STANNIOCALCIN-1 (STC1) AS A PUTATIVE MICROENVIRONMENT MARKER IN CHILDHOOD ACUTE LYMPHOBLASTIC LEUKEMIA (ALL)

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Leukemia cells interact with the bone marrow (BM) microenvironment, which provides them proliferative advantages. We stimulated BM stromal cells by co-cultivation with primary ALL cells or addition of ALL patient's plasma to the culture medium and then performed a microarray analysis of the gene expression in the stromal cells. Using quantitative RT-PCR analysis we showed that STC1 is among the genes that showed higher levels of activation in leukemia cells vs. controls. STC1 is is widely expressed in various tissues but neither its receptor nor its exact functions are known in mammals. STC1 cDNA was amplified from cells from healthy BM stromal cells and cloned into vectors for heterologous protein expression and yeast two-hybrid assays. STC1 protein was expressed in soluble form in insect cells using the baculovirus system and purification is currently optimized for both crystallization trials and spectroscopic analyses. Screening of human cDNA libraries from fetal brain, bone marrow and leucocytes, for STC1 interacting proteins, we found plasma membrane receptors, mitochondrial as well as nuclear proteins. The found proteins correspond well to several functional and localization data reported so far for STC1 and their possible functional meanings are discussed. Financial support: FAPESP, CNPq and LNLS.