Dear Editor,

I have read with interest the recent paper by Yu and coworkers on the putative effects of a semaphorin 5A variant, rs7702187, in the context of Parkinson’s disease. The authors conclude to a significant risk-enhancing role of this polymorphism in the western population on the grounds of data from 12 earlier case-control studies. While the OR given (0.87) is, by definition, risk-lowering, the approach taken to assessing the overall risk is a concern. To begin with, no meaningful insight is to be expected from a meta analysis that lags 4 years behind. Even so, the data collected are grossly incomplete in that some 10,600 cases and 15,233 controls are missing from publications that were available in 2010. Out of 15 studies collected, the authors appear to have dropped at least 6 without providing any further details. Of those studies that were retained, genotype data were extracted with errors or were added up to give incorrect allele counts. Methodological discrepancies have gone unnoticed, despite an earlier alert. Thus, some studies have referred to “T” as the major allele whereas others cite “A” as the major allele or leave the major allele undefined. Regardless of allele specifications in the original studies, the authors have arbitrarily assigned a “T” to the more frequent allele even if the data clearly pertained to allele “A”. As the substitution in question requires additional strand information to resolve uncertainties regarding the classification as “A” or “T”, the authors should have removed all studies that fail to provide such information. Hardy-Weinberg equilibrium data are missing, instead a cryptic “Quality score” of 5 is allocated to all studies retrieved. In the light of these open issues, I propose that the authors be given the opportunity to reevaluate rs7702187 in Parkinson’s disease.

Conflict of Interest

The Author declares that he has no conflict of interests. The author of this study did not receive any financial support for this submission.

References


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