Results of active surveillance in wild birds for HPAI in Italy

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EU Reference Laboratory for Avian Influenza and Newcastle Disease

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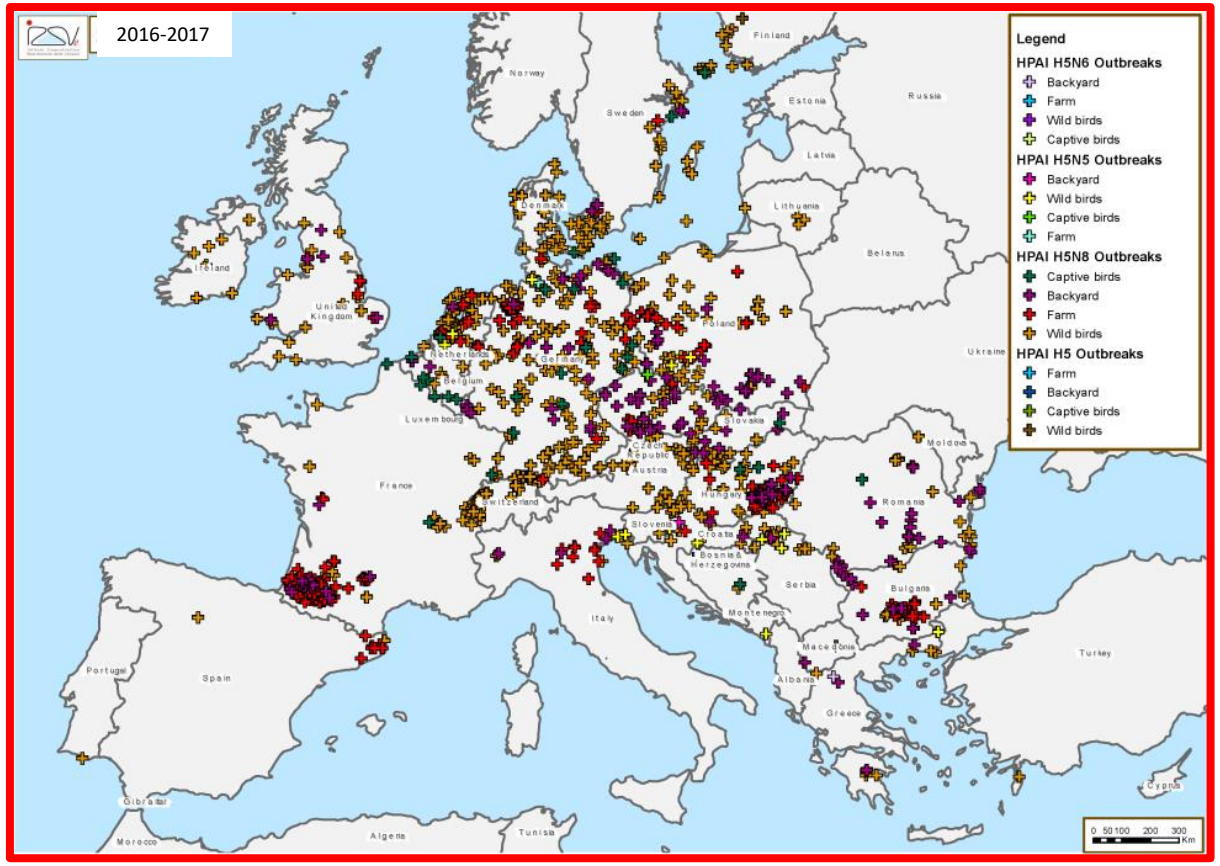
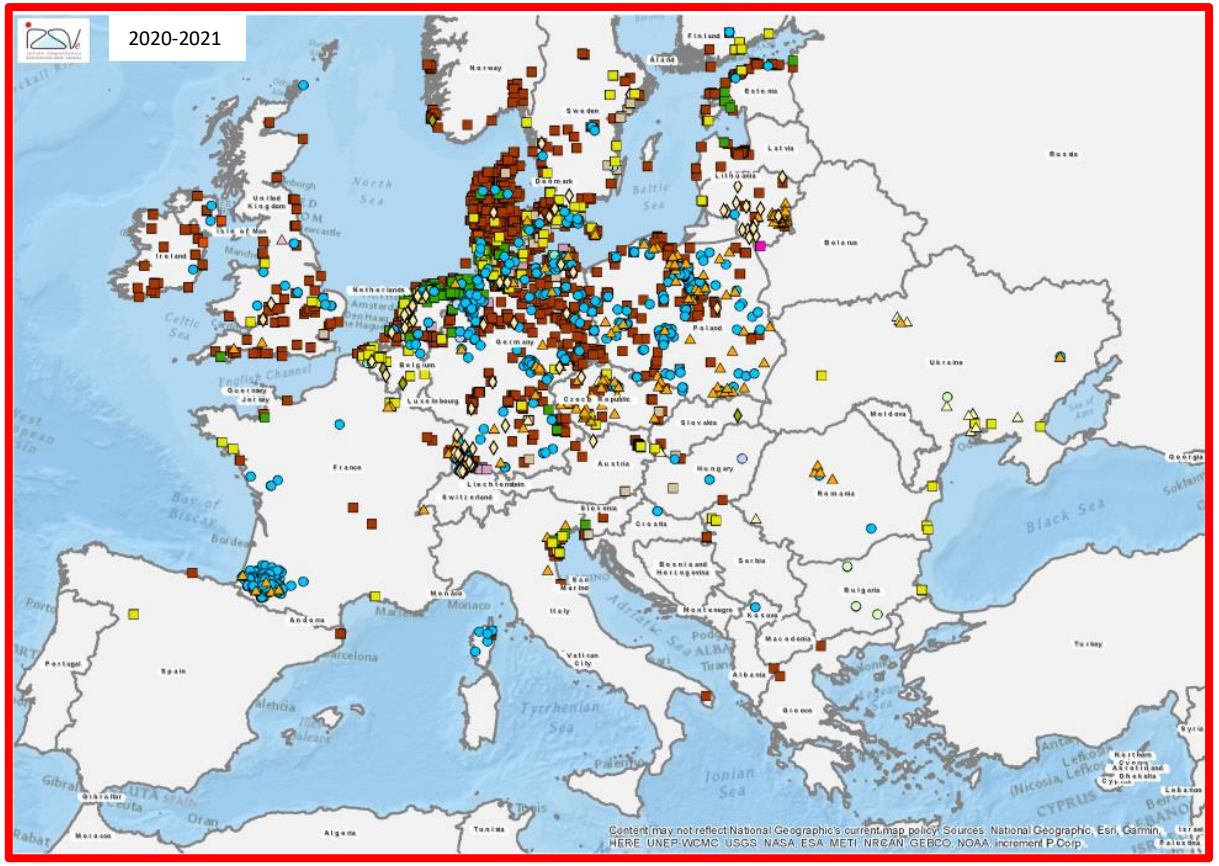
Background

HPAI H5 viruses belonging to clade 2.3.4.4b of the Goose/Guangdong/96 (GS/Gd) lineage





