Istituto Zooprofilattico Sperimentale delle Venezie

31st Annual Meeting

of the National Reference Laboratories for Avian Influenza and Newcastle Disease of European Union Member States

Istituto Zooprofilattico Sperimentale delle Venezie

Treviso
October 16-17, 2025

Update on Newcastle Disease in Europe

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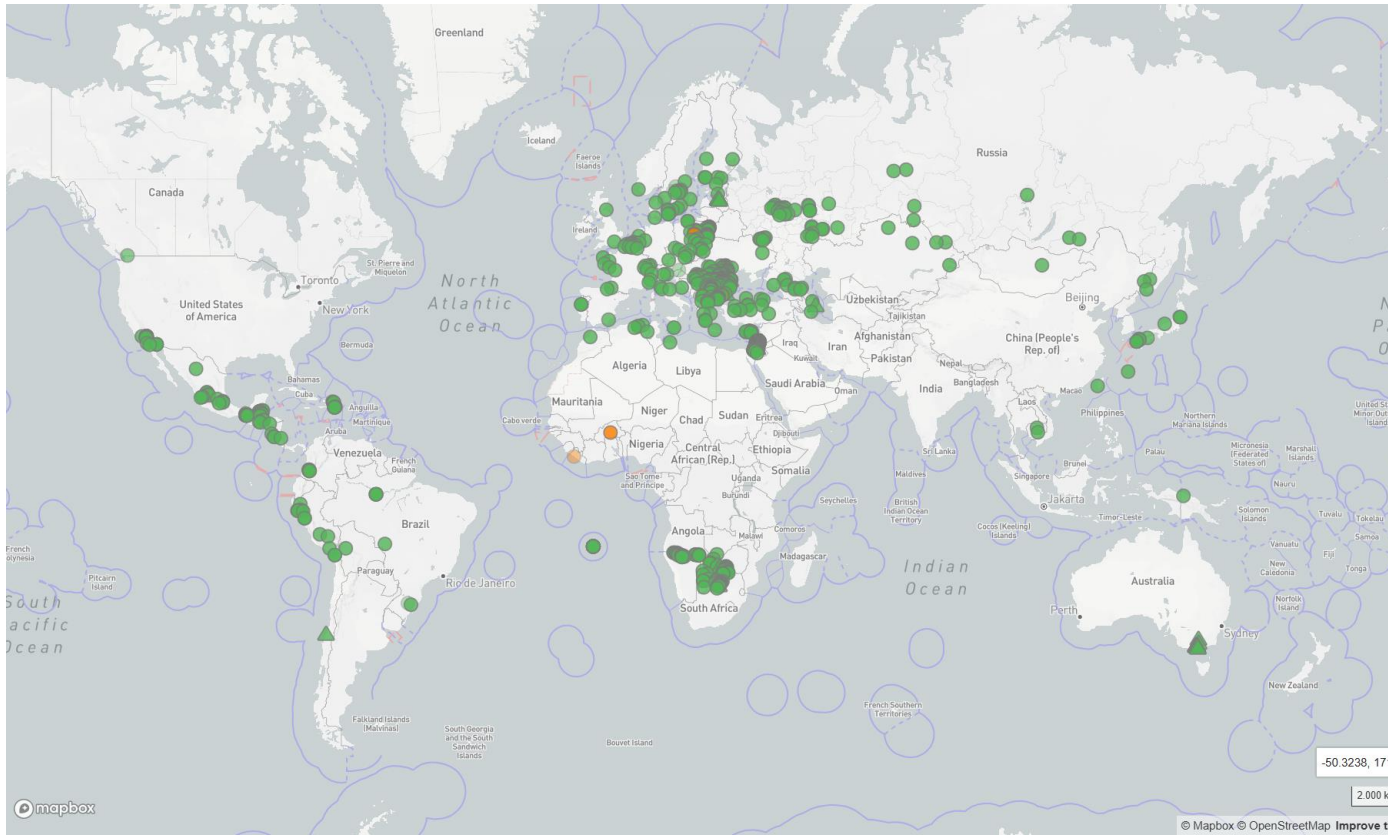
EURL AI/ND

Istituto Zooprofilattico Sperimentale delle Venezie (IZSVe), Padua, Italy

Trends of NDV notification to ADIS/WAHIS

D.J. Alexander (**2011**) "*Because of this worldwide impact, as recently as 1997, most of those working in the field would have considered ND* ***as the single most significant disease of poultry****. However, since that time it has been overshadowed by the emergence and spread of highly pathogenic avian influenza (HPAI) virus of subtype H5N1*"



Vaccination of household chickens results in a shift in young children's diet and improves child growth in rural Kenya

Elkanah Otiang, Jonathan Yoder, Shanthi Manian, +4, and Guy H. Palmer Authors Info & Affiliations

Edited by Xiang-Jin Meng, Virginia Polytechnic Institute and State University, Blacksburg, VA; received December 23, 2021; accepted April 1, 2022

