Erratum

In the article by Zhou et al., entitled 'Isolation and characterization of lytic phage vB_EcoM_JS09 against clinically isolated antibiotic-resistant avian pathogenic *Escherichia coli* and enterotoxigenic *Escherichia coli*' [Intervirology 2015;58:218–231, DOI: 10.1159/000437426], in figure 6, below TuIb it should be TuIa (see figure 6 below; the correction is given in red).

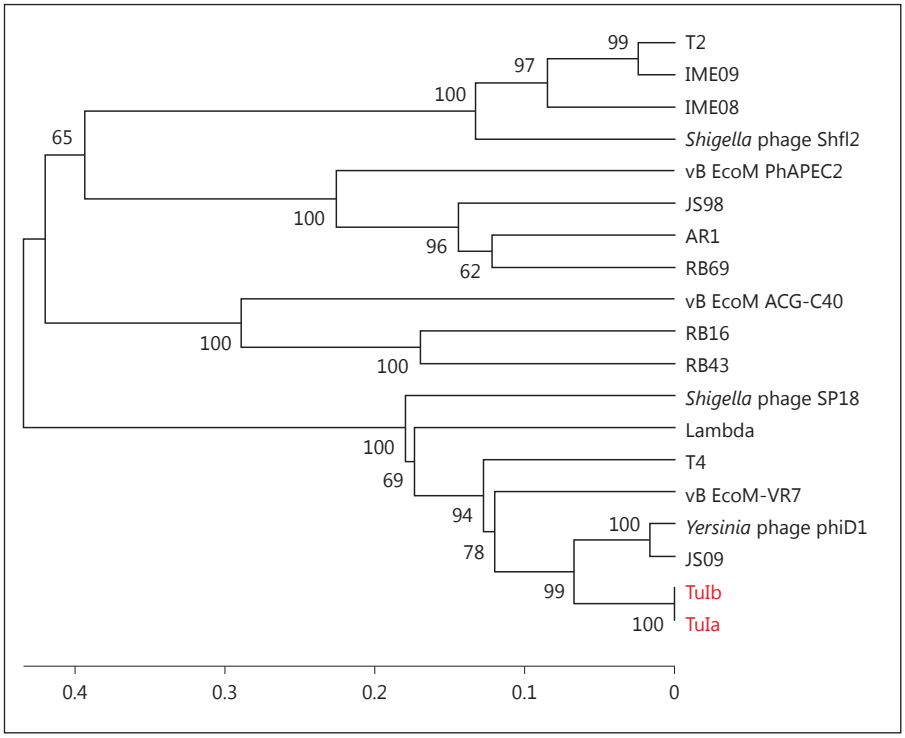

Fig. 6. Phylogenetic tree of genes identified as gp37 by homology searches of the nonredundant NCBI protein database. The topology and branch lengths correspond to the maximum likelihood (ML) inference. Bootstraps appear ordered as ML, neighbor joining, and maximum parsimony. Only bootstrap values greater than 60 are shown. The analysis credibility and genetic distance are shown as numbers. All of the phages are members of the Myoviridae family (except for siphovirus lambda phages), infecting *E. coli*. The rest of the phages belong to the T4 superfamily, with most of them infecting *E. coli*. However, *Shigella* phage Shfl2 infects *Shigella flexneri*, *Shigella* phage SP18 infects *S. sonnei*, and *Yersinia* phage phiD1 infects *Y. pestis*.