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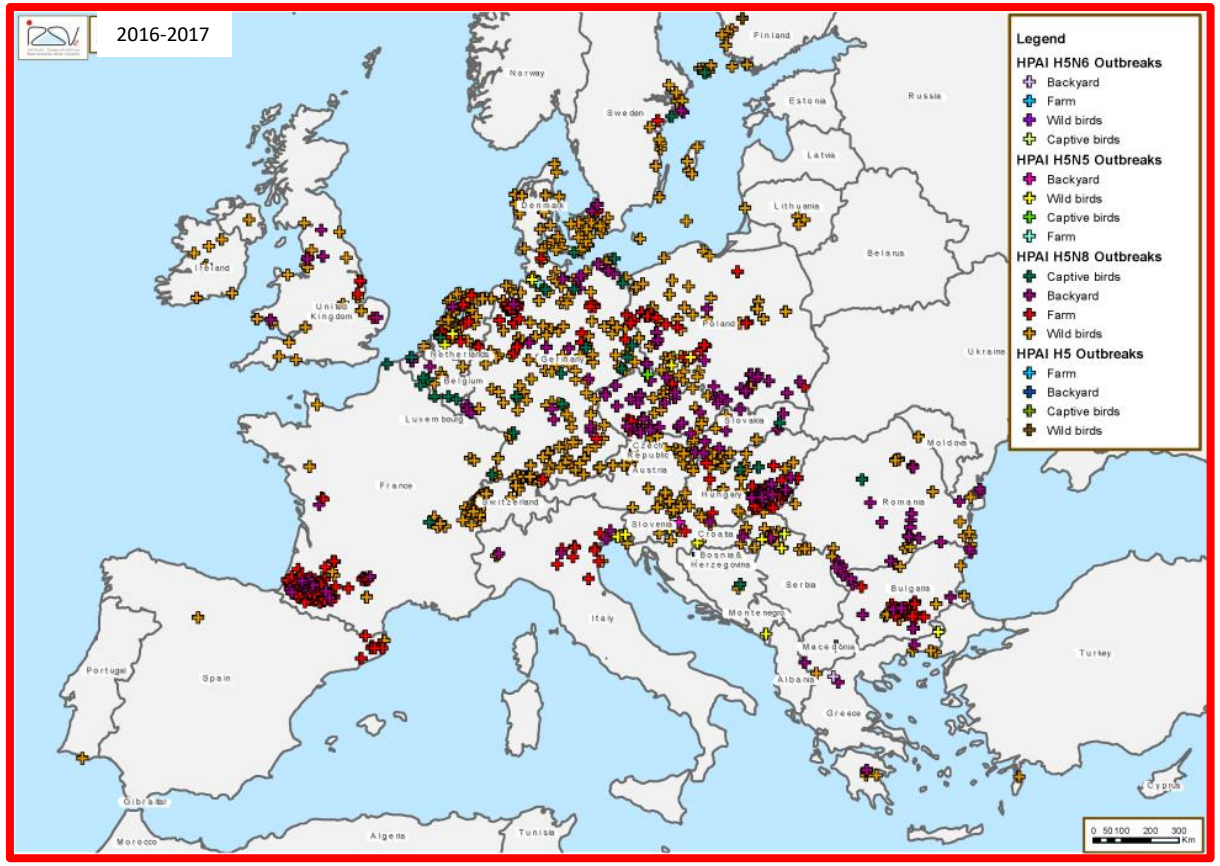
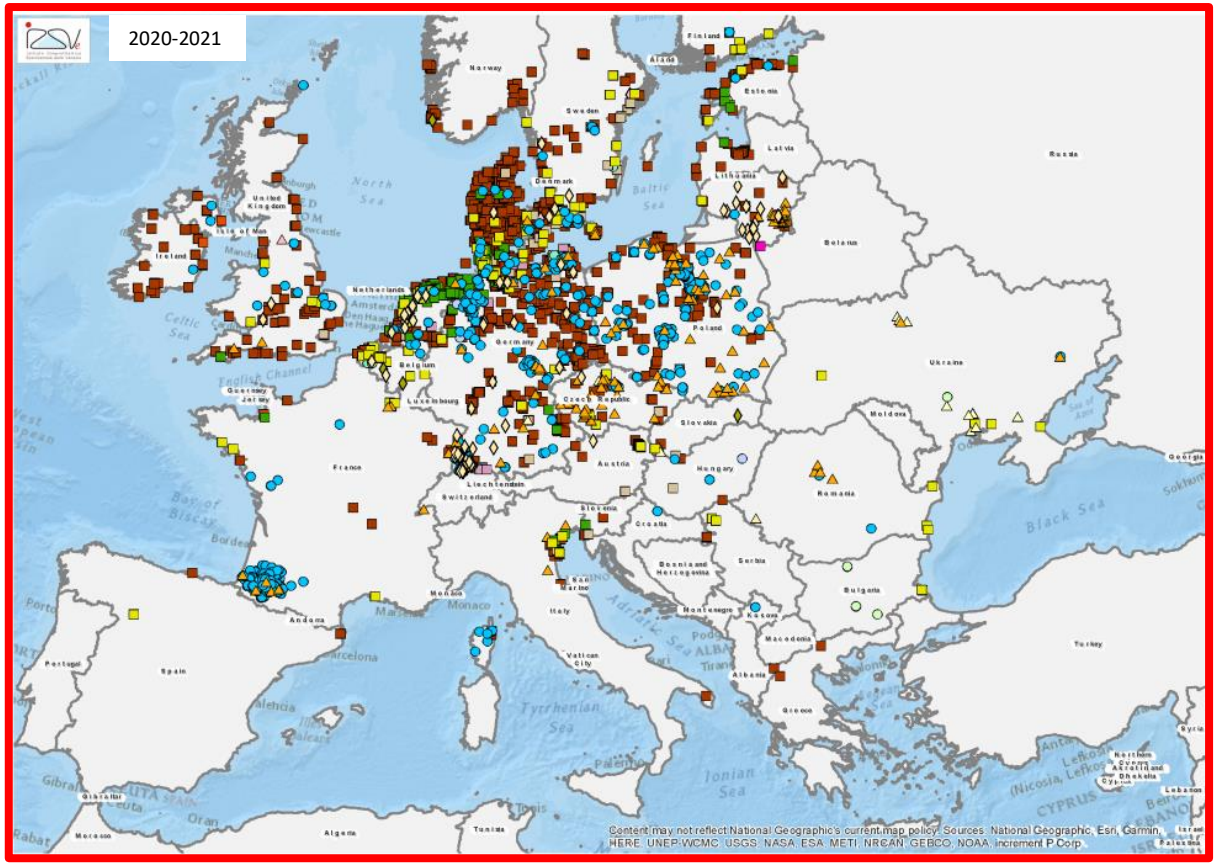




The Italian perspective

Decree of the Italian Ministry of Health of 14 March 2018: ancillary activities were implemented to enhance the AI National Surveillance Plan

Pilot surveillance activities in wetlands of the northern Italy

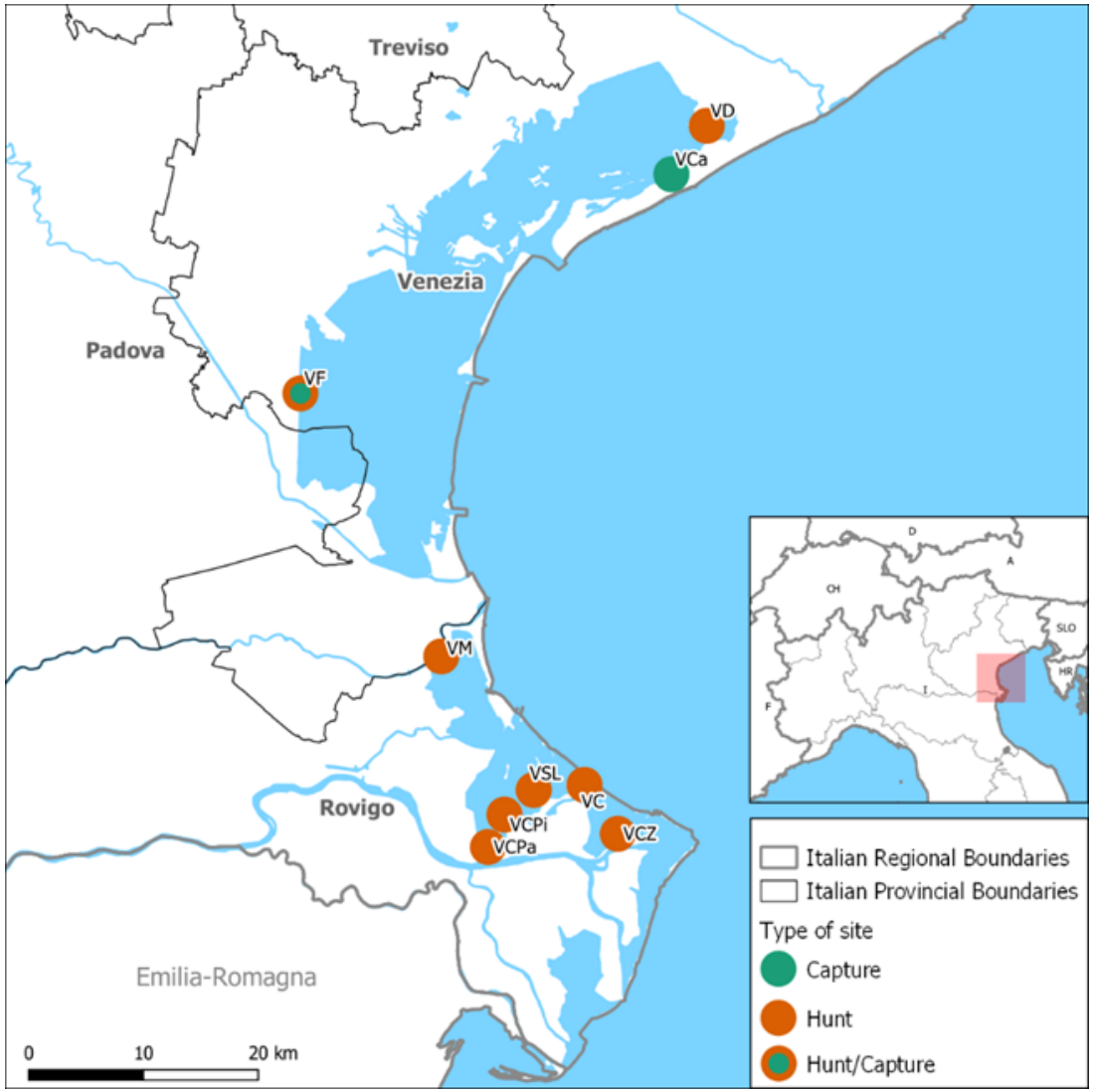
Strategic zone for the introduction of AIV *via* migratory flows

Early detection

Wild-domestic bird interface: unique combination of densely populated poultry areas(DPPAs) and wetlands

Risk-based

1. **Active Surveillance in hunted dabbling ducks (Nov 2020-Jan 2021)**
2. **Active Surveillance in birds Capture Station (Nov 2020-March 2021)**



Location of hunting sites (orange color) and capture sites (green color). V, Valle; **VCPa**, V. Ca Pasta (RO); **VCZ**, V. Ca Zuliani (RO); **VD**, V. Drago (VE); **VSL**, V. San Leonardo (RO); **VC**, V. Chiusa (RO); VCPi, V. Ca Pisani (RO); **VM**, V. Morosina (RO); **VF**, Valle Figheri (VE); **VCa**, Valle Cavallino.