June 6, 2022 | 119 (24) e2122389119 | https://doi.org/10.1073/pnas.2122389119

4.042 | 4 PDF EPUB

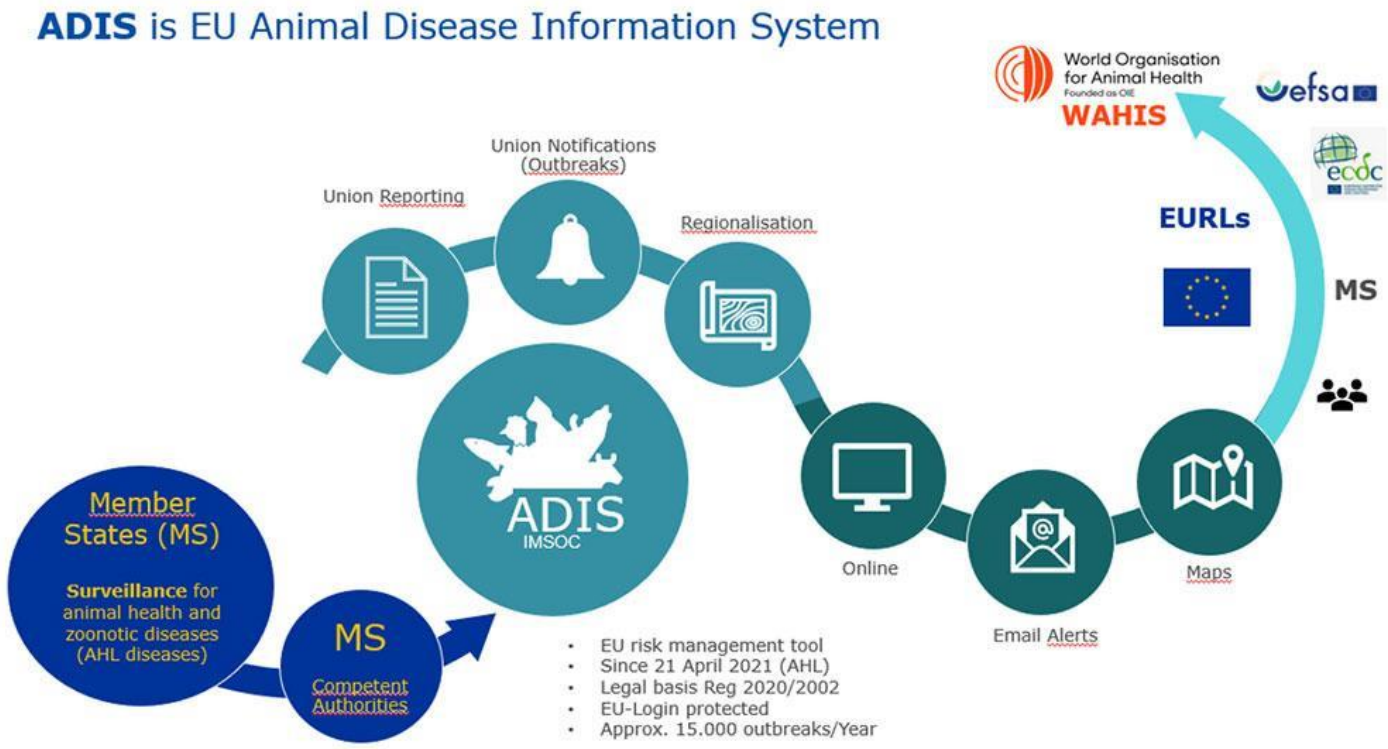
Significance

This randomized, controlled trial demonstrates that by relieving a constraint on household nutritional assets, here through reducing chicken mortality through vaccination, households make dietary choices for young children that increase consumption of protein- and micronutrient-rich foods and decrease relative consumption of high-carbohydrate, low-protein grains. The study provides causal evidence that this

