

The recent outbreak of avian leukosis virus subgroup J in Chinese local chickens, 2019

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Abstract

Avian leukemia caused by avian leukosis virus (ALV) is one of the most severe diseases endangering poultry health. When the eradication measures performed in commercial broilers and layers have achieved excellent results, ALV in some local chickens has gradually attracted extensive attention. Since late 2018, following the re-outbreak of ALV-J in white feather broilers in China, AL-like symptoms also suddenly broke out in some local flocks, leading to great economic losses. In this study, a systematic epidemiological survey was carried out in eight local chicken flocks in Jiangxi Province, China, and 71 strains were finally isolated from 560 samples, while the env sequences of them were successfully sequenced. All of those new isolates belong to subgroup J but they have totally different molecular features and were very different from the strains that emerged in white feather broilers recently, with some strains being highly consistent with those previously isolated from commercial broilers, layers and other flocks or even isolated from USA and Russian, suggesting these local chickens have been acted as reservoirs to accumulate various ALV strains for a long time. More seriously, phylogenetic analysis shows that there were also many novel strains emerging and in a separate evolutionary branch, indicating several new mutated ALVs are being bred in local chickens. Besides, ALV strains isolated in this study can be further divided into ten groups, while there were more or less groups in different chickens, revealing that ALV may cross propagate in those flocks. The above analysis explains the complex background and future evolution trend of ALV in Chinese local chickens, providing theoretical support for the establishment of corresponding prevention and control measures.

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