INTRODUCTION
Infectious Bronchitis Virus (IBV), belonging to family Coronaviridae, genus Coronavirus, is a positive-sense, single-stranded RNA virus of about 27.6 kb (5-UTR-1a/1b-S-3a-3b-E-M-5a-5b-N-3 UTR) causing major economic losses in avian industry (Jackwood and de Wit, 2013). In recent times, different genotypes apparently of Asian origin, have spread to other countries and continents, sometimes with relevant economic consequences (de Wit et al., 2011).

Since the mid 90’s a new IBV genotype, referred to as Q1, circulated in China (Yu et al., 2001). This genotype was reported for the first time in Italy in 2011, associated with an increase in mortality, kidney lesions and proventriculitidis (Toffan et al., 2011; Toffan et al., 2013). However, few information are available regarding the genomic features of this genotype despite its presence has been reported in Asia, Middle East, Europe and South America (Jackwood, 2012).

AIM
To sequence and characterize the complete genome of an IBV-Q1 like strain isolated in Italy

MATERIALS AND METHODS

1. IBV virus isolation and genotyping

2. Complete genome sequence and analysis

3. Evaluation of recombination events

RESULTS and DISCUSSIONS

4. S1 gene sequence analysis

Conclusions

For the first time an Italian IBV Q1-like strain complete genome was sequenced.

The development protocol can be useful also to sequence other IBV genotypes.

The origin of the vCoV/Ck/Italy/I2022/13 strain is still under investigation.

The availability of full genome IBV sequences on public databases is needed.