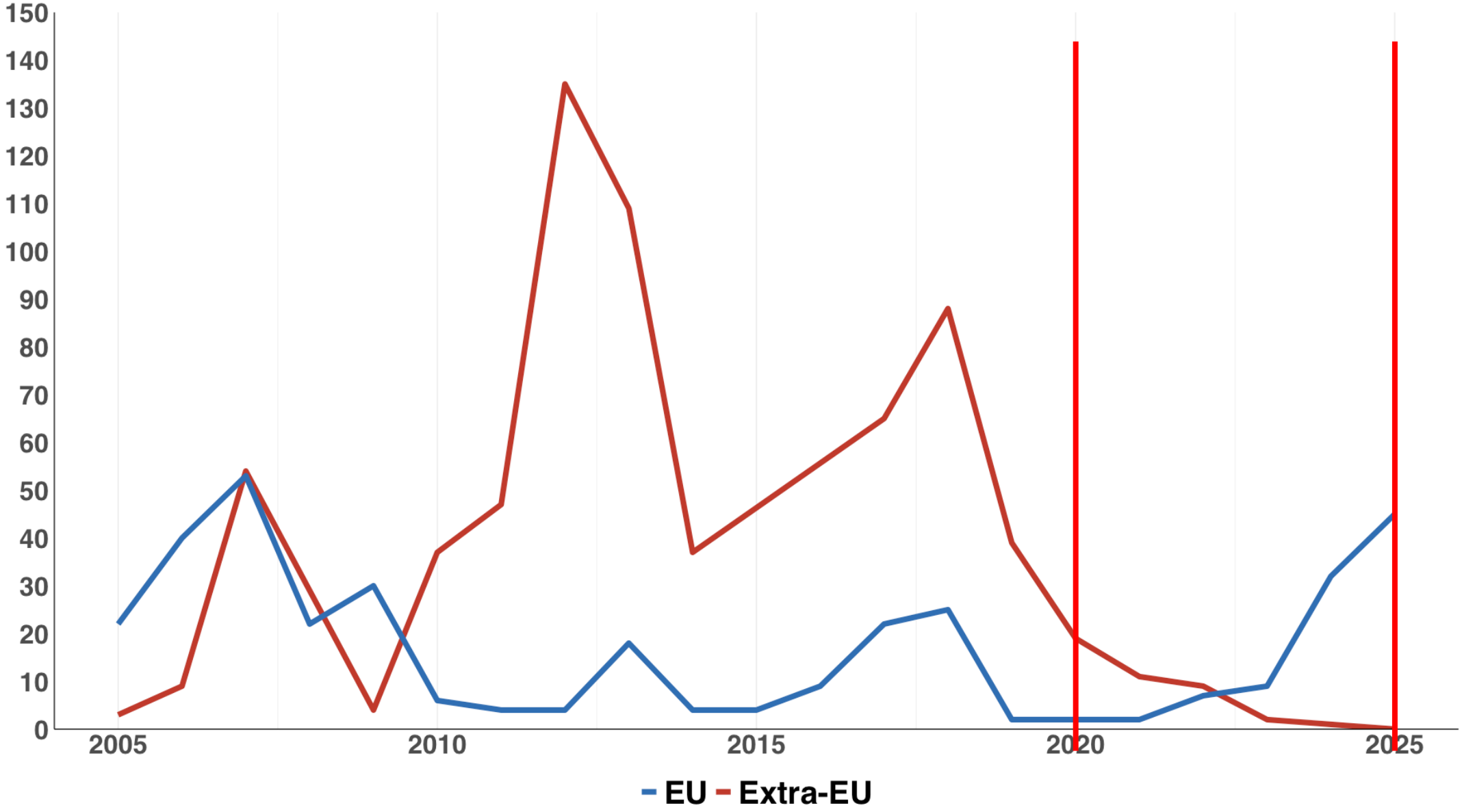
- In developing countries it still represent a threat to the livelihood of small scale farmers and rural communities while in many part of world the disease is controlled by vaccination

Trends of NDV notification to ADIS/WAHIS

- No perfect overlap of notification submitted to the EU Animal disease information system (ADIS) and the World Animal Health Information System (WAHIS), managed by the World Organisation for Animal Health (WOAH) but integration of the two systems is in progress.
- We used both databases to retrieve information on NDV outbreaks occurring in EU and Non-EU countries in the past 20 years.
- Integration of databases essential at the present stage to rapidly obtain more information. ADIS allows to easily obtain number of outbreaks. WAHIS more friendly interface to obtain additional information on outbreaks.



Trends of NDV notification to ADIS/WAHIS



Notification by EU-MSs and neighbouring countries 2020-2025 (excluding domestic columbiformes)

Year	Country	Species	Genotype	Number of outbreaks
2020	North Macedonia	Chicken	VII.2	3
2020-2022	Turkey	Domestic	VII.2	32
2020	Russia	Chicken, Turkeys	VII.1.1	9
2021-2022-2024	Sweden	Chicken	XIII.1.1	4
2021-2022	Republic of Kosovo	Chicken	VII.2	1
2022	Norway	Chicken	XIII.1.1	1
2022	Spain	Chicken	VII.2	3
2022	Sweden	Chicken	VI.2.1.1.2.2	1
2022	Switzerland	Chicken	VI.2.1.1.2.2.	1
2023	Moldova	Domestic	n.a.	1
2023-2025	Poland	Chicken, Turkeys	VII.1.1.	99
2025	Malta	Chicken	VII.1.1	2
2025	Slovenia	Chicken	VII.1.1	2
2025	Republic of Kosovo	Chicken	VII.2?	3
2025	North Macedonia	Chicken	VII.2	2
2025	Czech Rebublic	Chicken	VII.1.1	5
Total	**10 Countries**	**2 species?**	**4 genotypes**	**169**

