ABSTRACT

Plants constantly cope with various abiotic and biotic stress while interacting with the environment by utilizing their immunity. Computational biology has become one of the most important approaches in the study of plant biology with the assistance next-generation sequencing data analysis since mid-2000s. Although many core plant immune questions and functions of key elements in cytoskeleton have been revealed, there are still many foundational questions that remain mysterious. Plants may survive after experiencing biotic and abiotic stress, such as fungal infection and drought stress, but the detailed progress of the immune response is still not well-covered. Modern maize evolved in South America followed by key traits were selected under the influence of both nature and cultural preference, but the specific selection under culture influence is still unknown. While part of ACTIN DEPOLYMERIZING FACTOR (ADF), which is essential as one the actin-binding protein (ABP) of the plant cytoskeleton to regulate the plant's immune system's ability, is known, the multiple functions of ADFs remain unknown. As a result, this is a field of research where analysis through computational biology is necessary to answer questions about plant immunity, as well as to build biological models for it.

In this dissertation, I focus on using a combination of computation biology methods and plant biological knowledge to uncover the role of plant immunity in the response to biotic and abiotic stress, Incan cultural influence on selection of key traits of maize in South America and *ADF* gene family evolution and gene function prediction. First, I addressed the question of "why Fusarium virguliforme (*Fv*) is asymptomatic on monocot host and a symptomatic eudicot host" utilizing multiple methods, and I found that root senescence is a primary contributing factor underlying colonization and disease progression in symptomatic versus asymptomatic host–fungal interactions. Furthermore, I identified the role of NDR1 (NON-RACE-SPECIFIC DISEASE RISISTANCE1) in drought response by analyzing the transcriptional data from different treatments at various times. The results revealed that NDR1 is required for signaling processes associated with plant cell drought stress responses. Lastly, I identified the key traits that were selected by under Inca culture, including shorter growing season, greater stress-resistant, and sweeter taste, between ancient and modern maize in South America. This was achieved by utilizing a combination of several computational methods, along with influence of Incan culture and maize diversity. This study provides insights into the complex biocultural role that Inca culture had in determining the direction of maize diversity in South America. As the supplement, I predicted the potential functions of ADF by identifying the evolutionary history of the *ADF* gene family through expression pattern. The results uncovered the potential function of ADFs and provided direction for future research in traditional biology. In summary, my work has provided significant insights into the plant immunity by using computational biology knowledge.