Null Results in Brief

Association between Genetic Polymorphisms of Macrophage Scavenger Receptor 1 Gene and Risk of Prostate Cancer in the Health Professionals Follow-up Study

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Abstract

Background: Macrophage scavenger receptor 1 (MSR1) is involved in chronic inflammation, which is a risk factor for prostate cancer. Association studies assessing the relationship between sequence variants of MSR1 and prostate cancer are inconsistent. We hypothesized that sequence variants of MSR1 were associated with prostate cancer risk.

Methods: In a nested case-control design within the Health Professionals Follow-up Study, we identified 700 participants with prostate cancer diagnosed after they had provided a blood specimen in 1993 and before January 2000. Controls were 700 age-matched men without prostate cancer who had had a prostate-specific antigen test after providing a blood specimen. We genotyped three common (>5%) single nucleotide polymorphisms (SNP) that have been reported previously to be associated with risk of prostate cancer.

Results: None of these MSR1 SNPs nor estimated haplotypes were associated with prostate cancer risk (P for the global test for haplotypes = 0.89). These MSR1 SNPs also did not appear to be associated with higher-grade or advanced-stage prostate cancer.

Conclusion: The association between these sequence variants of MSR1 and the risk of prostate cancer was null. Further study of aggressive prostate cancer may be warranted, as we had limited power to assess these. (Cancer Epidemiol Biomarkers Prev 2008;17(4): 1001–3)
MSR1 and Prostate Cancer

Table 1. Characteristics of MSR1 SNPs

<table>
<thead>
<tr>
<th>SNP</th>
<th>Nucleotide change</th>
<th>Location</th>
<th>rs #</th>
<th>Controls</th>
<th>Cases</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Minor allele freq (%)</td>
<td>Hardy-Weinberg equilibrium P</td>
<td>Minor allele freq (%)</td>
<td>Hardy-Weinberg equilibrium P</td>
<td></td>
</tr>
<tr>
<td>PRO3</td>
<td>A→G</td>
<td>Promoter</td>
<td>rs433235</td>
<td>8.8</td>
<td>0.08</td>
</tr>
<tr>
<td>IVS5-59</td>
<td>C→A</td>
<td>Intron 5</td>
<td>N/A</td>
<td>4.9</td>
<td>&lt;0.01</td>
</tr>
<tr>
<td>P275A</td>
<td>C→G</td>
<td>Exon 6</td>
<td>rs3747531</td>
<td>5.1</td>
<td>0.95</td>
</tr>
</tbody>
</table>

Table 2. OR between MSR1 SNPs and haplotypes and the risk of prostate cancer

<table>
<thead>
<tr>
<th>SNP</th>
<th>Prevalence among controls, % (95% CI)</th>
<th>Global test P = 0.89</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>0 copies</td>
<td>1 copy</td>
</tr>
<tr>
<td></td>
<td>Case/control</td>
<td>OR (95% CI)</td>
</tr>
<tr>
<td>PRO3</td>
<td></td>
<td></td>
</tr>
<tr>
<td>IVS5-59</td>
<td></td>
<td></td>
</tr>
<tr>
<td>P275A</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Haplotype</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Hap1: ACG</td>
<td>85.3 (83.5-87.2)</td>
<td>20/16</td>
</tr>
<tr>
<td>Hap2: ACC</td>
<td>5.1 (3.9-6.2)</td>
<td>625/631</td>
</tr>
<tr>
<td>Hap3: CGG</td>
<td>4.8 (3.7-5.9)</td>
<td>641/635</td>
</tr>
<tr>
<td>Cumulative frequency (%)</td>
<td>92.5</td>
<td></td>
</tr>
</tbody>
</table>

NOTE: From left to right, the haplotypes above were composed of PRO3, IVS5-59, and P275A.

*p* tested the null hypothesis: OR1 copy = OR2 copies = 1.
rise to the cases and were composed of 94% Caucasians. Results were similar after the exclusion of non-Caucasians.

Chronic intraprostatic inflammation has been reported to increase the risk of prostate cancer (7). Our previous study (8) showed that variants in the innate immune gene TLR4 played a role in prostate cancer susceptibility. However, in our study and most previous studies, no association between sequence variants of MSR1 and prostate cancer risk has been observed.

Acknowledgments
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References
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