Genotype VII: Changes in the classification system

Sub/lineage Aldous et al., 2003	Sub/genotype Diel et al., 2012a, 2012b	Current study
Class II		
1	I a	I.1.1
	I b	I.2.
	I c	I.1.2.1
	I d	I.1.2.2
2	II	II
3a, 3f	III	III
3b	IV	IV
3c	V b	V; V.1
	V c	V.2
	V d	V
4bii *e*	VI a	VI.2.1.1.1
	VI n	VI.2.1.1.1
4b, 4bi, 4bii *d*	VI b	VI.1.1
	VI e	VI.1.2.2.2
	VI f	VI.1.2.2.1
	VI h	VI.1.2.1.2
4bii *f*	VI j	VI.2.1.1.2.1
	VI k	VI.2.1.1.2.2
4c	–	–
5a	VII a – one sequence	VII.2
	VIIi	
5d	VII b	VII.1.1
	VII b	VII.1.1
	VII j	VII.1.1
	VII l	VII.1.1
5c	VII e	VII.1.1
	VII f	VII.1.2
–	VII g (RF)	–
5a	VII h	VII.2
–	VII k	VII.2
5e	VII	VII, VII.2
3d	VIII	VIII
3e	IX	IX
1	X a	X
	X b	X
3 g	XI	XI
5b	XII a	XII.1
	XII b	XII.2
5b	XIII a	XIII.1.1
	XIII a	XIII.1.2
	XIII b	XIII.2.1
	XIII b	XIII.2.2
5 h, 7d	XIV	XIV
5f, 7c	XIV a	XIV.1
	XIV b	XIV.2
–	XV (RF)	XV (RF)
3d	XVI	XVI
5 g, 7a	XVII a	XVII
	XVII b	XVII
7b	XVIII a	XVIII.1
	XVIII b	XVIII.2
3c	V a	XIX
4a, 4d	VI c	XX
–	VI l	XXI
–	VI i	XXI.2
–	VI g	XXI.1.1
–	VI m	XXI.1.2
Class I		
6	1a	1.1.1
	1b	1.1.2
	1c	1.2
	1d	1.2

The viruses responsible for the fourth and fifth NDV panzootics belong to genotypes VII.1.1 and VII.2, respectively.

5a	VII a – one sequence	VII.2
	VIIi	
5d	VII b	VII.1.1
	VII b	VII.1.1
	VII j	VII.1.1
	VII l	VII.1.1
5c	VII e	VII.1.1
	VII f	VII.1.2
–	VII g (RF)	–
5a	VII h	VII.2
–	VII k	VII.2

Genotype VII in Europe (2019-2025)

F gene

Several genetically distinguishable viruses within genotype VII have been circulating in Europe over the past five years.

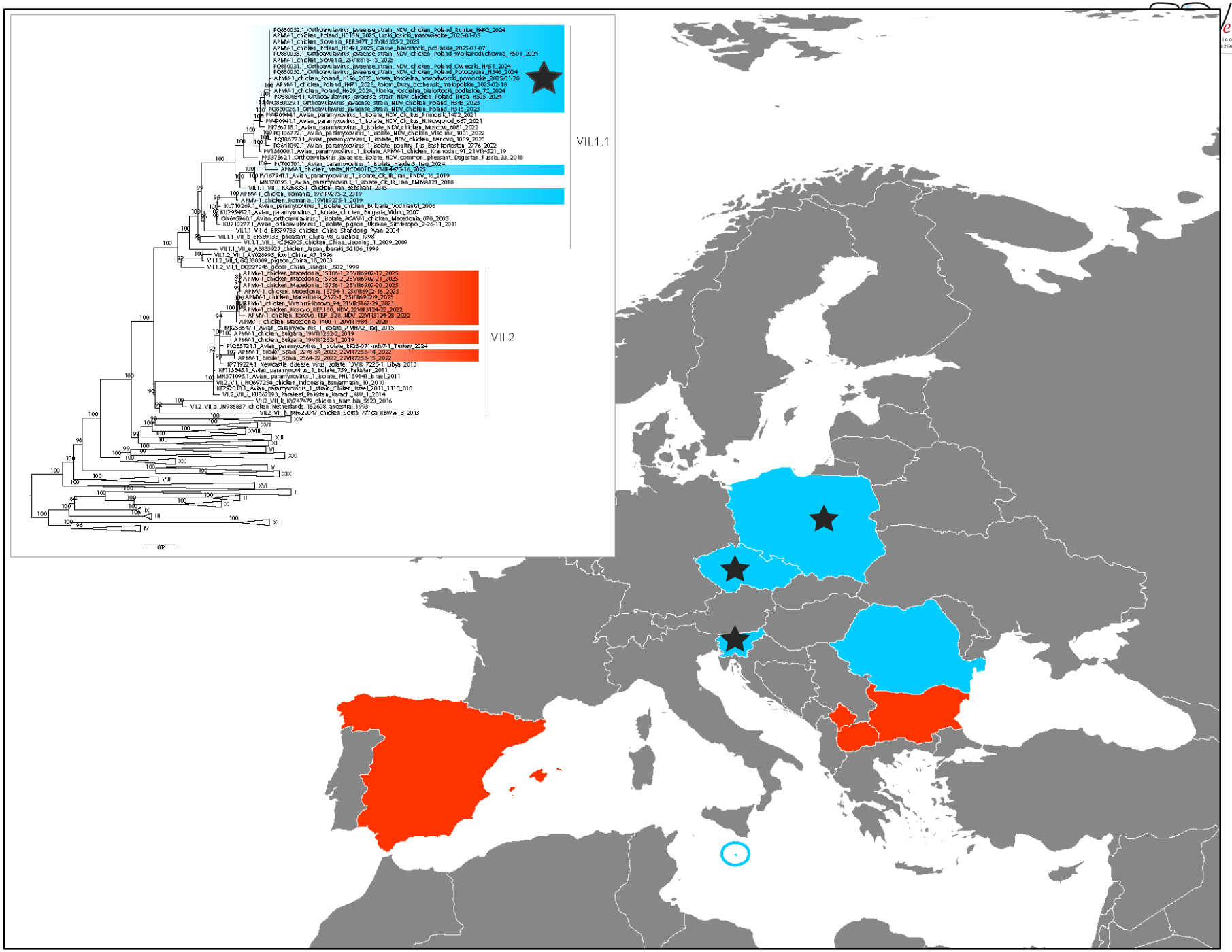
In particular, both VII.1.1 and VII.2 sub-genotypes have been identified co-circulating in the last five year.

