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Pattern recognition receptors (PRRs) and cancer: Molecular analysis of PRRs expression in several human cancer cell lines

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BACKGROUND: Pattern recognition receptors (PRRs) are the main sensors of pathogens and danger signals in innate immunity. They are mainly expressed by macrophages and dendritic cells of different organs. Toll like receptors (TLRs) are the most studied and best characterized PRRs, which are responsible for sensing pathogen associated molecular patterns (PAMP) and also products of inflamed tissues, which are called damage associated molecular patterns (DAMP). TLRs activation triggers signaling pathways that lead to activation of transcription factors such as nuclear factor- κ B and the interferon regulatory factors. These in turn lead to induction of immune and inflammatory genes, including such important cytokines as tumor necrosis factor- α and type I interferons. The contribution of PRRs in inflammation induced by microbial infection, tissue damage and cancer are a major topic in immunology as well as cancer biology and immunotherapy. Much evidence points to the role for PRRs and especially TLRs in immune and inflammatory diseases and increasingly in cancer. Cancer cell lines are one of the best models to study the biological roles of PRRs in cancer and tumor biology. The objectives of the present study were to analyze the expression of several PRRs including TLR2, TLR4, MyD88 and CD14 transcripts in several human cancer cell lines, namely: human glioblastoma cell line U87 MG, human acute monocytic leukemia cell line THP-1, and human lung adenocarcinoma epithelial cell line A549. Moreover, the expression level of these PRRs genes in peripheral blood mononuclear cells (PBMC) of healthy individuals was compared with those of the cancer cell lines. **RESULTS:** According to our results, human glioblastoma cell line U87 MG and human acute monocytic leukemia cell line THP-1 express TLR2, TLR4, MyD88 and CD14 transcripts. However, the expression analysis of these genes in human lung adenocarcinoma epithelial cell line A549 was not straightforward. Moreover, the quantitative gene expression studies revealed a differential expression of these genes in human cancer cell lines in comparison to the PBMC of healthy individuals. **CONCLUSION:** The different expression level of PRRs in human cancer cell lines in comparison to PBMC observed in this study can give more insights on PRRs mediated cancer pathology, which might have potential implications in future cancer immunotherapy.