The Toll Like Receptors (TLR) comprise a family of a transmembrane protein type I that have an extracellular domain of a leucine-rich repeat and an intracellular domain homologous to human interleukin 1. They are the primary molecular mechanism of the host to recognize the microorganisms, such as bacteria, fungi and viruses. Ten TLRs have been recognized for human, and the activation of TLR develops a signaling cascade that stimulates the immune system. The objective of this work was data and literature mining of polymorphisms of the TLR family and the association with the risk of cancer. The data and literature from the SNPs of TLRs were collected in dbSNP/NCBI. With exception of TLR3 and 8 they showed association with a variety of cancers. For TLR1 (rs4833095) prostate cancer; TLR2 (rs3804099) reduced risk of colon cancer associated with cigarette smoking and (rs3804100) Non Hodgkin Lymphoma (NHL), marginal zone lymphoma (MZL); TLR 4 (rs4986790) Prostate cancer, gastric MALT lymphomas, NHL, precancerous gastric lesions, (rs4986791) gallbladder cancer (GBC), gastric cancer, precancerous gastric lesions; TLR5 (rs5744174) gastric carcinogenesis; TLR6 (rs5743815) NHL, chronic lymphocytic lymphoma, Follicular lymphoma and diffuse large B-cell lymphoma; TLR7 (rs179008) Hodgkin’s lymphoma; TLR 9 (rs352140) cervical cancer, Hodgkin Lymphoma; TLR10 (rs11096955) Reduced risk of prostate cancer, (rs11096956) NHL, (rs11466657) Decreased meningioma risk. In the literature we can find a lot of conflicts with the data found about the SNPs and their association with different types of cancers. This can occur because of the heterogeneity of the SNPs and the ethnicity of the groups. To resolve these kinds of gaps, comprehensive genome association studies, using next generation sequencing, can be made in various populations to improve the linkage of TLRs mutations and cancers, as strategies to develop new biomarkers to diagnostic and personalized therapeutics.

Keys Word: Cancer, TLR, SNP.
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