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TXNRD2 (rs35934224) CT genotype and primary open-angle glaucoma: correspondence

Genótipo CT do *TXNRD2* (rs35934224) e glaucoma primário de ângulo aberto: correspondência

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Dear Editor,

We would like to share ideas on "TXNRD2 (rs35934224) CT genotype as possible protective marker for primary open-angle glaucoma in a Brazilian population[(1)]." Tenório et al. concluded that "*Our data suggest an association between TXNRD2 gene polymorphism (rs35934224) with primary open-angle glaucoma in an admixed Brazilian population*[(1)]. We agree TXNRD2 (rs35934224) CT genotype might be associated with primary open-angle glaucoma. The present report can give good data on genetic underlying background of glaucoma. In this study, Tenório et al. focused only a polymorphism.

Environmental confounding factors might be well controlled but there is a chance of effects of other genetic polymorphisms which are reported for association with primary open-angle glaucoma might still exist. Examples of those genetic polymorphisms are CDKN2B-AS1, GSTO1, GSTO2, GSTP1, GPX1OPA1, MFN1, and MFN2 polymorphisms[(2-4)]. Further studies on effects of other polymorphisms are very interesting.

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Reply to "TXNRD2 (rs35934224) CT genotype and primary open-angle glaucoma: correspondence"

Resposta a "Genótipo CT do *TXNRD2* (rs35934224) e glaucoma primário de ângulo aberto: correspondência"

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To the Editor:

We thank Sookaromdee and Wiwanitkit for their interest and comments on our manuscript. The authors have highlighted the importance of further studies to evaluate the effects of other polymorphisms on primary open-angle glaucoma (POAG). As published by Weinreb et al.[1], glaucoma is a multifactorial disease with incompletely understood pathophysiology. Bailey et al.[2] published a genome-wide association study (GWAS) describing 22 POAG-related single nucleotide polymorphisms (SNPs), of which 19 had been previously described. In addition, Bonnemaijer[3] confirmed the relationship of 15 SNPs with glaucoma in the African population.

Although GWAS studies are important to identify new common polymorphisms associated with diseases, this strategy has some limitations[4] that may lead to false-positive results. In addition, most studies were performed in European and North American populations; therefore, it is of fundamental importance to confirm these polymorphisms in other populations, such as the Brazilian, which has a highly admixed population. Therefore, we decided to verify the association of *TXNRD2* (rs35934224) with POAG in a Brazilian population.

As exposed in our work, we also have the conviction that further studies are needed to confirm these associations and try to better understand the disease pathophysiology to be able to propose curative therapies based on these data.

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