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PITX3 variants in Chinese patients with Parkinson's disease

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We have read with interest the recent report by Gui and coworkers on the role of *PITX3* variants in Parkinson's disease [1]. The authors are proposing that a newly identified exonic variant is associated with the phenotype in Chinese patients but other variants are not.

The data presented, however, generate more heat than light. Chi-square tests with Yates' correction conducted for rs2281983 and rs4919621 produce p values of 0.05, not 0.274 (table 2). For c.219G>A, p < 0.0001 is achieved (table 2). In order to put these results into perspective and to address the impact of multiple comparisons on the significance threshold, the authors may consider providing measures of LD between markers. Primer information is missing from table 1 and the DNA strand amplified is not specified. As a consequence, rs4919621 genotype data become uninformative. Allele frequencies for rs4919621 differ sharply from those previously published in the same ethnic group [2–4], presumably, because the authors are referring to the antiparallel strand. Finally, contrary to the authors' claim, the genotype distribution for rs3758549 in controls clearly violates Hardy Weinberg Equilibrium at p = 0.0064. No mention is made of subjects' relatedness which could account for the divergence. Alternatively, the method used for genotyping the entire sample may have introduced artefacts but this is not specified either.

We invite Gui and co-workers to append the information required so that the role of *PITX3* variants in Parkinson's disease may be fully appreciated.

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