Abstract

Transmembrane adaptor proteins (TRAPs) function as a scaffolding anchor for numerous signaling molecules and facilitate formation of large signaling complexes near the plasma membrane. They regulate spatio-temporal organization of signaling events in order to transduce fast and effective signal from surface receptors into the cell nucleus. The importance of described TRAPs in the development and proper functioning of immune cells in relation to their localization within lipid rafts is still under debate. The simple reason is the lack of a profound phenotype in knock-out mice. The described phenotypes observed in animals deficient in ITAM-containing adaptors of immunoreceptors as well as lipid raft adaptor Lat all lead to the block in the T-cell development and impaired TCR signaling. The subject of my diploma thesis is to perform bioinformatic search and filter candidate TRAP genes according to predicted and published data. Selected TRAP candidates were subjected to functional characterization. I checked for their localization to the plasma membrane and correlate their ectopic overexpression with the expression of CD69 surface Tcell activation marker. From 14 candidate TRAPs, only a single Pdzk1ip1 protein is probably localized to the plasma membrane but its expression does not influence CD69 upregulation before and after TCR stimulation. On the other hand, overexpression of cytoplasmic Crtap protein showed constitutive and TCR-induced upregulation comparable to the negative control Shp-1. On the basis of our experimental data we identified two potentially interesting candidate genes and we will proceed with the extended functional characterization. We plan to look at the effects of overexpression/downregulation of candidate genes on the development and activation of immune cells in mouse *in vivo* model of hematopoietic engraftment.

Key words: lipid rafts, transmembrane adaptor proteins (TRAPs), candidate TRAPs, membrane localization, CD69