Author's response to reviews

Title: Association analysis between HOXD9 genes and the development of developmental dysplasia of the hip in Chinese female Han population

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Author's response to reviews: see over
Dear editor,

Thanks a lot for having reviewed our manuscript. Now we have revised the manuscript according to the reviewers’ comments. Most of the revisions are in the manuscript marked with red. Some explanations regarding the revisions of our manuscript are as follows.

Response to Reviewer:

Thanks for your comments to our manuscript. We have revised our manuscript according to your comments.

1. Provide descriptive information on severity of dysplasia and basic demographics (e.g., mean, standard deviation of the age distribution).

Thank you very much for your suggestion. We are very sorry for hadn’t collected the information on severity of dysplasia. And the patients are 5.81±3.55 months (Mean±SD) old, while the controls are 6.47±4.15 months (Mean±SD) old.

2. Discuss differences/similarities in allele frequencies in bilateral vs unilateral DDH.

Thank you very much for your helpful comment; since there were only 11 bilateral DDH patients, we hadn’t computed the different allele frequencies between patients with bilateral DDH vs. unilateral DDH. But we showed the data of allele frequencies and genotype in table 1.

3. Fix Table 1 - need to provide haplotype frequencies for cases and controls separately; need to make this (a) more readable table(s).

Thanks a lot for the suggestion; we have added them in table 1 in the revised content according to your suggestion.
4. Address reviewer’s suggestion regarding clarifying the statistical analysis (i.e., simply adding a sentence saying you calculated odds ratios and 95% confidence intervals isn't enough. The reader needs to know what groups are you combining and comparing? What is the referent group?

Thank you for your comment; we have added them in certain part in the revised content according to your suggestion in revised “Genetic and statistical analysis” section, as followed:

“Allele frequencies and genotype distribution of patients and controls were determined by allele-counting method and analyzed with Pearson chi-square tests using Statistic Package for the Social Science (SPSS) version 10.0. To assess the strength of relationship in the allele distribution, the odds ratios (OR) and 95% confidence intervals (95% CI) were computed. First, we analyzed the Hardy-Weinberg equilibrium of SNP rs711822 and rs711819 in both patient group and control group. Then, the allele frequencies and genotype distribution of the two tag SNPs were compared between patients and controls. Finally, the haplotype frequencies of the two tag SNPs were calculated and analyzed. And we defined the LD map of CHB population in Hapmap databases as the reference category. The estimated statistical significance was $P<0.05$. ”