Hunted dabbling ducks

- 8 wetlands selected for the active surveillance (Province of Rovigo and Venice)
- 15 samplings from November 2020 to January 2021 (a total of **823 hunted** aquatic birds were sampled via oropharyngeal swab (**OS**), cloacal swab (**CS**) and feather swab (**FS**)

337 EW	220 ET	111 Ma	49 Ga	94 NS	12 NP
					
Eurasian wigeon	*Eurasian teal*	*Mallard*	*Gadwall*	*Northern shoveler*	*Northern pintail*

2449 animal swabs were investigated for AIV (M-gene, H5,H7,H9). The identified viruses were characterized and pathotyped by sequencing. AI viruses were easily isolated in SPF chicken eggs from selected samples

Molecular detection and prevalence of AIVs in different biological samples collected from **hunted dabbling ducks** (Veneto region, Northern Italy, 2020-2021). Blue, HPAIV circulation; yellow, LPAIV circulation; green, HPAIV and LPAIV co-circulation.

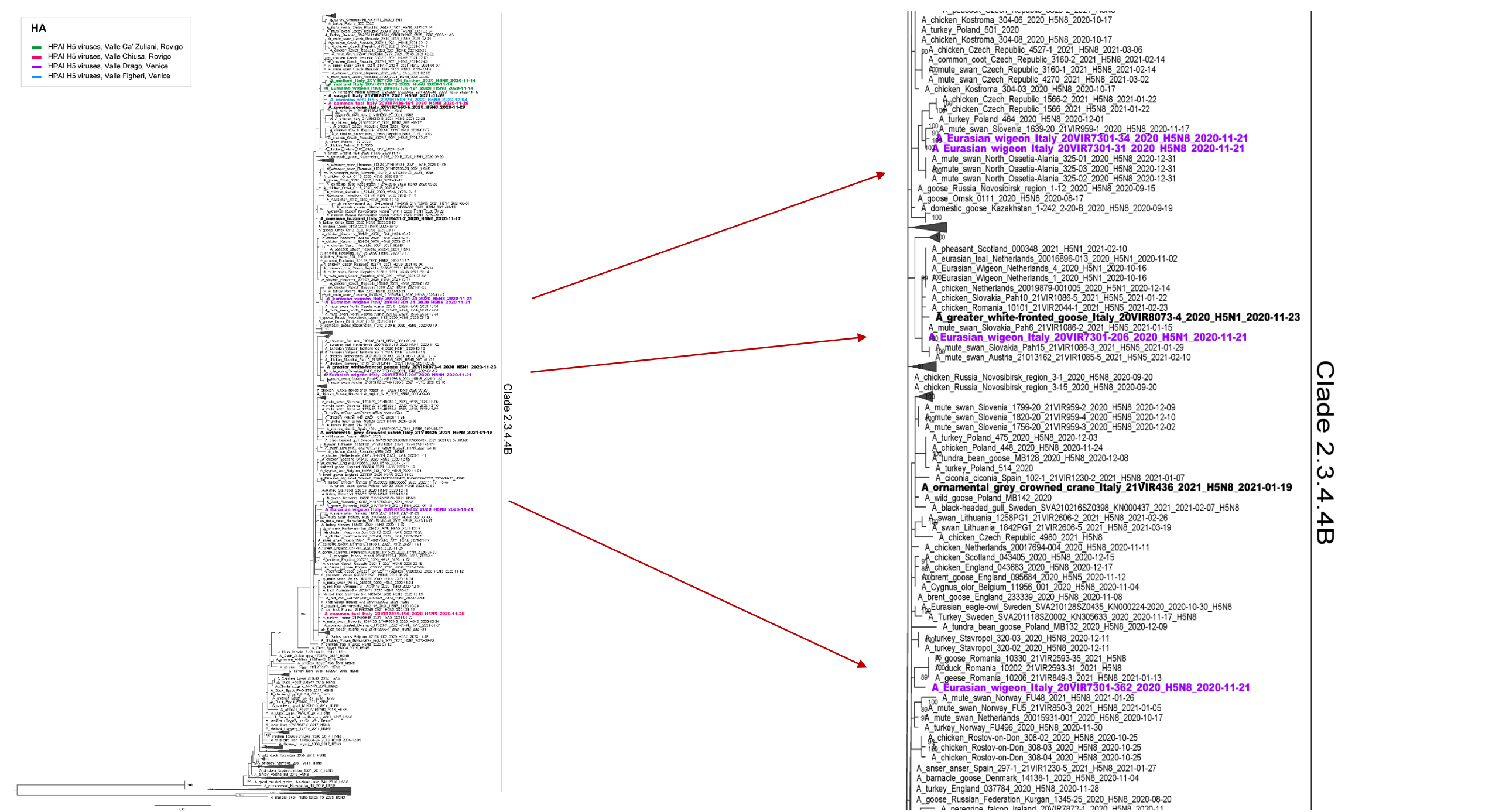
HVSS ID	Sampling yy-mm-dd	Eurasian Teal				Gadwall				Northern Pintail				Eurasian Wigeon				Mallard				Northern Shoveler				Dabbling ducks			
		ET	Pos. N. (%)			Ga	Pos. N. (%)			NP	Pos. N. (%)			EW	Pos. N. (%)			Ma	Pos. N. (%)			NS	Pos. N. (%)			DD	Pos. N. (%)		
			OS	CS	FS		OS	CS	FS		OS	CS	FS		OS	CS	FS		OS	CS	FS		OS	CS	FS		OS	CS	FS
VCPa-1st	20-11-09	7	0	1 (14.3)	0	19	0	0	0	1	0	0	0	6	0	2 (33.3)	0	8	0	0	0	13	0	0	0	54	0	3 (5.6)	0
VCZ-1st	20-11-16	1	0	0	0	5	0	0	1(20)	4	0	0	0	10	1 (10)	2 (20)	0	19	1 (5.3)	1 (5.3)	2 (10.5)	1	0	0	0	40	2 (5)	3 (7.5)	3 (7.5)
VD-1st	20-11-21	0	—	—	—	4	0	0	0	5	0	0	0	100	10 (10)	9 (9)	5 (5)	0	—	—	—	11	0	1 (9.1)	1 (9.1)	120	10 (8.3)	10 (8.3)	6 (5)
VSL-1st	20-11-21	8	0	0	0	0	—	—	—	0	—	—	—	54	2 (3.7)	3 (5.6)	1 (1.9)	8	0	0	0	40	0	0	0	110	2 (1.8)	3 (2.7)	1 (0.9)
VC-1st	20-11-26	32	2 (6.3)	0	2 (6.3)	2	0	0	0	0	—	—	—	16	0	0	2 (12.5)	8	0	0	1 (12.5)	4	0	0	0	62	2 (3.2)	0	5 (8.1)
VD-2nd	20-11-28	0	—	—	—	0	—	—	—	0	—	—	—	20	0	0	—	0	—	—	—	0	—	—	—	20	0	0	—
VCPi	20-12-07	46	1 (2.2)	0	0	0	—	—	—	0	—	—	—	2	0	0	0	2	0	0	0	0	—	—	—	50	1 (2)	0	0
VCPa-2nd	20-12-15	1	0	0	0	3	0	0	0	0	—	—	—	89	3 (3.4)	4 (4.5)	1 (1.1)	5	0	0	0	2	0	0	0	100	3 (3)	4 (4)	1 (1)
VM-1st	20-12-22	60	1 (1.7)	0	0	2	0	0	0	0	—	—	—	0	—	—	—	23	0	0	0	1	0	0	0	86	1 (1.2)	0	0
VC-2nd	21-01-09	20	0	0	0	1	0	0	0	0	—	—	—	16	0	0	0	4	0	0	0	4	0	0	0	45	0	0	0
VD-3rd	21-01-11	15	0	1 (6.7)	0	0	—	—	—	0	—	—	—	15	0	0	0	0	—	—	—	0	—	—	—	30	0	1 (3.3)	0
VSL-2nd	21-01-16	1	0	0	0	0	—	—	—	0	—	—	—	4	0	0	0	6	0	0	0	7	0	1 (14.3)	0	18	0	1 (5.6)	0
VF	21-01-24	1	0	0	0	11	0	0	0	2	0	0	0	2	0	0	0	15	0	0	0	8	0	1 (12.5)	0	39	0	1 (2.6)	0
VCZ-2nd	21-01-25	3	1 (33.3)	0	0	0	—	—	—	0	—	—	—	3	1 (33.3)	0	2 (66.7)	5	1 (20)	0	1 (20)	2	1(50)	0	0	13	4 (30.8)	0	3 (23.1)
VM-2nd	21-01-30	25	0	1 (4)	0	2	0	0	0	0	—	—	—	0	—	—	—	8	0	0	0	1	0	0	0	36	0	1 (2.8)	0
Total duck & Pos. (%)	20-11-09 21-01-30	220	5 (2.3)	3 (1.4)	2 (0.9)	49	0	0	1 (2)	12	0	0	0	337	17 (5)	20 (5.9)	11 (3.3)	111	2 (1.8)	1 (0.9)	4 (3.6)	94	1 (1.1)	3 (3.2)	1 (1.1)	823	25 (3)	27 (3.3)	19 (2.3)

