constructive questions and his respectful demeanor towards presenters under pressure were greatly appreciated. His research on Sunflower Genomics, Phenomics, and tolerance to abiotic stresses has been highly inspiring and valuable to my work. I have promised to send him a copy of my paper once it is published and I am grateful for his support and guidance. I wish him continued success and good health.

Another notable suggestion came from Dr. CREUX from FABI, who recommended integrating heatmaps of expression profiling under environmental stresses with images of cis-acting elements located in promoters, using the same gene order. This advice addressed a longstanding issue I faced, as the separation of these two types of data made it difficult to observe their relationship. Following Dr. CREUX's suggestion, I will forego the phylogenetic tree for gene arrangement and instead present the heatmaps and cis-acting element images in the same gene order. This approach will enhance the clarity of the connections between cis-acting elements and expression profiling for readers.

The feedback and suggestions from both Professor Langlade and Dr. CREUX have been immensely beneficial, enhancing my understanding and guiding my future analyses. I am deeply thankful to the Student Conference Award and ISA for providing me with the opportunity to present my work, interact with distinguished scholars, and broaden my academic horizons.

Photo Gallery

The electronic photo album includes memorable moments from the conference, including photographs of new friends made during the event. These images capture the essence of the conference experience and the valuable interactions that occurred.