Sub genotype VII.1.1

Viruses identified in **Poland** (2023-2025) and **Slovenia** (2025) are clustering together and show the highest similarity to viruses previously detected in Russia.

Based on the partial F gene sequence, it seems that the viruses identified last August in **Czech Republic** also belong to this genetic cluster.

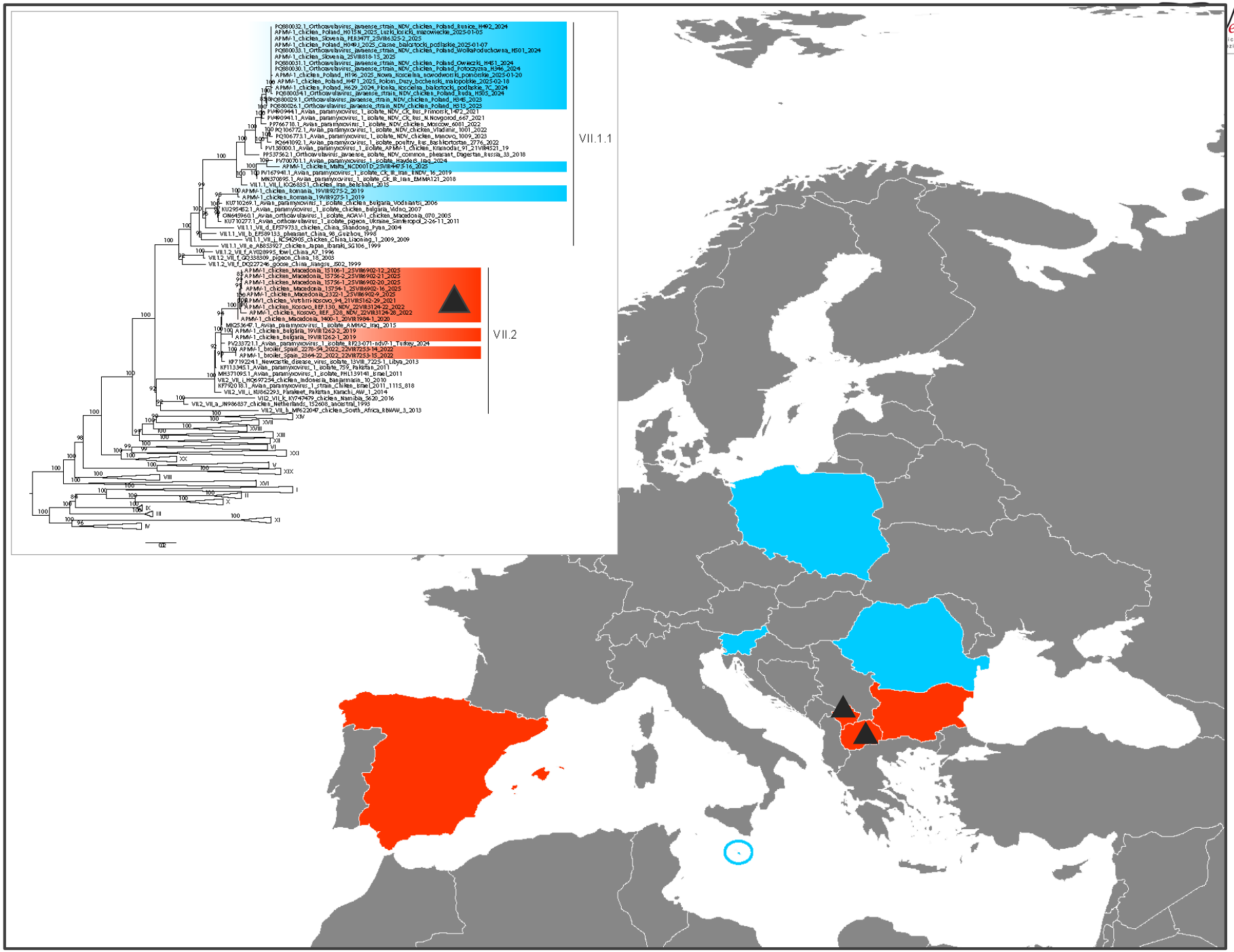
In 2025, the same sub-genotype was identified in **Malta**, but the Maltese virus was genetically distinct from the Poland/Slovenia/Czech republic cluster (similarity 95%), suggesting a separate introduction from an unknown source (highest similarity of 98.85% with a virus identified in Iraq in 2024).



