Abstract

Transmembrane adaptor proteins play an important role in signal transduction cascades emanating from immune cell receptors leading to cellular effector mechanisms. Despite the lack of enzymatic function, their sequence contains interaction motifs which organize other proteins in time and space and initiates building of the signaling complexes.

Functionally the most important and for the longest time known TRAPs are the ones associated with immune receptors. Their deficiency has severe impacts on the signal transduction and knock-out mice show dramatic phenotypes. The deficiency of Lat - the first discovered TRAP, which is not constitutively associated with immune receptors – has comparable effects on signaling in lymphocytes. The difference between the first group of TRAPs and Lat is not only the type of association with receptors, but also the lack of tyrosine – based activation motifs (ITAMs) in Lat, but Lat contains several other binding motifs also based on the phosphorylation of tyrosine. The group of TRAPs similar to Lat up today contains eight members, but all of them, except of Lat, has only very mild or undetectable phenotype in the knock-out mice.

In this work I searched the protein databases for proteins with the characteristics of TRAP using the bioinformatic tools. Based on our results, it looks that the majority of TRAPs have been already discovered. We have found only a few proteins, which share the characteristics similar to TRAPs. We had to loose the TRAP definition (we have allowed the existence of the intracellular domains) in order to select 14 candidate genes.

The expression of candidate genes in different mouse tissues and cells have been measured using real – time PCR. From the expression data some of our candidates seem to have similar expression profile as the most important TRAP Lat (Acpl2, Pdzk1ip1), some others change their expression upon T – cell activation (Acpl2, Skip).

In the next phase of the research we would like to focus on some of the most promising candidate genes and perform *in vitro* reporter transcription assay. We will also try to understand whether these genes affects immune system development and function *in vivo* using the mouse model based on the hematopoietic stem cells transplantation with altered expression level of our candidate genes.