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A Meta-Analysis of Non-Coding Polymorphisms Linked to Pre-Cancerous Lesions and Cervical Cancer

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Abstract

Objectives: To investigate the risk of SNPs found in non-coding areas of genes linked to cervical cancer. Neity, as well as publishing bias and statistical signifcance as measured by the p-value.

Methods: To uncover literature containing the relationship between single nucleotide polymorphisms with cervical cancer, the PubMed database was extensively searched using text-mining tools. If case-control studies matched the selection criteria, they were examined for the meta-analysis until June 2020. Each case-control study's polymorphisms were examined for the existence of genotype data before being separated into groups based on precancerous and cancerous cervix situations. The odds ratio and 95% confdence intervals (CI) were used to explore the impact of polymorphisms using various genetic models (allele, dominant, recessive, heterozygous and homozygous). The p-value was also used to assess heterogeneity, publication bias, and statistical signifcance.

Results: The meta-analysis evaluated 120 studies covering 48 distinct non-coding SNPs with 37,123 cases and 39,641 control data. For 43, 8, and 11 SNPs, the genotype data was divided into Cancer, Precancer, and "Cancer + Precancer" groups. The meta-analysis found 21 and 1 SNPs to be signifcant in the Cancer and "Cancer + Precancer" categories, respectively. rs1143627 (IL1B), rs1800795 (IL6), rs1800871 (IL10), rs568408 (IL12A), rs3312227 (IL12B), rs2275913 (IL17A), rs5742909 (CTLA4), rs1800629 (TNF), and rs4646903 (CYP1A1) were discovered to increase risk of cervical cancer in at least three.

Conclusion: We identifed potential non-coding SNPs corresponding to various cytokines like interleukins (ILs), tumour necrosis factor (TNF), interferon (IFN) and other immune related genes like toll like receptor (TLR), cytotoxic T-lymphocyte associated protein (CTLA) and matrix metalloproteinase (MMP), as signifcant with increased pooled OR in this meta-analysis pointing to risk association of the immune-related genes in cervical carcinogenesis.

Introduction

Materials and Method

Data collection

Classi cation of study population based on the condition of cervical cells

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