**SMP-CONTAINING PROTEINS AT MEMBRANE CONTACT SITES: SUBCELLULAR LOCALIZATION AND CHARACTERIZATION.**

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Membrane contact sites (MCS) are microdomains where two membranes of two different organelles are in close apposition, but they do not fuse. MCS are essential for non-vesicular transport of lipids. This lipid transport is mediated by several families of proteins which all of them contain a lipid transport domain, as the synaptotagmin-like mitochondrial lipid-binding (SMP) domain. The most studied SMP protein is Arabidopsis SYT1 which is known to be involved in tolerance to multiple abiotic stresses. Later studies in other SMP proteins of the same family have shown that SYT1 and homologous such as SYT3 or SYT5 gave similar results. However, little information is available about the role other SMP proteins in plants. We have studied the occurrence of additional SMP proteins in A. thaliana and S. lycopersicum. In order to identify these proteins, SMP sequences from human and yeast were used to identify their remote orthologues in A. thaliana and S. lycopersicum, allowing the identification of several putative encoding SMP domains. We have found that some of the identified proteins are exclusive of plants as they do not have direct orthologs in yeast nor human. Transient expression in N. benthamiana leaves followed by confocal microscopy was used to study the subcellular localization of these proteins. Our results show that some of these proteins are localized at ER-Golgi contact sites and two other proteins at ER-Chloroplast sites. Finally, to determine whether these proteins are involved in abiotic stress tolerance, we have analysed the root growth and seed germination rates of Arabidopsis mutants for these genes under different conditions. Some of these mutants have shown different germination rates in media supplemented with NaCl and different rates of expanded cotyledons in media supplemented with ABA. These results suggest that some these proteins may be implicated in abiotic stress signalling through an ABA-dependent pathway.