Author's response to reviews

Title: Clinical Features and Phylogenetic Analysis of Coxsackievirus A9 in Northern Taiwan in 2011

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Dear Editor

We clarified within the manuscript how the strains were randomly selected: We selected the first sequence from every eight consecutive cases from current study and 13 sequences were selected to build a phylogenetic tree (Page 8, the last line).

Thank you very much for your consideration.

Sincerely yours,

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