Highly Pathogenic Avian Influenza H5N5 and H5N8 in wild birds in Italy

STANDING COMMITEE ON PLANTS, ANIMALS, FOOD AND FEED

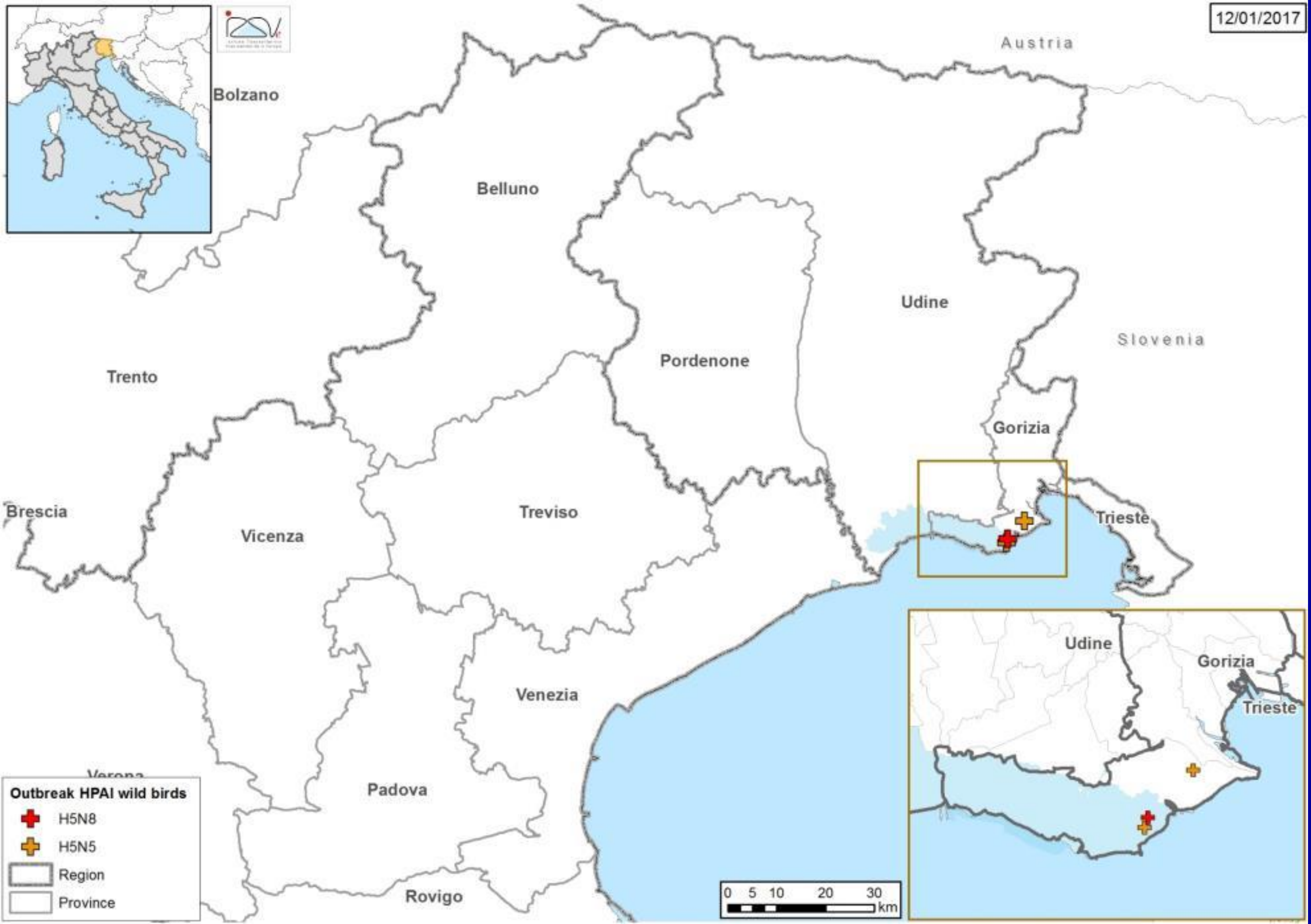
Section Animal Health and Welfare

17-18 January 2017

HPAI H5 outbreaks

- First case was an Eurasian Wigeon (*Anas penelope*) confirmed positive by the National Reference Laboratory for **Influenza A virus subtype H5N5** on 29 December
- All of the three cases were found near wetlands (Grado lagoon)

Conf. Date	Region	Province	Species	Strain
29/12/2016	Friuli Venezia Giulia	Gorizia (Grado lagoon)	Eurasian Wigeon (*Anas penelope*)	H5N5
05/01/2017	Friuli Venezia Giulia	Gorizia (Grado lagoon)	Eurasian Wigeon (*Anas penelope*)	H5N8
10/01/2017	Friuli Venezia Giulia	Gorizia	Gadwal (*Anas strepera*)	H5N5



12/01/2017

Austria
Bolzano
Belluno
Udine
Slovenia
Trento
Pordenone
Gorizia
Brescia
Vicenza
Treviso
Trieste
Venezia
Verona
Padova
Rovigo
Udine
Gorizia
Trieste
Outbreak HPAI wild birds
H5N8
H5N5
Region
Province
0 5 10 20 30 km