Sub genotype VII.2

There is evidence of an apparent re-emergence of an earlier virus in the Balkans: Viruses detected in **North Macedonia** in 2025 cluster with those detected in North Macedonia in 2020 and in Kosovo in 2021.

The viruses detected in North Macedonia in 2025 are genetically distinct from those reported in Spain (2022) and Bulgaria (2019), consistent with separate introduction events.

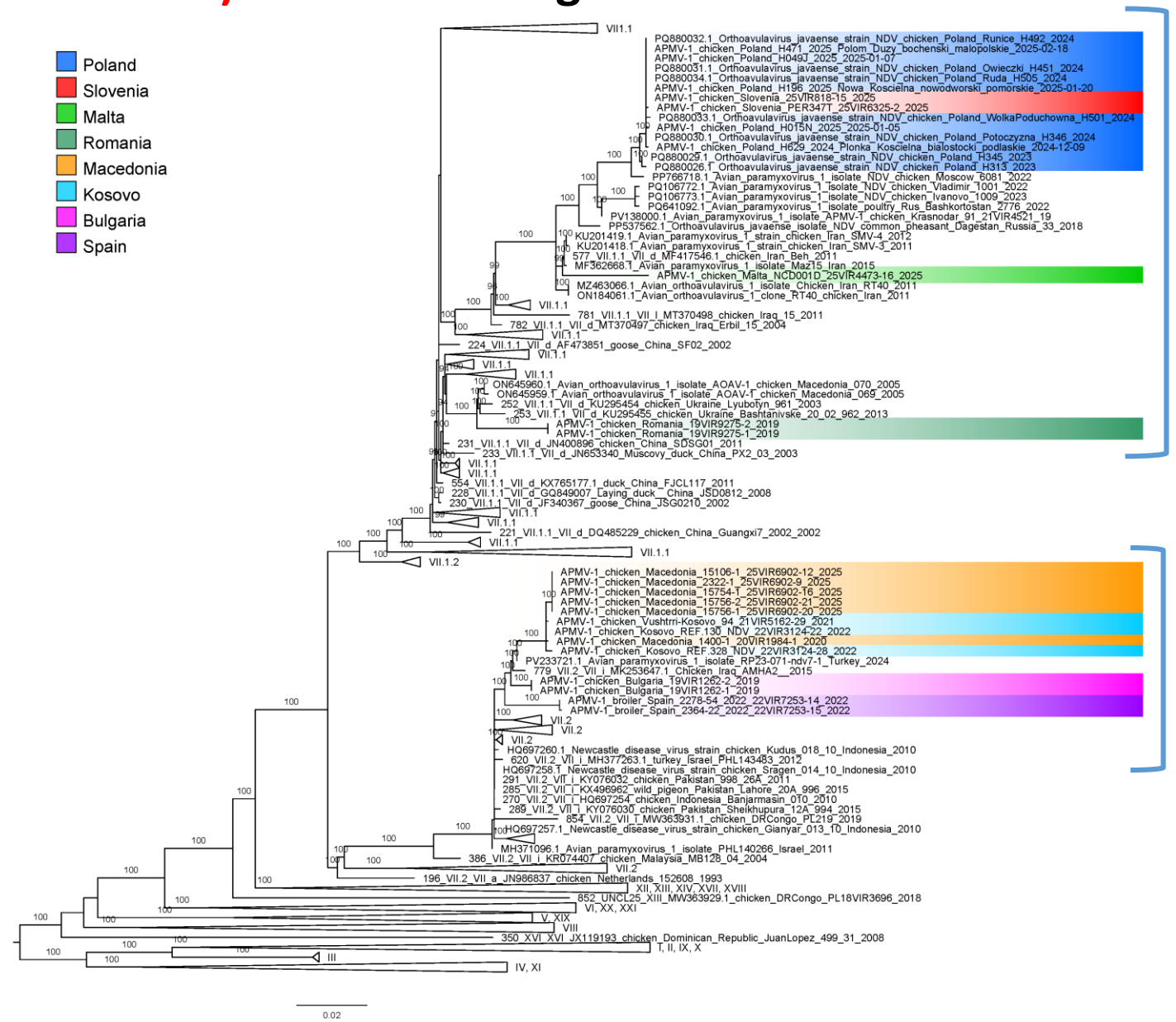


Genotype VII in Europe (2019-2025)

HN gene

The HN-gene phylogenetic tree mirrors that of the F gene.

