Author’s response to reviews

Title: In vitro characterization of novel and functional regulatory SNPs in the promoter region of IL2 and IL2R alpha in a Gabonese population

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Version: 3 Date: 30 July 2012

Author’s response to reviews: see over
Dear Distinguished editor,

We herewith submit a manuscript entitled “In vitro characterization of novel and functional regulatory SNPs in the promoter region of IL2 and IL2R alpha in a Gabonese population” to be considered for publication in BMC medical genetics. On behalf of all authors, I hereby affirm that all authors have read the manuscript and agreed to its submission. This study has no financial insights. We hereby certify that this manuscript consists of original and unpublished work which is not under consideration for publication elsewhere.

The selection pressure imposed by the parasite has a functional consequence on the immune genes leading to altered immune function. Of which regulatory T cells (Tregs) induced by parasites during infectious challenges modulate or thwart T effector cells mechanism. In this study, we identified and investigated regulatory polymorphisms in the immune gene IL2 and its receptor IL2R alpha (also known as CD25) in Gabonese individuals exposed to plentiful parasitic infections. We identified two reported variants each for IL2 and its receptor IL2R alpha gene loci. In addition, two novel variants, -83 /-84 CT deletions (ss410961576) for IL2 and -409C/T (ss410961577) for IL2R alpha were identified. We further validated all identified promoter variants for their allelic gene expression using transient transfection assays. Three promoter variants of the IL2 locus revealed no significant expression of the reporter gene. The identified novel variant (ss410961577C/T) of the IL2R alpha revealed a significant higher expression of the reporter gene in comparison to the major allele (P<0.05). In addition, the rs12722616C/T variant of the IL2R alpha locus altered the transcription factor binding site TBP (TATA box binding protein) and C/EBP beta (CCAAT/enhancer binding protein beta) that are believed to regulate the Treg function.

We do believe that the identified regulatory SNPs in this current study will be of greater interest to readers of BMC medical genetics and provide useful information for understanding the relevance of sequence polymorphisms in populations exposed to many parasitic diseases and may serve as a basis to study disease susceptibility in association studies. I will be obliged if you can go through our draft. Many thanks for your time and effort.

Sincerely

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