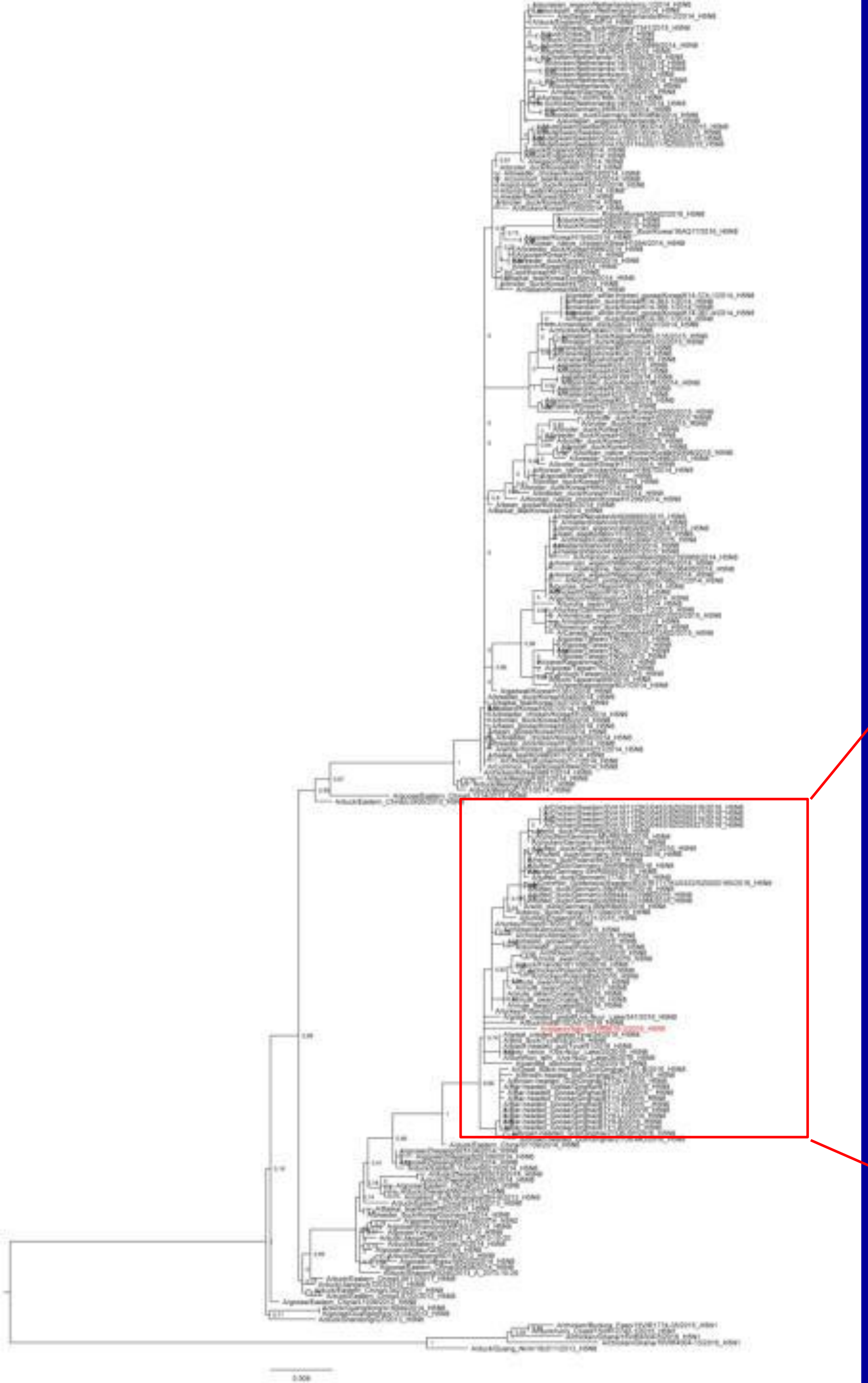
Main control measures in Italy

- Veterinary controls on biosecurity and emergency procedures
- Enhanced monitoring of dead wild birds with possible AI infection
- Reinforcement of biosecurity measures (e.g. birds indoor)
- Evaluation of mortality rates and feed consumption, and sampling of turkeys, laying hens, fattening ducks and geese (20 tracheal/cloacal swabs)
- Ban on the use of live decoy birds for hunting activities

Phylogenetic analysis of H5N5 virus

- The HA gene of the virus A/wigeon/Italy/16VIR9616-3/2016 (H5N5) clusters with H5N8 viruses detected in 2016 in Europe, Russia, Mongolia, India and China (genetic similarity 98.35-99.1%);
- HA gene shows the highest similarity (99.1%) with two viruses identified in Poland in December 2016;
- Analysis on N gene showed that N5 sequence is closely related to a virus detected in Singapore in 2015;
- No additional glycosylation sites or molecular markers of adaptation to mammalian hosts have been identified in the HA gene.

ML phylogenetic tree of the HA gene



Thank you