**Unveiling the influence of transmembrane domains in plants against drought stress**

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**Identification of transmembrane proteins is necessary not only for furthering knowledge, but also in highlighting the means of how plants may have survived against stressors up until now.**

**Introduction**

Stress, although a fundamental and necessary stimulus for living organisms, can ultimately result in the demise of plants. An array of innate mechanisms within the plant are activated during stressful events, regardless of whether it is a short or long time. With the ever-growing concern of climate change resulting in an onslaught of high temperatures and periods of drought, further identifying and characterizing mechanisms mentioned above may help increase plant survivability. Much of what drives the response to stress is made up of transmembrane proteins, which are proteins located within the cell membrane and have many functions. Most of what is known of transmembrane proteins and the domains that they inhabit derive from animals and humans. Those of plant origin and their function are still unknown, as only 1 percent of transmembrane proteins have been sequenced (Fleishman et al., 2006). Highlighting the ever growing need in sequencing and identifying protein classes to provide further insight to the make-up of plants at a cellular level.

Transmembrane proteins are characterized by one of two protein domains, which is dependent on the structure that said protein possesses. Even if they are classified by their structure, alpha-helices, or beta barrels, the number of proteins classified as transmembrane due to their location in the cell membrane is vast and continuously increasing. Their use in animal and human research is extensive, with some used for drug research and even as a biomarker for malignant tumors (Zhou et al., 2022). Studies utilizing these proteins for health-related research demonstrate the potential of utilizing transmembrane proteins to improve the health and productivity of plants. Improving plant productivity is even more true for the plants classified as crops used for both human and animal consumption, as the ever-increasing population has elevated the need to produce enough to feed each mouth. However, for this to occur, the identification of said proteins must continue.

**Recent Progress**

Although there has been extensive research identifying and illustrating the specific proteins and their functionality within the membrane of mammals, much has yet been discovered within the Kingdom Plantae. Even more so when focusing on the transmembrane proteins that assist in the responses against various stressors that a plant may experience in their lifetime. Plant productivity drives the continuing existence of all living creatures on earth, thus locating proteins that assist in this productivity and ultimately survivability is necessary. Although there may be differences across species, identifying transmembrane proteins and their domains may open a means of alteration of the genetic code to increase their ability to thrive. A group of researchers were able to identify a certain protein family in the faba bean that allows seedlings to withstand periods of drought (Zhao et al., 2024). With the emergence of more advanced sequencing technology, researchers have also begun to identify different proteins in the cereal family, Arabidopsis, and many more plants and crops.

***Identification of transmembrane proteins resistant against abiotic stressors***

Faba beans, considered legumes, are renowned for their high-quality protein, dietary fiber, and essential nutrients (Zhao et al., 2024). Although it is considered to be one of the top legumes produced in the world, limitations on improving yield have arisen. Limitations have arisen to the exposure of abiotic stressors, in this case, drought, which arises from the environment and not from another living being. Abiotic stress can occur for many reasons, such as strong winds and drought (Al-Saharin et al., 2022). Although they have thrived until now, allowing them to be considered one of the four top legume crops produced, identifying internal mechanisms could be enhanced to improve their adaptability against abiotic stress. Thaumatin-like proteins (TLPs) have been identified in plants and other organisms. These proteins have been found to hold different roles within plants (Zhao et al., 2024), with their function also allowing plants to respond against both biotic and abiotic stress. Although this family of proteins is known to be in many plant species, it does not automatically indicate that they would be present in the faba bean. Even if they are found within this plant, it is still being determined how vigorously this protein family is combating drought.

With this in mind, researchers out of Zhang et al. lab conducted a study aiming to identify and quantify the functionality of TLPs within two varieties of beans. First, with the use of sequences already generated by the lab.

Researchers were able to identify within the faba bean genome regions of conserved cysteine residues and Thaumatin signature. This confirms the presence of the Thaumatin-like proteins within the faba bean, which is necessary for the purpose of this study.

**Discussion**

Results from the study are promising as they elucidate that the presence of these protein families allows for drought resistance in the faba bean. More importantly, the number and degree of TLPs found within the faba bean allows for further knowledge to be obtained. This may open a new avenue in research to occur with the intent of modified proteins to improve drought resistance in other species of faba beans. which hold a potential to occur as Zhao et al., did find that overexpression of the TLPs in tobacco plants resulted in an enhanced drought resistance. As the two species utilized were known for their drought-resistance, it does indicate that not all faba beans in production are the same.

A concern that is raised is if this translatability to the plants from lab to practice. In this study, the plant samples that were used were raised outside of their normal environment.

**References**

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