Comment on “A meta-analysis of influence of MSMB promoter rs10993994 polymorphisms on prostate cancer risk”

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Dear Editors,

With strong interests, we had read a recent article, “A meta-analysis of influence of MSMB promoter rs10993994 polymorphisms on prostate cancer risk”1, which was published online in European Review for Medical and Pharmacological Sciences. However, we had a great conversation about several important issues about this meta-analysis.

First, all included case-control studies were published before December 2015, which was outdated, so this meta-analysis should be updated. In addition, several articles may be left out. Based on above two factors, we reidentified related articles about the MSMB rs10993994 polymorphism on prostate cancer (PCa) risk. We found other literature involving 8 cases-control studies (21808 PCas and 20326 controls). We listed the characteristics of the additional studies in Table I2-8.

Second, classical meta-analysis should include five genetic models, including allelic comparison, homozygous model, heterozygous model, dominant comparison, and recessive comparison9. There were only four genetic models to analysis the associations between rs10993994 polymorphism and PCa risk. The heterozygous model (CT vs. CC) also should be included in the paper.

Third, it was necessary to assess the included research literature, the quality of observational studies usually was evaluated by the Newcastle-Ottawa Scale (NOS); moreover, PRISMA 2009 checklist also should be shown. To better understand the correlations of rs10993994 polymorphism and PCa susceptibility, other evaluation indicators should be looked out. We maybe pay more attention on whether the polymorphism has certain correlations with Gleason score and TNM stage, which may offer significant markers for the diagnosis and prognosis of PCa and contribute to explaining the heterogeneity.

Table I. Characteristics of the additional studies in the meta-analysis.

<table>
<thead>
<tr>
<th>Authors</th>
<th>Year</th>
<th>Population</th>
<th>Ethnic group</th>
<th>Numbers</th>
<th>P for HWE</th>
<th>Genotype methods</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mhatre et al²</td>
<td>2015</td>
<td>Indian</td>
<td>Asian</td>
<td>50</td>
<td>30</td>
<td>0.171 PCR</td>
</tr>
<tr>
<td>Shui et al³</td>
<td>2014</td>
<td>Americans</td>
<td>Caucasian</td>
<td>10487</td>
<td>11024</td>
<td>0.996 Taqman</td>
</tr>
<tr>
<td>Ho et al⁴</td>
<td>2012</td>
<td>Scotland</td>
<td>Caucasian</td>
<td>242</td>
<td>264</td>
<td>0.406 PCR</td>
</tr>
<tr>
<td>Chang et al⁵</td>
<td>2011</td>
<td>African</td>
<td>African-American</td>
<td>4040</td>
<td>3748</td>
<td>0.996 PCR</td>
</tr>
<tr>
<td>Eeles et al⁶</td>
<td>2008</td>
<td>British</td>
<td>Caucasian</td>
<td>1854</td>
<td>1894</td>
<td>0.955 Hapman</td>
</tr>
<tr>
<td>Eeles et al⁶</td>
<td>2008</td>
<td>British Australians</td>
<td>Caucasian</td>
<td>1960</td>
<td>2104</td>
<td>0.992 Hapman</td>
</tr>
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<td>Eeles et al⁶</td>
<td>2008</td>
<td>British Australians</td>
<td>Caucasian</td>
<td>1308</td>
<td>1262</td>
<td></td>
</tr>
<tr>
<td>Wang et al⁷</td>
<td>2009</td>
<td>Chinese</td>
<td>Asian</td>
<td>200</td>
<td>200</td>
<td>0.0003 PCR</td>
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<tr>
<td>Cui et al⁸</td>
<td>2012</td>
<td>Chinese</td>
<td>Asian</td>
<td>1667</td>
<td>1525</td>
<td>NA PCR</td>
</tr>
</tbody>
</table>

Abbreviations: PCa, Prostate cancer; HWE, Hardy-Weinberg equilibrium; NA, not available.
A meta-analysis of influence of MSMB promoter rs10993994 polymorphisms on prostate cancer risk

Conflict of Interest
The Authors declare that they have no conflict of interests.

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References
2) Mhatre DR, Mahale SD, Khatkhatay MI, Achrekar SK, Desai SS, Jagtap DD, Dhabalia JV, Tongaonkar HB, Dandekar SP, Varadkar AM. The rs10993994 in the proximal MSMB promoter region is a functional polymorphism in Asian Indian subjects. Springerplus 2015; 4: 380.