A Heterologous System Examination of JACKDAW Mutant Variants' Effects on Complex Formation With SHORT-ROOT and SCARECROW

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Distinct features of transcription factors play a primary role in plant growth and development. Understanding the root development of plants can further develop a more robust, improved version of plant roots. Previous studies show how JACKDAW, a transcription factor crucial for plant development and root formation, interacts with SHORT-ROOT and SCARECROW, two transcription factors involved in asymmetric cell division and root development. This research identified the possible necessary domains and amino acids within the JACKDAW protein that facilitate their interaction by studying the effect of JACKDAW mutant variants on the localization of SHORT-ROOT and SCARECROW. This was done within a heterologous mammalian expression system, HeLa cells. Point-mutations of JKD were induced using primers. HeLa cells were cultured to provide the expression system of the study. All proteins were co-transfected into the cells using transfection reagents. Expression levels were observed using a scanning laser confocal microscope and fluorescent levels were measured using ImageJ software. JACKDAW point mutations showed fluctuating percentages of SHORT-ROOT and SCARECROW localization. Moreover, JKD point mutations caused different levels of SHORT-ROOT nuclear retention. Accordingly, such results showed that the specific sub regions of JACKDAW play an important role in the localization of SHORT-ROOT and SCARECROW. These findings can be involved in regulating cell layering and the development of roots by controlling SHORT-ROOT nuclear retention. Such regulation and control of development, especially in roots, will allow plants to possibly extend their roots to further destinations underground, which is the main source of water in Saudi Arabia, and other global regions.

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