Molecular pathotyping and subtyping of AIVs detected in different biological samples collected from captured hunted dabbling ducks (Veneto region, Northern Italy, 2020-2021).

HVSS ID (yy-mm-dd)	AIV Pos H-duck ID	Sex	Age	OS virological results			CS virological results			FS virological results		
				AIV M gene	AIV P-T	AIV S-T	AIV M gene	AIV P-T	AIV S-T	AIV M gene	AIV P-T	AIV S-
VCPa-1st (20-11-09)	H1_ET	n.a.	n.a.	-	n.d.	n.d.	Pos.	LPAI	H5Nx	-	n.d.	n.d.
	H2_EW	n.a.	n.a.	-	n.d.	n.d.	**Pos.**	**HPAI**	**H5Nx**	-	n.d.	n.d.
	H3_EW	n.a.	n.a.	-	n.d.	n.d.	Pos.	LPAI	H9Nx	-	n.d.	n.d.
VCZ-1st (20-11-16)	H4_EW	n.a.	n.a.	-	n.d.	n.d.	**Pos.**	**HPAI**	**H5Nx**	-	n.d.	n.d.
	H5_EW	n.a.	n.a.	**Pos.**	**HPAI**	**H5N8**	**Pos.**	**HPAI**	**H5Nx**	-	n.d.	n.d.
	H6_Ga	n.a.	n.a.	-	n.d.	n.d.	-	n.d.	n.d.	Pos.	LPAI	HxNx
	H7_Ma	n.a.	n.a.	-	n.d.	n.d.	-	n.d.	n.d.	Pos.	LPAI	HxNx
	H8_Ma	n.a.	n.a.	-	n.d.	n.d.	-	n.d.	n.d.	**Pos.**	**HPAI**	**H5N8**
	H9_Ma	n.a.	n.a.	**Pos.**	**HPAI**	**H5N8**	**Pos.**	**HPAI**	**H5N8**	-	n.d.	n.d.
VD-1st (20-11-21)	H10_EW	F	J	**Pos.**	**HPAI**	**H5N8**	**Pos.**	**HPAI**	**H5Nx**	-	n.d.	n.d.
	H11_EW	F	J	**Pos.**	**HPAI**	**H5Nx**	**Pos.**	**HPAI**	**H5Nx**	-	n.d.	n.d.
	H12_EW	F	A	Pos.	n.a.	H5Nx	-	n.d.	n.d.	-	n.d.	n.d.
	H13_EW	F	J	-	n.d.	n.d.	-	n.d.	n.d.	**Pos.**	**HPAI**	**H5Nx**
	H14_EW	M	A	-	n.d.	n.d.	Pos.	n.a.	H5Nx	-	n.d.	n.d.
	H15_EW	F	J	**Pos.**	**HPAI**	**H5N8**	-	n.d.	n.d.	-	n.d.	n.d.
	H16_EW	F	J	**Pos.**	**HPAI**	**H5N8**	-	n.d.	n.d.	-	n.d.	n.d.
	H17_EW	F	J	-	n.d.	n.d.	**Pos.**	**HPAI**	**H5Nx**	-	n.d.	n.d.
	H18_EW	M	A	-	n.d.	n.d.	-	n.d.	n.d.	**Pos.**	**HPAI**	**H5Nx**
	H19_EW	F	J	**Pos.**	**HPAI**	**H5Nx**	Pos.	n.a.	H5Nx	-	n.d.	n.d.
	H20_EW	M	J	Pos.	n.a.	H5Nx	-	n.d.	n.d.	-	n.d.	n.d.
	H21_EW	M	J	-	n.d.	n.d.	**Pos.**	**HPAI**	**H5Nx**	-	n.d.	n.d.
	H22_EW	F	J	**Pos.**	**HPAI**	**H5N8**	-	n.d.	n.d.	-	n.d.	n.d.
	H23_EW	M	A	-	n.d.	n.d.	-	n.d.	n.d.	**Pos.**	**HPAI**	**H5Nx**
	H24_EW	M	J	**Pos.**	**HPAI**	**H5Nx**	**Pos.**	**HPAI**	**H5Nx**	**Pos.**	**HPAI**	**H5Nx**
	H25_EW	F	A	**Pos.**	**HPAI**	**H5Nx**	-	n.d.	n.d.	-	n.d.	n.d.
	H26_EW	M	J	-	n.d.	n.d.	Pos.	n.a.	H5Nx	-	n.d.	n.d.
	H27_EW	M	J	-	n.d.	n.d.	**Pos.**	**HPAI**	**H5N1**	-	n.d.	n.d.
	H28_EW	M	J	-	n.d.	n.d.	-	n.d.	n.d.	**Pos.**	**HPAI**	**H5Nx**
	H29_NS	F	J	-	n.d.	n.d.	**Pos.**	**HPAI**	**H5Nx**	-	n.d.	n.d.
	H30_NS	F	J	-	n.d.	n.d.	-	n.d.	n.d.	**Pos.**	**HPAI**	**H5Nx**
VSL-1st (20-11-21)	H31_EW	n.a.	n.a.	**Pos.**	**HPAI**	**H5N8**						
	H32_EW	n.a.	n.a.	-	n.d.	n.d.						
	H33_EW	n.a.	n.a.	**Pos.**	**HPAI**	**H5N8**						

Cont.

