GENETIC POLYMORPHISMS ASSOCIATED WITH COLORECTAL CANCER RISK
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BACKGROUND
Colorectal cancer (CRC) is currently the most frequent malignant gastrointestinal disease. Some recent publications have proposed that genetic polymorphisms (Single Nucleotide Polymorphism, SNP) in different genes may be potential markers of CRC risk.

PURPOSE
This study aimed to determine the association of SNP in KIF9, PLCE1, MLH1, CYP2E1, TP53 and SMAD7 genes with susceptibility to the development of CRC.

MATERIAL AND METHODS
A retrospective case-control study was performed, where 126 cases and 169 controls CRC of Caucasian ethnicity were included. The genotypes of the selected polymorphisms from KIF9, PLCE1, MLH1, CYP2E1, TP53 and SMAD7 genes were determined in different individuals using the real-time PCR with TaqMan probes. Then, the results were analyzed under different genetic models (additive, genotypic, allelic, dominant and recessive) to look for an association between them and CRC risk.

RESULTS
G allele from SNP MLH1 rs1800734 was found to be a protector marker for CRC in the genotypic model (OR AG vs AA: 0.17; 95% CI: 0.05-0.49; p: 0.0015. OR GG vs AA: 0.31; 95% CI: 0.10-0.80; p: 0.0217), beside gender and BMI in the multivariate statistical model, while the rest of polymorphisms were not found associated with CRC risk.

<table>
<thead>
<tr>
<th>Variable</th>
<th>Ref (OR: 1.00)</th>
<th>Odds Ratio</th>
<th>95% CI</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>MLH1 rs1800734 AG</td>
<td>AA</td>
<td>0.17</td>
<td>0.05-0.49</td>
<td>0.00152</td>
</tr>
<tr>
<td>MLH1 rs1800734 GG</td>
<td>AA</td>
<td>0.31</td>
<td>0.10-0.80</td>
<td>0.02170</td>
</tr>
<tr>
<td>Gender</td>
<td>Mujer (♀)</td>
<td>1.82</td>
<td>1.06-3.15</td>
<td>0.03205</td>
</tr>
<tr>
<td>Obesity</td>
<td>No</td>
<td>0.58</td>
<td>0.34-1.00</td>
<td>0.04950</td>
</tr>
</tbody>
</table>

CONCLUSION
AA genotype from SNP MLH1 rs1800734 is a marker of CRC risk.