RISK POLYMORPHISMS IN ORAL LEUKOPLAKIA: A SYSTEMATIC REVIEW

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Introduction
The greatest challenge is to predict which oral leukoplakia (OL) will be able to progress to oral squamous cell carcinoma.
Purpose
Generally, the systematic reviews and meta-analysis of polymorphisms are focused in genes related to unique cellular process; in this work, our goal was to identify studied genes in last decade and to know which ones are related to the risk of developing OL.
Method
Eligible gene/polymorphism studies were identified by electronic searches. Individual participant data of 2054 Oral Leukoplakia and 3493 controls from 16 genetic studies were analyzed, yielding adjusted (tobacco, gender, age and alcohol) odds ratios (OR) and 95% confidence intervals (CIs) comparing cases with controls.
Results
The following genes/polymorphisms were seen to have significant association with increased risk of *OL*: CYPA1 (m1/m2), XDP (Gln/Gln), GSTM1 (null), and P53 (intron 6). In contrast, COX-2 (exon 10), P53 (intron 3), XRCC3 (GG), and PRKDC (rs7003908) polymorphisms are associated with a diminished risk of OL.
Conclusions
According to the results of this work, we conclude that all genotypes are heterozygous or homozygous for the polymorphic variants; and the people with genotypes CYP1A1 m1/m2, XDP Gln/Gln, GSTM1 null, P53 intron 6, XRCC3 rs861539, COX2 -765 have high risk of presented OL, and therefore they are more exposed to oral cancer risk.