Notably, the 2025 strains from **North Macedonia** encode an HN protein of **577 amino acids**, compared with **571** in other Genotype VII viruses detected in Europe

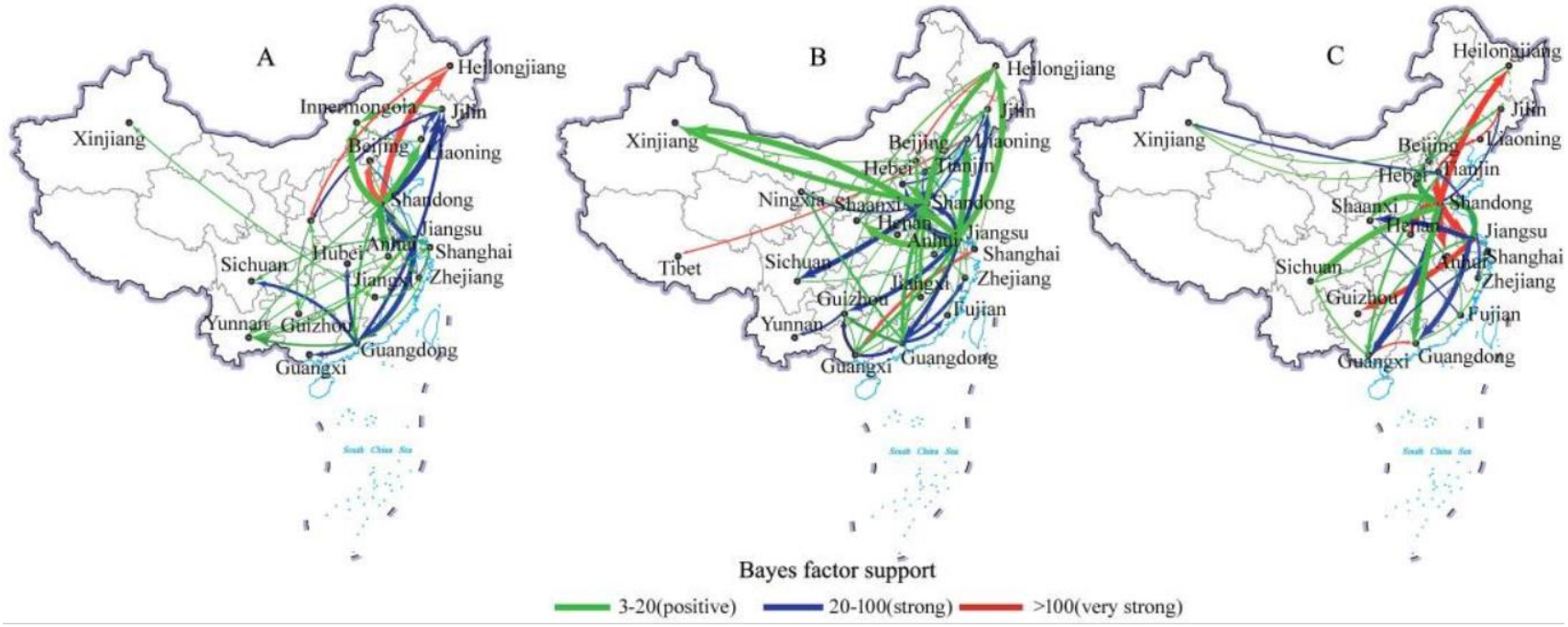


Sub-genotype **VII.1.1**

Sub-genotype **VII.2**

Source of introductions for virulent APMV-1 viruses

- In endemic countries the main source of infection to domestic birds is likely due to lateral spread because of sublcinical within the poultry sector with potential contribution of backyard poultry as demonstrated by numerous papers

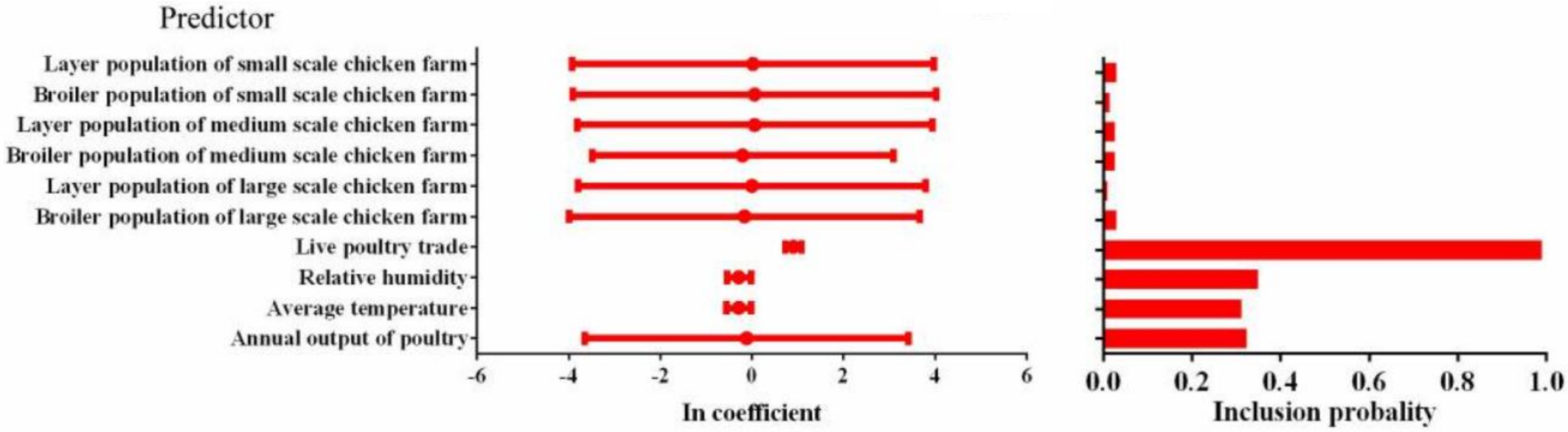


(A) VI-F gene, (B) VII-F gene (subsample one), (C) VII-HN gene. The line colour represents the relative strength by which the rates are supported: very strong (BF > 100, red lines), strong (20 < BF < 100, blue lines) and positive (3 < BF < 20, green lines). The thickness of the arrows indicates increasing number of Markov jumps between locations.

