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Disruption of Arabidopsis thaliana dihydrolipoyl acetyltransferase gene expression using T-DNA and RNA interference

Arabidopsis thaliana is commonly used as a model organism for plant functional genomics research. The genome is relatively small and has been completely sequenced, the complete life cycle is relatively short, it is amenable to genetic manipulation, and is closely related to economically important crop plants. It is evident from the results of the A. thaliana genome sequencing project that many proteins are encoded by small multi-gene families. What is the reason for this apparent redundancy? One possibility is that the functions of the genes are vital for plant survival and the genome has accumulated "backup" copies, in case the primary gene is damaged. Another possibility is that genes that appear alike actually play some specialized role. For example, one gene might be expressed only in flowers while another is expressed in the leaves. The A. thaliana includes three genes for the important respiratory enzyme dihydrolipoyl acetyltransferase (E2). Two of the genes encode a protein with a single lipoyl domain, while the third has two lipoyl domains. A good way to study the function of multiple genes is to disrupt their expression. The most common method of gene disruption in plants uses what is called "T-DNA insertional mutagenesis." This method produces non-functional proteins. Another, relatively new, method uses RNA interference (RNAi) to prevent protein translation. RNAi uses a naturally occurring pathway to destroy the mRNA prior to translation of the protein. By using a combination of these two methods of molecular manipulation we will be closer to answering the question of why these genes exist in duplicate.

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