Genetics and Molecular Research

Letter to the Editor

Reply to commentary by D. Elleder and J. Hejnar on the article "Avian sarcoma and leukosis virus gag gene in the *Anser anser domesticus* genome" published in Genetics and Molecular Research 14 (4): 14379-14386 to the letter published in Genet. Mol. Res. 15 (1): gmr.15014956

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Dear Editor,

I should thank to the questioner and these questions are very valuable. Here, I want to give some opinions for it.

In letter, questioner mentions that the gag sequences we got are too homologous with chicken sequence, unlike other Galliformes birds. Actually, endogenous avian sarcoma and leukosis virus (enASLV) sequences are variable in the Galliformes birds, and geese have split with chicken

for a long time. However, it is hard to have a final conclusion about conservation of gag gene in waterfowl, because geese have no vertical relation with Galliformes birds; specially domestic geese have a very different background. Moreover, the sequences we got are only part of gag gene, and the complete sequence is still unknown. As known, some endogenous retrovirus (ERV) sequences were inserted into the ancient bird genome. There is an assumption that ASLV has infected the common ancestors of Galliformes and Anseriformes before differentiation. Of course, as questioner referred to, a possible horizontal transmission between chicken and domestic goose might occur in the process of domestication. In this study, we wanted to verify hypothesis using PCR technology and designed an experiment to do it. Our results showed the probability. Also, questioner referred that they cannot get any PCR product with same primers in domestic goose and swan. I am not aware of their experiments, because I do not know any information about their samples and conditions. I only emphasize that our reaction conditions are designed to optimize the PCR program. Additionally, they said they did not find any ALSV sequences in swan goose genome (GCA_000971095.1). We also did a mapping on it using BLAST and we failed to find any hit too. Although we failed to locate the gag sequence, we still could not make sure the validity of gene mapping on current version reference sequences. The biggest problem is that this version reference only have lots of scaffolds and this means it still have many assembly errors and gaps. So we believe that the ASLV is still “hidden” in the unknown genomic region.

Indeed, there is a possibility that chicken sequences might contaminate samples. For this reason, we are hurrying to repeat our experiment. I hope we can take enough time, one or two months to finish it. Thank you.