

Discovery of a novel recombinant avian orthoreovirus in China

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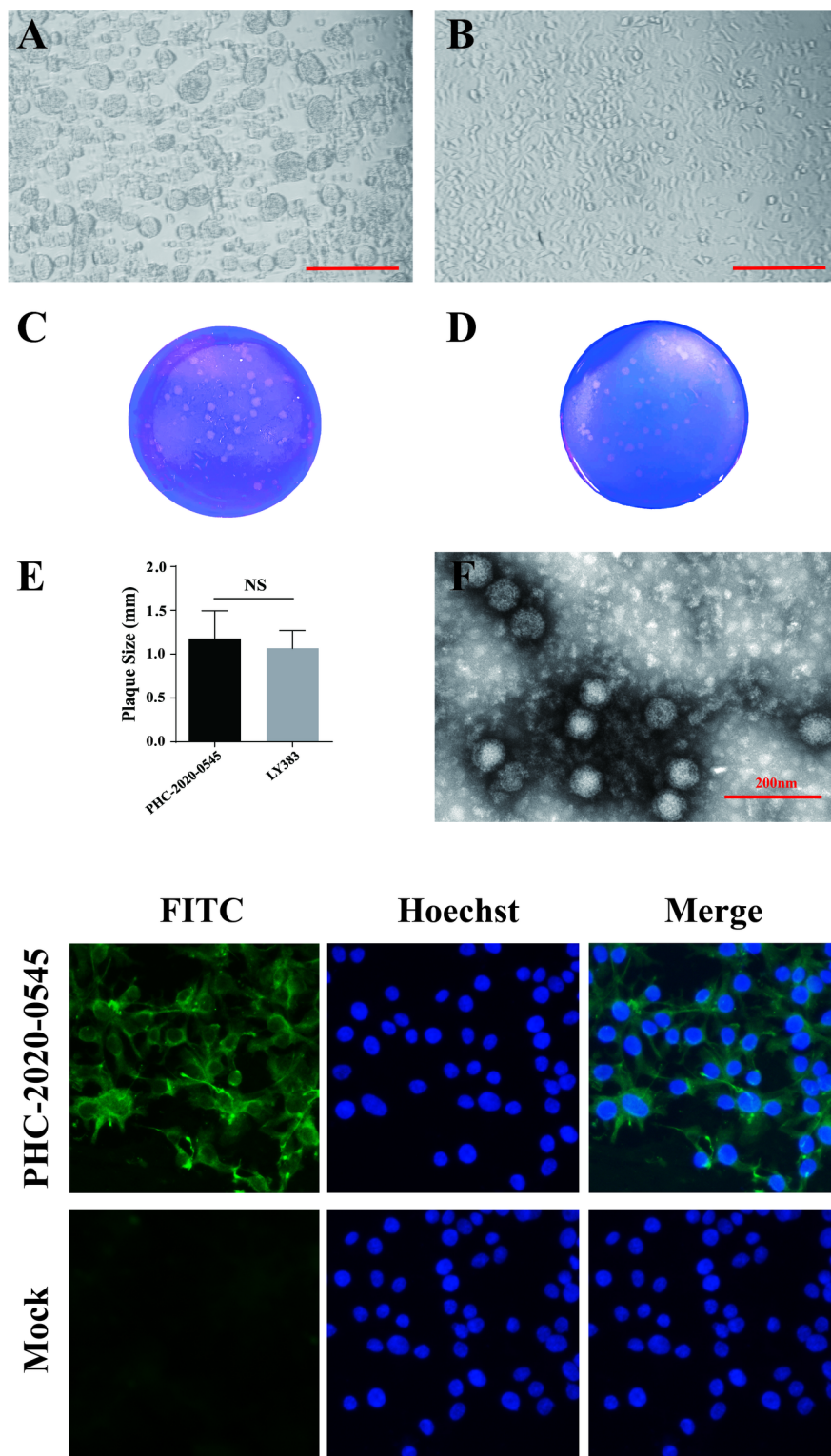
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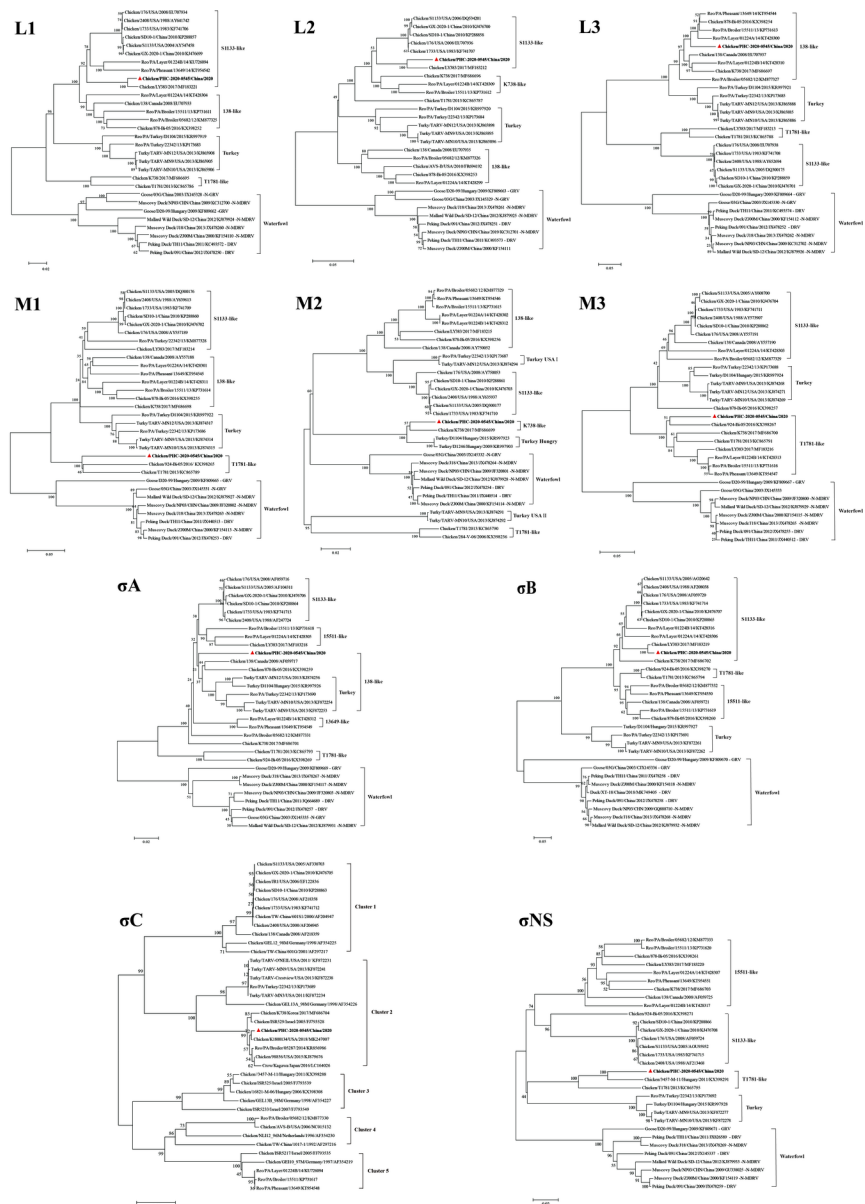
Abstract

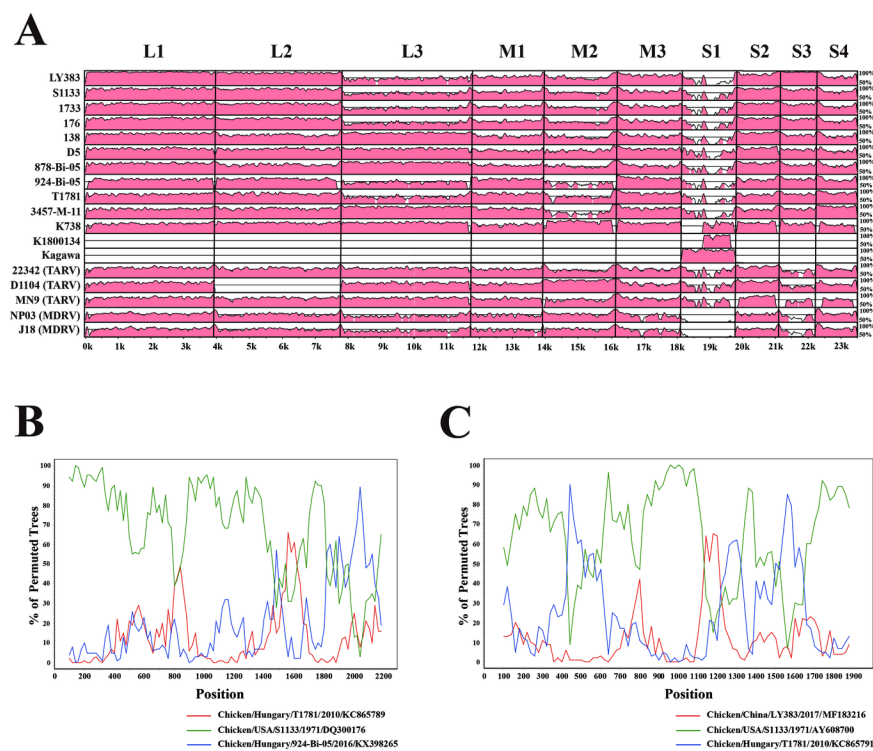
In mid-2020, using next-generation sequencing (NGS) technology, we identified a divergent cluster 2 avian orthoreovirus (ARV) variant named PHC-2020-0545, isolated