Cloning and Functional Characterization of the \textit{Fatty Acid Elongase 1} (\textit{Fae1}) Gene from High Erucic \textit{Crambe Abyssinica} Cv. Prophet

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The strategic goal of our research is to modify high erucic acid rapeseed (HEAR) germplasm to increase the content of very long chain fatty acids (VLCFAs, particulary erucic 22:1c13) in the seed oil for industrial applications. The 3-ketoacyl-CoA synthase (\textit{Fatty Acid Elongase - FAE}) catalyzing the condensation reaction plays a key role in determining the chain length of fatty acid products found in seed oils and is one of the rate-limiting enzymes for VLCFA production in developing seeds. Looking for more efficient fatty acid elongase genes, we selected \textit{Crambe abyssinica} as a source based on the fact that this plant is capable of producing significant amounts of erucic acid in the seeds (60% of total fatty acids). Using a PCR based approach, a cDNA of a putative embryo \textit{FAE} was obtained showing high homology to known plant fatty acid elongases. To study the function of the protein encoded by the \textit{Crambe FAE}, the coding region was linked to the \textit{GAL1}-inducible promoter in the yeast expression vector pYES2.1/V5-HisTOPO and to the strong seed-specific napin promoter and subsequently transformed into \textit{Saccharomyces cerevisiae} and \textit{Arabidopsis thaliana} plants, respectively. Results from these heterologous expression experiments with the \textit{Crambe FAE} will be presented.