HVSS ID (yy-mm-dd)	AIV Pos. H-duck ID	Sex	Age	OS virological results			CS virological results			FS virological results		
				AIV M gene	AIV P-T	AIV S-T	AIV M gene	AIV P-T	AIV S-T	AIV M gene	AIV P-T	AIV S-
VC-1st (20-11-26)	H34_Ma	n.a.	n.a.	-	n.d.	n.d.	-	n.d.	n.d.	Pos.	n.a.	H5Nx
	H35_ET	n.a.	n.a.	**Pos.**	**HPAI**	**H5N8**	-	n.d.	n.d.	-	n.d.	n.d.
	H36_ET	n.a.	n.a.	-	n.d.	n.d.	-	n.d.	n.d.	Pos.	n.a.	H5Nx
	H37_ET	n.a.	n.a.	-	n.d.	n.d.	-	n.d.	n.d.	Pos.	n.a.	H5Nx
	H38_ET	n.a.	n.a.	**Pos.**	**HPAI**	**H5N5**	-	n.d.	n.d.	-	n.d.	n.d.
	H39_EW	n.a.	n.a.	-	n.d.	n.d.	-	n.d.	n.d.	Pos.	n.a.	H5Nx
	H40_EW	n.a.	n.a.	-	n.d.	n.d.	-	n.d.	n.d.	Pos.	n.a.	H5Nx
VCPi (20-12-07)	H41_ET	n.a.	n.a.	Pos.	LPAI	HxNx	-	n.d.	n.d.	-	n.d.	n.d.
VCPa-2nd (20-12-15)	H42_EW	n.a.	n.a.	**Pos.**	**HPAI**	**H5N8**	**Pos.**	**HPAI**	**H5N8**	-	n.d.	n.d.
	H43_EW	n.a.	n.a.	**Pos.**	**HPAI**	**H5N8**	**Pos.**	**HPAI**	**H5N8**	**Pos.**	**HPAI**	**H5N8**
	H44_EW	n.a.	n.a.	**Pos.**	**HPAI**	**H5N1**	-	n.d.	n.d.	-	n.d.	n.d.
	H45_EW	n.a.	n.a.	-	n.d.	n.d.	**Pos.**	**HPAI**	**H5N1**	-	n.d.	n.d.
	H46_EW	n.a.	n.a.	-	n.d.	n.d.	**Pos.**	**HPAI**	**H5N1**	-	n.d.	n.d.
VM-1st (20-12-22)	H47_ET	n.a.	n.a.	**Pos.**	**HPAI**	**H5N8**	-	n.d.	n.d.	-	n.d.	n.d.
VD-3rd (21-01-11)	H48_ET	M	J	-	n.d.	n.d.	Pos.	LPAI	HxNx	-	n.d.	n.d.
VSL-2nd (21-01-16)	H49_NS	n.a.	n.a.	-	n.d.	n.d.	Pos.	LPAI	HxNx	-	n.d.	n.d.
VF (21-01-24)	H50_NS	M	J	-	n.d.	n.d.	Pos.	LPAI	HxNx	-	n.d.	n.d.
VCZ-2nd (21-01-25)	H51_Ma	n.a.	n.a.	**Pos.**	**HPAI**	**H5N8**	-	n.d.	n.d.	**Pos.**	**HPAI**	**H5N8**
	H52_EW	n.a.	n.a.	**Pos.**	**HPAI**	**H5N8**	-	n.d.	n.d.	**Pos.**	**HPAI**	**H5N8**
	H53_NS	n.a.	n.a.	**Pos.**	**HPAI**	**H5N8**	-	n.d.	n.d.	-	n.d.	n.d.
	H54_ET	n.a.	n.a.	**Pos.**	**HPAI**	**H5N8**	-	n.d.	n.d.	-	n.d.	n.d.
	H55_EW	n.a.	n.a.	-	n.d.	n.d.	-	n.d.	n.d.	**Pos.**	**HPAI**	**H5N8**
VM-2nd (21-01-30)	H56_ET	n.a.	n.a.	-	n.d.	n.d.	Pos.	LPAI	HxNx	-	n.d.	n.d.


HA
HPAI H5 viruses, Valle Ca' Zuliani, Rovigo
HPAI H5 viruses, Valle Chiusa, Rovigo
HPAI H5 viruses, Valle Drago, Venice
HPAI H5 viruses, Valle Figheri, Venice
Clade 2.3.4.4B
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A_turkey_Poland_501_2020
A_chicken_Kostroma_304-08_2020_H5N8_2020-10-17
A_chicken_Czech_Republic_4527-1_2021_H5N8_2021-03-06
A_common_coot_Czech_Republic_3160-2_2021_H5N8_2021-02-14
A_mute_swan_Czech_Republic_3160-1_2021_H5N8_2021-02-14
A_mute_swan_Czech_Republic_4270_2021_H5N8_2021-03-02
A_chicken_Kostroma_304-03_2020_H5N8_2020-10-17
A_chicken_Czech_Republic_1566-2_2021_H5N8_2021-01-22
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A_chicken_Netherlands_20019879-001005_2020_H5N1_2020-12-14
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A_turkey_Poland_514_2020
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A_brent_goose_England_095684_2020_H5N5_2020-11-12
A_Cygnus_olor_Belgium_11956_001_2020_H5N8_2020-11-04
A_brent_goose_England_233339_2020_H5N8_2020-11-08
A_Eurasian_eagle-owl_Sweden_SVA210128SZ0435_KN000224-2020_2020-10-30_H5N8
A_Turkey_Sweden_SVA201118SZ0002_KN305633_2020_2020-11-17_H5N8
A_tundra_bean_goose_Poland_MB132_2020_H5N8_2020-12-09
A_turkey_Stavropol_320-03_2020_H5N8_2020-12-11
A_turkey_Stavropol_320-02_2020_H5N8_2020-12-11
A_goose_Romania_10330_21VIR2593-35_2021_H5N8
A_duck_Romania_10202_21VIR2593-31_2021_H5N8
A_geese_Romania_10206_21VIR849-3_2021_H5N8_2021-01-13
A_Eurasian_wigeon_Italy_20VIR7301-362_2020_H5N8_2020-11-21
A_mute_swan_Norway_FU48_2021_H5N8_2021-01-26
A_mute_swan_Norway_FU5_21VIR850-3_2021_H5N8_2021-01-05
A_mute_swan_Netherlands_20015931-001_2020_H5N8_2020-10-17
A_turkey_Norway_FU496_2020_H5N8_2020-11-30
A_chicken_Rostov-on-Don_308-02_2020_H5N8_2020-10-25
A_chicken_Rostov-on-Don_308-03_2020_H5N8_2020-10-25
A_chicken_Rostov-on-Don_308-04_2020_H5N8_2020-10-25
A_anser_anser_Spain_297-1_21VIR1230-5_2021_H5N8_2021-01-27
A_barnacle_goose_Denmark_14138-1_2020_H5N8_2020-11-04
A_turkey_England_037784_2020_H5N8_2020-11-28
A_goose_Russian_Federation_Kurgan_1345-25_2020_H5N8_2020-08-20
A_peregrine_falcon_Ireland_20VIR7872-1_2020_H5N8_2020-11
Clade 2.3.4.4B

Captured dabbling ducks

- 2 wetlands selected for active surveillance in Province of Venice: Valle Figheri wetland (14 samplings from November 2020 to March 2021) and Valle Cavallino wetland (2 samplings in February 2021)

- **521** captured aquatic birds were sampled via oropharyngeal swab (**OS**), cloacal swab (**CS**) and feather swab (**FS**)

4 EW	374 ET	61 Ma	2 Ga	1 CSh	79 NP
					
Eurasian wigeon	*Eurasian teal*	*Mallard*	*Gadwall*	*Common shelduck*	*Northern pintail*

1563 animal swabs were investigated for AIV (M-gene, H5,H7,H9). The identified viruses were characterized and pathotyped by sequencing. AI viruses were easily isolated in SPF chicken eggs from selected samples

Molecular detection and prevalence of AIVs in different biological samples collected from **captured dabbling ducks** (Veneto region, Northern Italy, 2020-2021). Blue, HPAIV circulation; yellow, LPAIV circulation; green, HPAIV and LPAIV co-circulation.

TSS ID	Sampling yy-mm-dd	Eurasian Teal				Gadwall				Northern Pintail				Eurasian Wigeon				Mallard				Common Shelduck				Dabbling ducks			
		ET	Pos. N. (%)			Ga	Pos. N. (%)			NP	Pos. N. (%)			EW	Pos. N. (%)			Ma	Pos. N. (%)			CSh	Pos. N. (%)			DD	Pos. N. (%)		
			OS	CS	FS		OS	CS	FS		OS	CS	FS		OS	CS	FS		OS	CS	FS		OS	CS	FS		OS	CS	FS
VF-1	20-11-12	24	1 (4.2)	0	0	0	–	–	–	0	–	–	–	0	–	–	–	3	0	0	0	0	–	–	–	27	1 (3.7)	0	0
VF-2	20-11-12	10	0	1 (10)	0	0	–	–	–	0	–	–	–	0	–	–	–	3	0	0	0	0	–	–	–	13	0	1 (7.7)	0
VF-3	20-11-27	24	0	2 (8.3)	0	0	–	–	–	0	–	–	–	0	–	–	–	2	0	0	0	0	–	–	–	26	0	2 (7.7)	0
VF-4	20-12-04	68	15 (22.1)	4 (5.9)	9 (13.2)	0	–	–	–	0	–	–	–	0	–	–	–	1	0	0	0	0	–	–	–	69	15 (21.7)	4 (5.8)	9 (13)
VF-5	20-12-11	36	7 (19.4)	0	1 (2.8)	0	–	–	–	0	–	–	–	0	–	–	–	2	0	0	0	0	–	–	–	38	7 (18.4)	0	1 (2.6)
VF-6	20-12-18	24	2 (8.3)	1 (4.2)	0	0	–	–	–	0	–	–	–	0	–	–	–	2	0	0	0	0	–	–	–	26	2 (7.7)	1 (3.8)	0
VF-7	20-12-23	6	0	0	0	0	–	–	–	0	–	–	–	0	–	–	–	1	0	0	0	0	–	–	–	7	0	0	0
VF-8	21-01-07	10	0	1 (10)	0	0	–	–	–	0	–	–	–	0	–	–	–	1*	0	0	0	0	–	–	–	11	0	1 (9.1)	0
VF-9	21-01-14	6	0	0	0	0	–	–	–	0	–	–	–	0	–	–	–	10	0	0	1 (10)	0	–	–	–	16	0	0	1 (6.3)
VF-10	21-01-22	40	0	2 (5)	0	0	–	–	–	0	–	–	–	0	–	–	–	6**	0	0	0	0	–	–	–	46	0	2 (4.3)	0
VF-11	21-01-29	51	1 (2)	3 (5.9)	0	2	0	0	0	0	–	–	–	0	–	–	–	9	1 (11.1)	0	0	0	–	–	–	62	2 (3.2)	3 (4.8)	0
VF-12	21-02-22	19	0	0	0	0	–	–	–	0	–	–	–	0	–	–	–	2	0	0	0	0	–	–	–	21	0	0	0
VF-13	21-02-25	29	0	2 (6.9)	0	0	–	–	–	0	–	–	–	0	–	–	–	5	0	0	0	0	–	–	–	34	0	2 (5.9)	0
VF-14	21-03-05	9	0	0	0	0	–	–	–	0	–	–	–	0	–	–	–	14	0	0	0	0	–	–	–	23	0	0	0
VCa-1	21-02-12	18	0	0	0	0	–	–	–	74	0	3 (4.1)	0	4	0	0	0	0	–	–	–	1	0	1 (100)	0	97	0	4 (4.1)	0
VCa-2	21-02-15	0	–	–	–	0	–	–	–	5	0	1 (20)	0	0	–	–	–	0	–	–	–	0	–	–	–	5	0	1 (20)	0
Total duck & Pos. (%)	20-11-12 21-03-05	374	26 (7)	16 (4.3)	10 (2.7)	2	0	0	0	79	0	4 (5.1)	0	4	0	0	0	61	1 (1.6)	0	1 (1.6)	1	0	1 (100)	0	521	27 (5.2)	21 (4)	11 (2.1)

