◼ **RESPONSE**

To: Urusa Thaenkham and Yukifumi Nawa Double Strand Problems: Reverse DNA Sequences Deposited in the DNA Database

Sun Huh

Department of Parasitology, College of Medicine, Hallym University, Chuncheon 200-702, Korea

Dear Editor,

Thank you very much for the detection of errors in the primer and vector sequences from the NCBI sequence data for the worms that were used for phylogenic analysis of our previous papers [1,2]. According to the recommendations by Drs. Urusa Thaenkham and Yukifumi Nawa, I deleted the primer sequences of both sides (JB3 and JB4.5) of all deposited sequences of 10 parasite species in GenBank. Furthermore, the reverse DNA sequence (JB4.5) has been transformed to the forward DNA sequence (JB3). Cloning vector sequences (GenBank No. AF181884, AY055380, and AF096233) have been removed. Those upgraded gene sequences will be updated in 2-3 weeks in GenBank.

I apologize for any inconvenience and confusion originated from sequence data which I submitted to GenBank.

REFERENCES

1. Lee SU, Huh S, Sohn WM, Chai JY. Sequence comparisons of 28S ribosomal DNA and mitochondrial cytochrome c oxidase subunit I of *Metagonimus yokogawai*, *M. takahashii* and *M. miyatai*. Korean J Parasitol 2004; 42: 129-135.
2. Lee SU, Huh S. Variation of nuclear and mitochondrial DNAs in Korean and Chinese isolates of *Clonorchis sinensis*. Korean J Parasitol 2004; 42: 145-148.