

Molecular detection and chracterization of infectious bronchitis virus from Libya.

ABSTRACT

Infectious bronchitis virus (IBV) is a very dynamic and evolving virus, causing major economic losses to the global poultry industry. Recently, the Libyan poultry industry faced severe outbreak of respiratory distress associated with high mortality and dramatic drop in egg production. Tracheal and cloacal swabs were analyzed for several poultry viruses. IBV was detected using SYBR Green I real-time PCR detection based on the nucleocapsid (N) gene. Sequence analysis of the partial N gene indicated high similarity (~ 94%) to IBV strain 3382/06 that was isolated from Taiwan. Even though the IBV strain 3382/06 is more similar to that of the Mass type H120, the isolate has been implicated associated with intertypic recombinant of 3 putative parental IBV strains namely H120, Taiwan strain 1171/92 and China strain CK/CH/LDL/97I. Complete sequencing and antigenicity studies of the Libya IBV strains are currently underway to determine the evolution of the virus and its importance in vaccine induced immunity. In this paper we documented for the first time the presence of possibly variant IBV strain from Libya which required dramatic change in vaccination program.

Keyword: Libya; Infectious bronchitis; Molecular characterization.