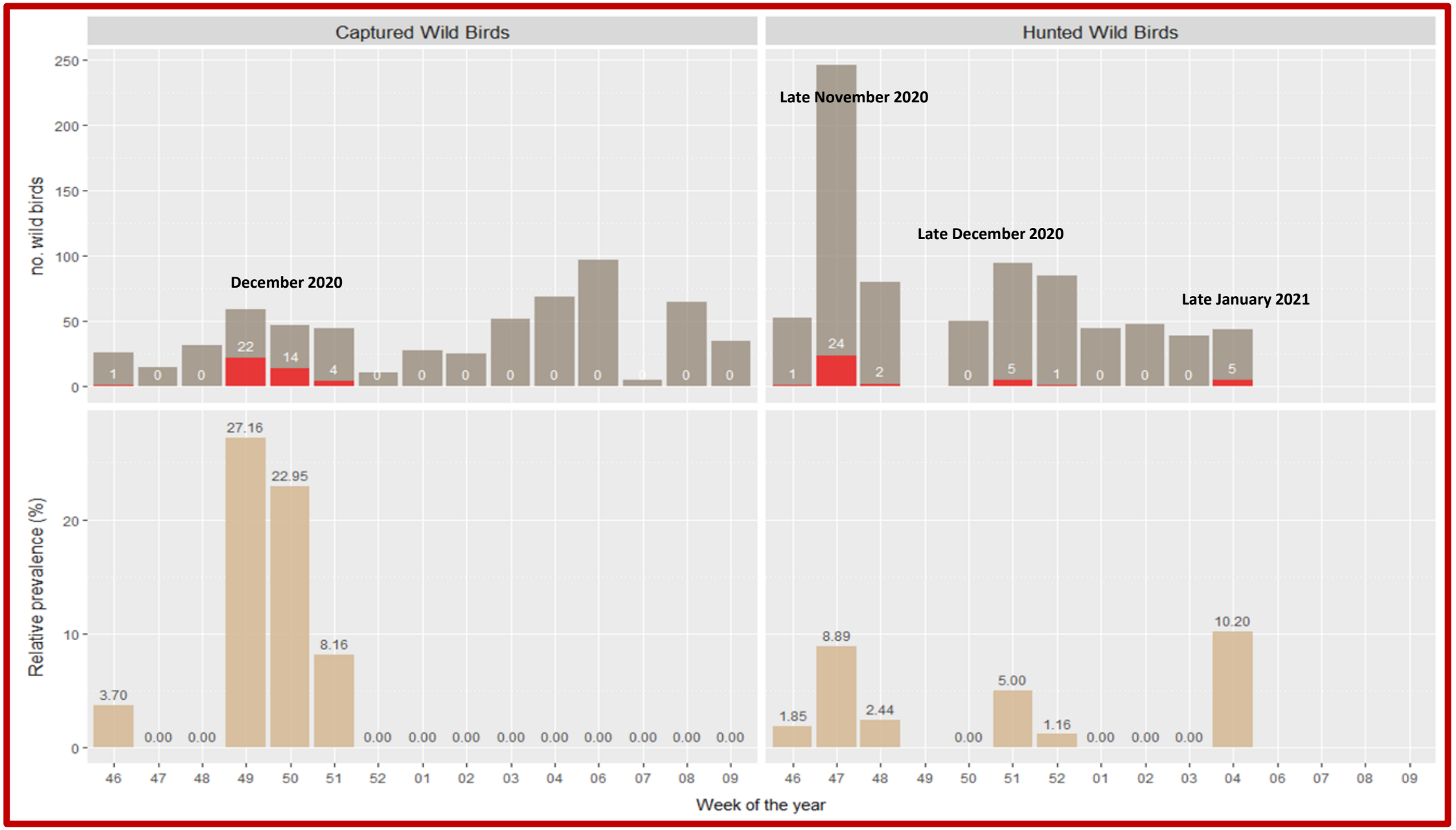
Molecular pathotyping and subtyping of AIVs detected in different biological samples collected from captured dabbling ducks (Veneto region, Northern Italy, 2020-2021).

TSS ID (yy-mm-dd)	AIV Pos C-duck ID	Sex	Age	OS virological results			CS virological results			FS virological results		
				AIV M gene	AIV P-T	AIV S-T	AIV M gene	AIV P-T	AIV S-T	AIV M gene	AIV P-T	AIV S-
VF-1 (20-11-12)	C1_ET	M	J	**Pos.**	**HPAI**	**H5Nx**	-	n.d.	n.d.	-	n.d.	n.d.
VF-2 (20-11-20)	C2_ET	F	A	-	n.d.	n.d.	Pos.	LPAI	H5Nx	-	n.d.	n.d.
VF-3 (20-11-27)	C3_ET	M	J	-	n.d.	n.d.	Pos.	LPAI	HxNx	-	n.d.	n.d.
	C4_ET	M	J	-	n.d.	n.d.	Pos.	LPAI	HxNx	-	n.d.	n.d.
VF-4 (20-12-04)	C5_ET	F	J	**Pos.**	**HPAI**	**H5Nx**	-	n.d.	n.d.	-	n.d.	n.d.
	C6_ET	M	J	**Pos.**	**HPAI**	**H5Nx**	-	n.d.	n.d.	-	n.d.	n.d.
	C7_ET	F	J	**Pos.**	**HPAI**	**H5Nx**	-	n.d.	n.d.	-	n.d.	n.d.
	C8_ET	F	J	**Pos.**	**HPAI**	**H5Nx**	**Pos.**	**HPAI**	**H5Nx**	-	n.d.	n.d.
	C9_ET	F	J	**Pos.**	**HPAI**	**H5Nx**	-	n.d.	n.d.	**Pos.**	**HPAI**	**H5Nx**
	C10_ET	F	A	Pos.	LPAI	HxNx	-	n.d.	n.d.	-	n.d.	n.d.
	C11_ET	F	A	**Pos.**	**HPAI**	**H5Nx**	-	n.d.	n.d.	-	n.d.	n.d.
	C12_ET	M	J	**Pos.**	**HPAI**	**H5N8**	**Pos.**	**HPAI**	**H5Nx**	-	n.d.	n.d.
	C13_ET	M	A	**Pos.**	**HPAI**	**H5Nx**	-	n.d.	n.d.	-	n.d.	n.d.
	C14_ET	F	J	**Pos.**	**HPAI**	**H5Nx**	-	n.d.	n.d.	-	n.d.	n.d.
	C15_ET	M	J	**Pos.**	**HPAI**	**H5N8**	**Pos.**	**HPAI**	**H5Nx**	-	n.d.	n.d.
	C16_ET	F	J	-	n.d.	n.d.	Pos.	LPAI	HxNx	-	n.d.	n.d.
	C17_ET	F	J	**Pos.**	**HPAI**	**H5Nx**	-	n.d.	n.d.	-	n.d.	n.d.
	C18_ET	F	J	**Pos.**	**HPAI**	**H5Nx**	-	n.d.	n.d.	**Pos.**	**HPAI**	**H5Nx**
	C19_ET	F	J	**Pos.**	**HPAI**	**H5Nx**	-	n.d.	n.d.	-	n.d.	n.d.
	C20_ET	M	A	**Pos.**	**HPAI**	**H5N1**	-	n.d.	n.d.	**Pos.**	**HPAI**	**H5Nx**
	C21_ET	M	J	-	n.d.	n.d.	-	n.d.	n.d.	**Pos.**	**HPAI**	**H5Nx**
	C22_ET	F	J	-	n.d.	n.d.	-	n.d.	n.d.	**Pos.**	**HPAI**	**H5Nx**
	C23_ET	M	J	-	n.d.	n.d.	-	n.d.	n.d.	**Pos.**	**HPAI**	**H5Nx**
	C24_ET	F	A	-	n.d.	n.d.	-	n.d.	n.d.	**Pos.**	**HPAI**	**H5Nx**
	C25_ET	F	J	-	n.d.	n.d.	-	n.d.	n.d.	**Pos.**	**HPAI**	**H5Nx**
	C26_ET	F	J	-	n.d.	n.d.	-	n.d.	n.d.	**Pos.**	**HPAI**	**H5Nx**
VF-5 (20-12-11)	C27_ET	M	J	**Pos.**	**HPAI**	**H5N8**	-	n.d.	n.d.	-	n.d.	n.d.
	C28_ET	F	J	**Pos.**	**HPAI**	**H5N8**	-	n.d.	n.d.	-	n.d.	n.d.
	C29_ET	F	J	**Pos.**	**HPAI**	**H5N8**	-	n.d.	n.d.	-	n.d.	n.d.
	C30_ET	F	J	**Pos.**	**HPAI**	**H5N1-N8**	-	n.d.	n.d.	-	n.d.	n.d.
	C31_ET	F	A	**Pos.**	**HPAI**	**H5N8**	-	n.d.	n.d.	-	n.d.	n.d.
	C32_ET	F	J	**Pos.**	**HPAI**	**H5N8**	-	n.d.	n.d.	-	n.d.	n.d.
	C33_ET	F	J	**Pos.**	n.a.	**H5N8**	-	n.d.	n.d.	-	n.d.	n.d.
	C34_ET	F	J	-	n.d.	n.d.	-	n.d.	n.d.	**Pos.**	**HPAI**	**H5N8**