from tendons of 33-day-old broilers with leg swelling in China. Sequence comparison and phylogenetic analysis of results revealed that the isolate strain was genetically distinct from all known ARV strains in M1 and M3 genes, and the σC coding gene was quite different from the identified ARV strains grouped into other genotyping cluster. The recombination analysis revealed that multiple segmental recombination, intra-segmental recombination and accumulation of point mutations might contribute to the emergence of this isolate. The broilers infected with the PHC-2020-0545 strain showed typical clinical symptoms of tarsal joint swelling, and the isolate mainly affected the movement, digestion and metabolism of broilers. Although the mortality of broilers caused by the isolate was very low, the results of viral load detection revealed that it had strong replication ability in vivo. In addition, the infection route of the isolate is related to its pathogenicity to broilers. Therefore, we determined that the PHC-2020-0545 field strain is a unique novel recombinant ARV strain, which might become prevalent in Chinese broiler flocks.

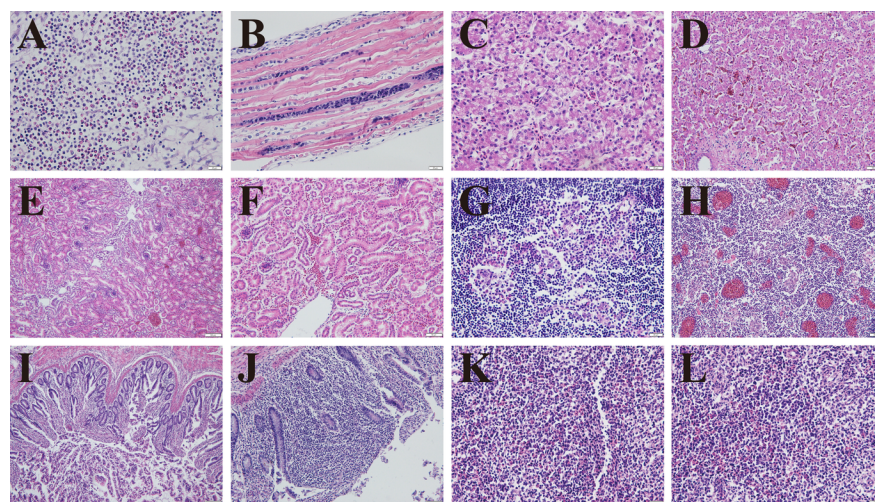
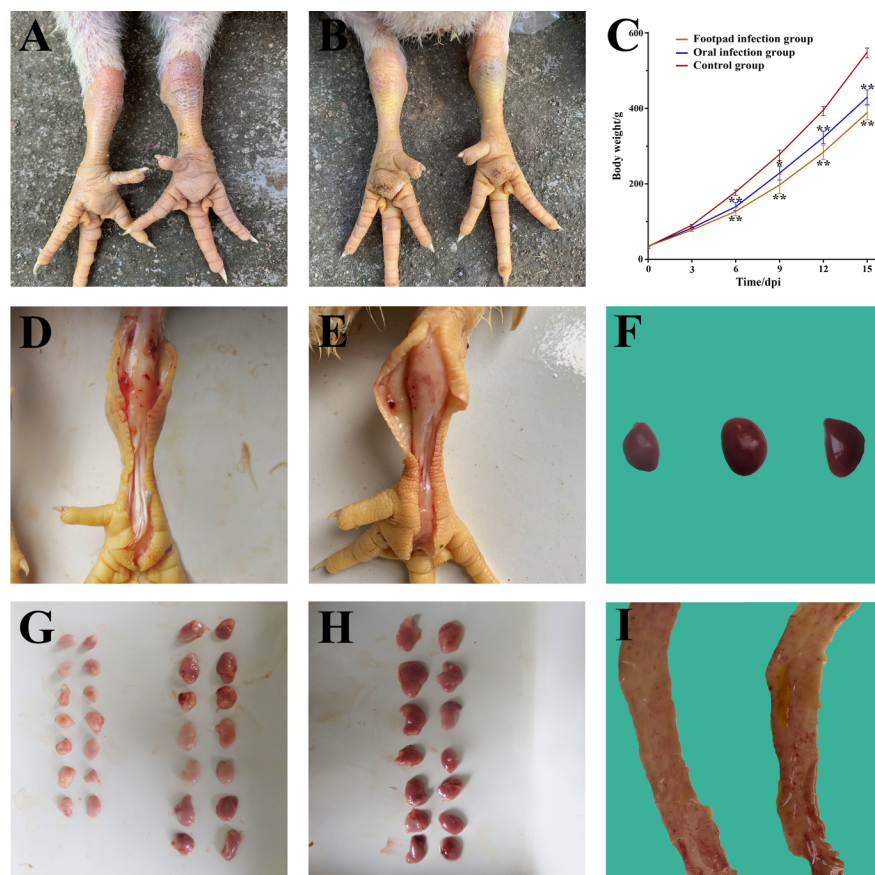
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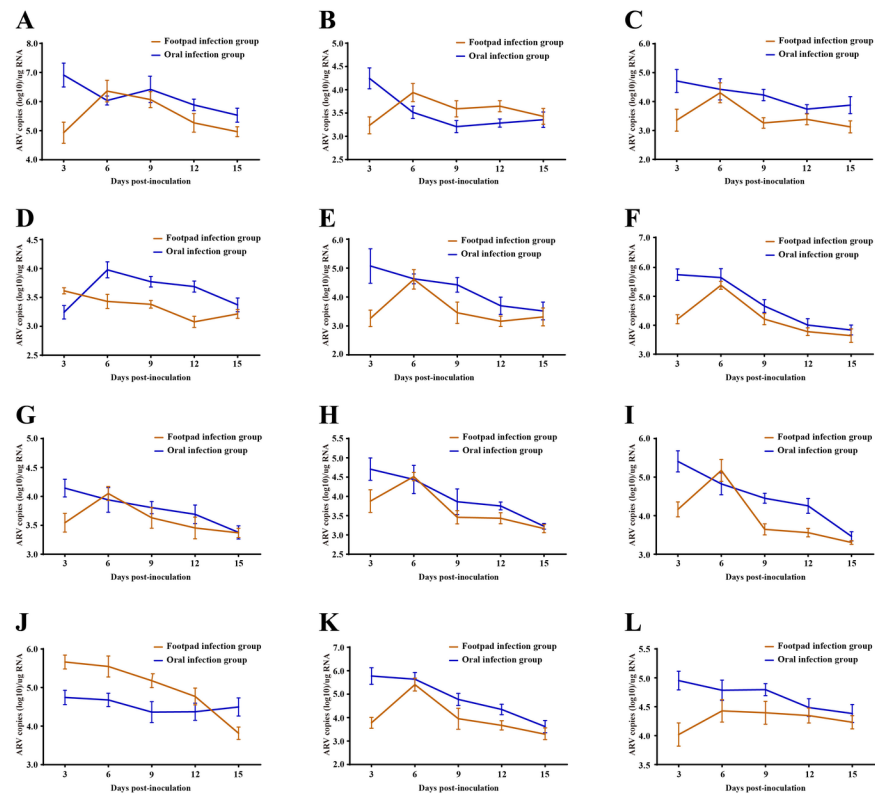
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