

Characterization of Western European field isolates and vaccine strains of avian infectious laryngotracheitis virus by restriction fragment length polymorphism and sequence analysis

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Schlüsselwörter

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Problemstellung und Zielsetzung

Infectious laryngotracheitis (ILT) is a dramatic disease of the upper respiratory tract in poultry. The causative agent is a herpesvirus. In Switzerland around 5 to 20 outbreaks are registered every year. The virus is enzootic in fancy breeds. The aim of this study is to further characterize a collection of around 100 isolates from Western Europe by molecular methods and establish a test for quick diagnosis of suspect field outbreaks. In addition we expect to gain more information on the diversity of isolates, on the possible role of vaccine strains in clinical disease and on epidemiological aspects in fancy breeds. Consequences for control will be discussed.

Material und Methoden

The examined 104 isolates, collected from acute outbreaks during the last 35 years, originated from Switzerland (48), Germany (21), Sweden (14), the United Kingdom (9), Italy (5), Belgium (4), Austria (2) and Norway (1). PCR was performed to amplify a 2.1-kb DNA fragment of ILTV using primers generated for the thymidine kinase (TK) gene. Restriction fragment length polymorphism analysis was carried out of the PCR products using endonuclease *Hae*III.

Ergebnisse und Bedeutung

98 field isolates showed the same cleavage pattern and were identical to both vaccine strains (clone 1). Two other clones were detected (clone 2: 5 Swiss isolates; clone 3: 1 Swedish isolate). The high genetic similarity regarding the TK gene did not allow a differentiation between field and vaccine strains. New clones primarily originated from noncommercial poultry. The latency and longer circulation of the virus in noncommercial poultry seems to favor the development of new clones.

Publikationen, Poster und Präsentationen

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