Cont.

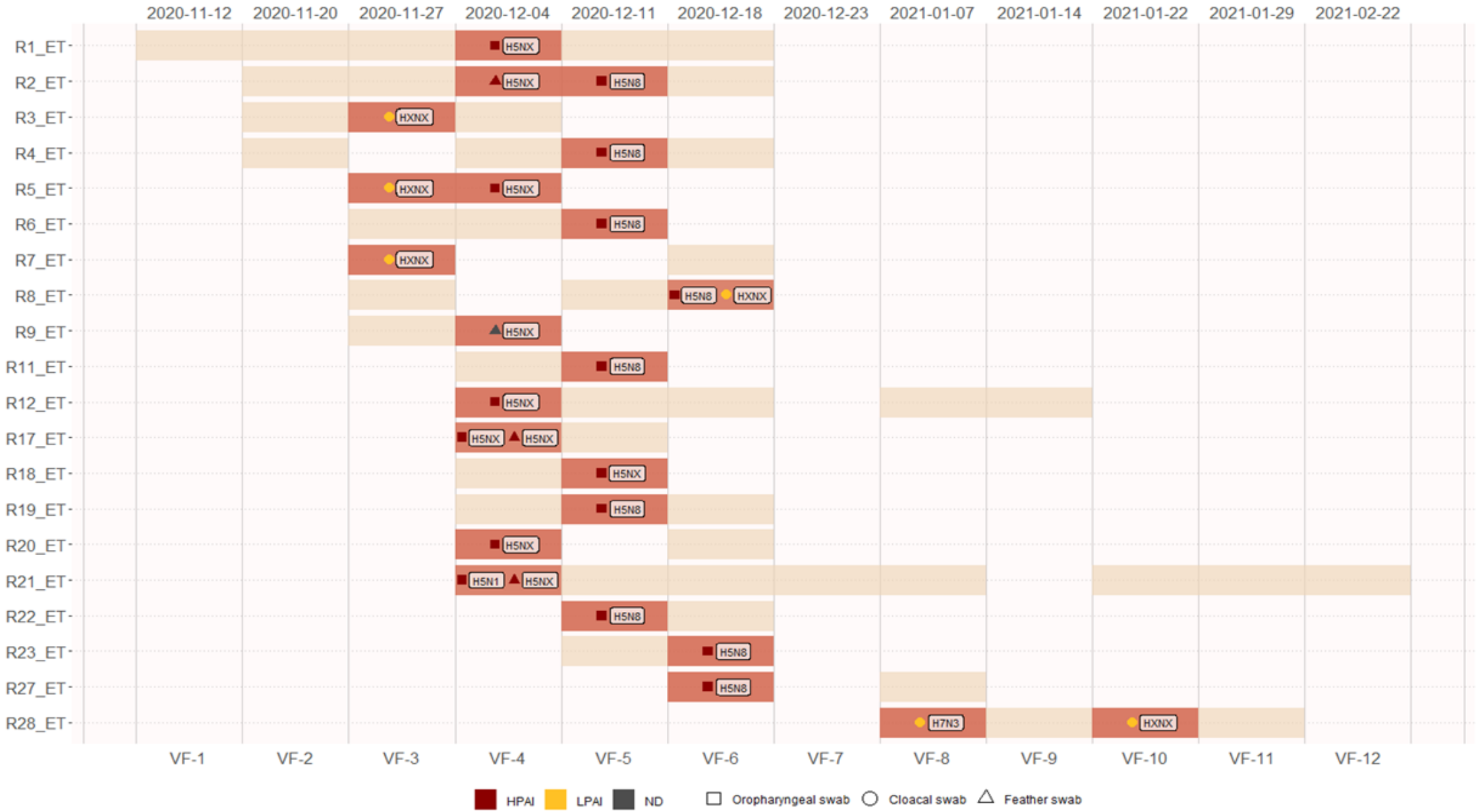
TSS ID (yy-mm-dd)	AIV Pos. C-duck ID	Sex	Age	OS virological results			CS virological results			FS virological results		
				AIV M gene	AIV P-T	AIV S-T	AIV M gene	AIV P-T	AIV S-T	AIV M gene	AIV P-T	AIV S-
VF-6 (20-12-18)	C35_ET	F	J	**Pos.**	**HPAI**	**H5N8**	-	n.d.	n.d.	-	n.d.	n.d.
	C36_ET	M	J	**Pos.**	**HPAI**	**H5N8**	-	n.d.	n.d.	-	n.d.	n.d.
	C37_ET	F	J	-	n.d.	n.d.	Pos.	LPAI	HxNx	-	n.d.	n.d.
VF-8 (21-01-07)	C38_ET	F	J	-	n.d.	n.d.	Pos.	LPAI	H7N3	-	n.d.	n.d.
VF-9 (21-01-14)	C39_Ma	F	J	-	n.d.	n.d.	-	n.d.	n.d.	Pos.	LPAI	H9Nx
VF-10 (21-01-22)	C40_ET	F	J	-	n.d.	n.d.	Pos.	LPAI	HxNx	-	n.d.	n.d.
	C41_ET	F	J	-	n.d.	n.d.	Pos.	LPAI	HxNx	-	n.d.	n.d.
VF-11 (21-01-29)	C42_ET	M	J	Pos.	LPAI	HxNx	-	n.d.	n.d.	-	n.d.	n.d.
	C43_ET	F	J	-	n.d.	n.d.	Pos.	LPAI	HxNx	-	n.d.	n.d.
	C44_ET	M	J	-	n.d.	n.d.	Pos.	LPAI	HxNx	-	n.d.	n.d.
	C45_ET	F	J	-	n.d.	n.d.	Pos.	LPAI	HxNx	-	n.d.	n.d.
	C46_Ma	M	J	Pos.	LPAI	HxNx	-	n.d.	n.d.	-	n.d.	n.d.
VF-13 (21-02-25)	C47_ET	F	J	-	n.d.	n.d.	Pos.	LPAI	HxNx	-	n.d.	n.d.
	C48_ET	M	J	-	n.d.	n.d.	Pos.	LPAI	HxNx	-	n.d.	n.d.
VCa-1 (21-02-12)	C49_CSh	F	J	-	n.d.	n.d.	Pos.	LPAI	H5Nx	-	n.d.	n.d.
	C50_NP	A	M	-	n.d.	n.d.	Pos.	LPAI	HxNx	-	n.d.	n.d.
	C51_NP	A	F	-	n.d.	n.d.	Pos.	LPAI	HxNx	-	n.d.	n.d.
	C52_NP	J	F	-	n.d.	n.d.	Pos.	LPAI	HxNx	-	n.d.	n.d.
VCa-1 (21-02-15)	C53_NP	n.a.	n.a.	-	n.d.	n.d.	Pos.	LPAI	HxNx	-	n.d.	n.d.

HPAI epidemic curves in captured and hunted wild birds during late autumn-winter seasons 2020-2021 in Northern Est Italy

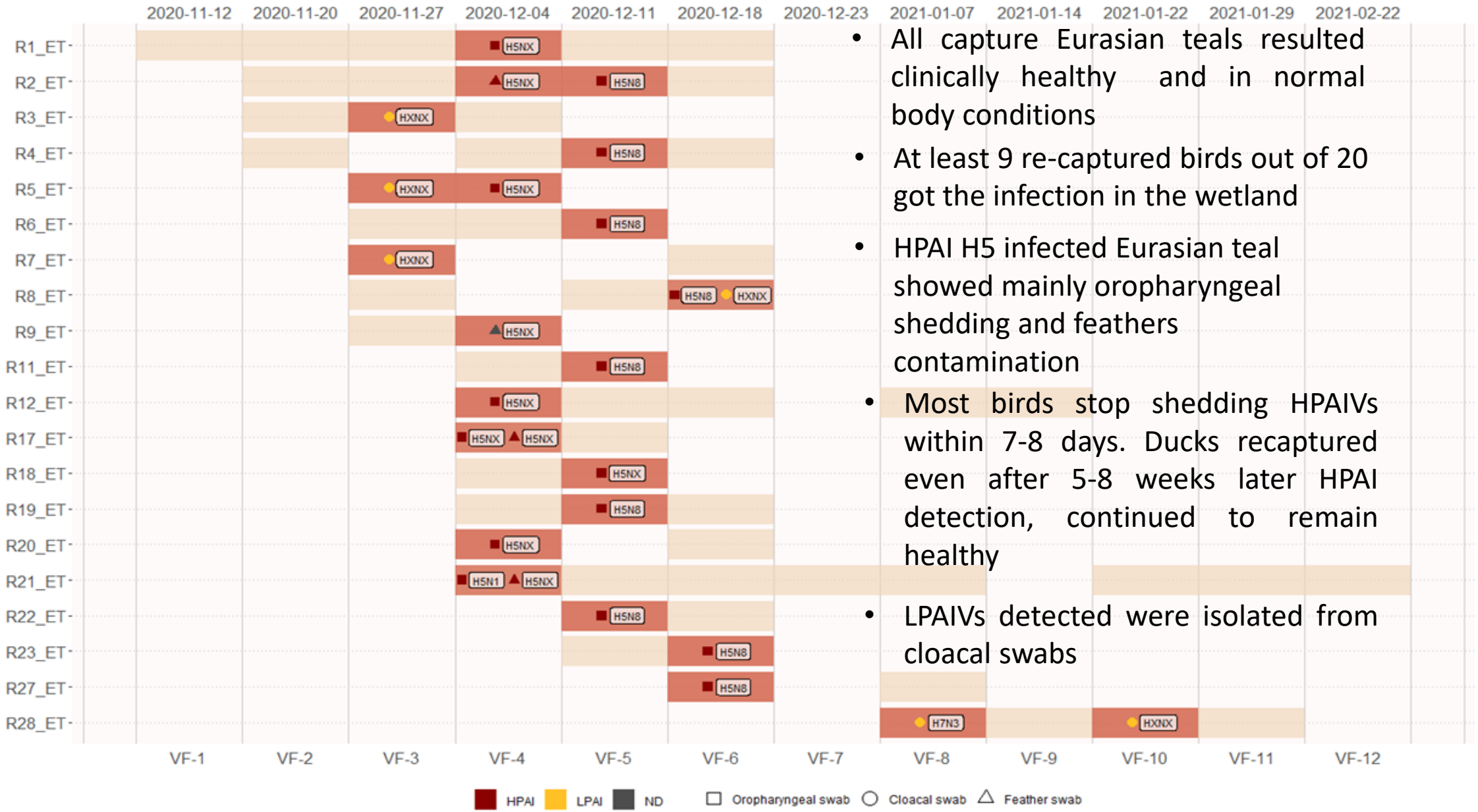


Capture station in Valle Figheri (Venice province)

Progression of the HPAI H5 clade 2.3.4.4b infection in naturally infected wild migratory Eurasian teals



Progression of the HPAI H5 clade 2.3.4.4b infection in naturally infected wild migratory Eurasian teals



- All capture Eurasian teals resulted clinically healthy and in normal body conditions
- At least 9 re-captured birds out of 20 got the infection in the wetland
- HPAI H5 infected Eurasian teal showed mainly oropharyngeal shedding and feathers contamination
- Most birds stop shedding HPAIVs within 7-8 days. Ducks recaptured even after 5-8 weeks later HPAI detection, continued to remain healthy
- LPAIVs detected were isolated from cloacal swabs

Conclusions

- The results obtained in these studies are particular and reflect a different scenario to the one observed last winter in northern European countries

- Late autumn - early winter seems to be the period at higher risk of introduction of HPAIVs from migratory birds in southern European countries

- The early detection of HPAIV presence in wintering migratory wild birds must lead MS to the immediate implementation of adequate risk mitigation measures

Conclusions

- Our findings confirm previous scientific evidences of Eurasian teal and Eurasian wigeon as long-distance vectors of HPAI H5Nx GsGd viruses 2.3.4.4b, since the infection may often occur asymptomatically despite evident oropharyngeal and cloacal viral shedding

- Our data show that it is more probable to detect H5 HPAI clade 2.3.4.4b in oropharyngeal and feather swabs of dabbling ducks rather than in cloacal swabs.

- In order to detect more efficiently the early introduction of novel HPAI viruses, passive surveillance should be complemented by a targeted active surveillance tailored to each country

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Active Surveillance for Highly Pathogenic Avian Influenza Viruses in Wintering Waterbirds in Northeast Italy, 2020–2021

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Abstract: The increasing involvement of wild waterfowl in H5 Highly Pathogenic Avian Influenza Virus (HPAIV) circulation continues to pose a threat to animal and public health worldwide. In winter 2020–2021, two field surveillance activities were carried out on a weekly basis, through virological and serological analyses, in 823 hunted and 521 trapped migratory aquatic birds in northeast Italy. Sixty Eurasian teals were recaptured several times, which allowed us to follow the progression of the HPAI H5 infection in naturally infected wild waterfowl. Oropharyngeal, cloacal, and feather swabs (OS, CS and FS) were collected from each duck and tested by real time rRT-PCR Type A influenza. The identified viruses were characterized and pathotyped by sequencing. Several viruses belonging to three different HPAI H5 subtypes were detected: H5N8, H5N5, and H5N1. High prevalence of infection with HPAI H5 clade 2.3.4.4b during November–December 2020 (up to 27.1%) was observed in captured Eurasian teals, while infection rates in hunted dabbling ducks, mainly Eurasian wigeons, showed the highest prevalence of infection in November 2020 (8.9%) and January 2021 (10.2%). All HPAI positive birds were also clinically healthy when recaptured weeks apart. The OS and FS showed the highest detection efficiency of HPAIV. Our results highlight that HPAI passive surveillance should be complemented by a targeted active surveillance to more efficiently detect novel HPAI viruses.

Keywords: avian influenza virus; HPAI H5 subtypes clade 2.3.4.4b; migratory aquatic bird; active surveillance

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1. Introduction

It has long been known that wild aquatic birds enable the perpetuation of low-pathogenic avian influenza viruses (LPAIVs) that, in poultry, can occasionally evolve into highly pathogenic (HP) strains. However, in recent years, the increasing involvement of these reservoir hosts in H5 HPAIV circulation and spread has opened a new scenario in which HPAI H5 viruses belonging to clade 2.3.4.4 of the Goose/Guangdong/96 (GS/Gd) lineage pose an even greater threat to poultry and wild birds worldwide. Reassortment events between these HPAI H5 and LPAIVs of wild bird origin have led to generation of different variants that have been periodically spread by wild birds across continents [1–3].

In the autumn–winter season of 2020–2021, following the confirmation of several HPAI outbreaks of the H5 subtype among wild and domestic birds in western Russia and Kazakhstan in May–September 2020, all European Union (EU) member states were urged to intensify surveillance activities and to increase biosecurity measures in the poultry sector to avoid new avian influenza outbreaks. Actually, these eastern affected areas are known

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Thank you for attention

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