Adapted from: Du J, Xia J, Li S, Shen Y, Chen W, Luo Y, Zhao Q, Wen Y, Wu R, Yan Q, Huang X, Cao S, Han X, Cui M, Huang Y. Evolutionary dynamics and transmission patterns of Newcastle disease virus in China through Bayesian phylogeographical analysis. PLoS One. 2020 Sep 29;15(9):e0239809.

Source of introductions for virulent APMV-1 viruses

- In endemic countries the main source of infection to domestic birds is likely due to lateral spread because of subclinical infections are frequent in vaccinated poultry with potential contribution from backyard poultry.
- Therefore in endemic countries and bordering regions or states the main threat is represented by trade (including hobbyists)



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Wild birds and virulent APMV-1 viruses

- Scarce literature on the role of wild birds in the epidemiology of virulent viruses
- Most of the literature indicates that wild birds do not represent the major reservoir of virulent ND viruses with pigeons, doves, and double-crested cormorants being the exception (Brown and Bevins, 2017). However, spillover to wild birds of class II viruses derived from strains used in poultry reported very

Cormorants as a Pote
Important Reservoir a
Newcastle Disease Vi
Asian Continent

Kobey Karamendin[1,2] and Aidyn Kydyrmanov[1,2]*

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National Agrarian University, Almaty, Kazakhstan

Despite numerous disease prevention measures
disease (ND) remains one of the most signific
especially in developing countries. It is known that
order, are the main carrier of lentogenic (non-patho
virus (NDV) in nature. But the question of the rese
NDV in nature still remains open. In the 1970s,
during epizootics among cormorants, velogenic N
concluded that cormorants play an important role
NDV in North America. New data have been obt
NDV strains in wild birds in Central Asia: VIIb and X
cormorants for the first time in Kazakhstan. Intere
in poultry in Central and Southern Asia were phyl
cormorants that support the idea that cormorants
velogenic NDV in developing countries of Asia. Th
may contribute to the distribution of the virus thro

Identification of Newca
subgenotype VII.2 in wi

Nuri Turan[1], Cemal Ozsemir[1], Aysun Yilmaz[1], Utku Y. (
Aydin Gurel[2], Ahmet Kutukcu[1], Kubra Ozsemir[3], H. Em
Mehmetcan Yaramanoglu[1], B. Kaan Tekelioğlu[4], Serha
Huseyin Yilmaz[1*]

Abstract

Background: Newcastle disease viruses (NDVs) can sp
investigated the frequency of NDV in both non-migra
flyway, in Istanbul, Turkey. Birds were trapped using n
spring seasons of 2016 and 2018. In total, 297 birds be
according to species and sex, and flocked oropharyng
also collected from 115 mallards caught by hunters ar
the Veterinary Faculty of Istanbul university-Cerrahpasa
public to Veterinary Faculty. A total of 619 flocked oro
extracted from swabs and tissue samples. Real-time RT

Results: There was no amplification in real time RT-PC
amplification of NDV-F gene was observed in orophar
and Mallard), and in tissue samples taken from 2 little
analyses of these 5 samples for NDV-F gene showed great similarity with NDV subgenotype VII.2 viruses. Al

Article

Newcastle Disease Genotype
Wild Birds in Egypt

Amal A. M. Eid [1], Ashraf Hussein [1], Ola Hassanin [1], R
Jean-Remy Sadeyen [2], Hanan M. F. Abdien [4], Klaudia

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Abstract: Newcastle Disease
has caused multiple outbrea
the prevalence and genetic
governorates. A total of 37 o
flocks including chickens, d
regions within 13 governora
eggs revealed 91 swab sam
suggestive of virus presence
in 85 samples. The geograp
birds, migratory, and non-mi
six NDV genome sequences
NDV strains carried high vi
to class II within genotype V

check for updates

Citation: Eid, A.A.M.; Hussein, A.; Hassanin, O.; Elbakrey, R.M.; Daines, R.; Sadeyen, J.-R.; Abdien, H.M.F.;

Journal of Wildlife Diseases, 47(2), 2011, pp. 433–441
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CHARACTERIZATION OF VELOGENIC NEWCASTLE DISEASE VIRUSES ISOLATED FROM DEAD WILD BIRDS IN SERBIA DURING 2007

Dejan Vidanović,[1] Milanko Šekler,[1] Ružica Ašanin,[2] Nenad Milić,[2] Jakov Nišavić,[2] Tamaš Petrović,[3] and Vladimir Savić[4,5]

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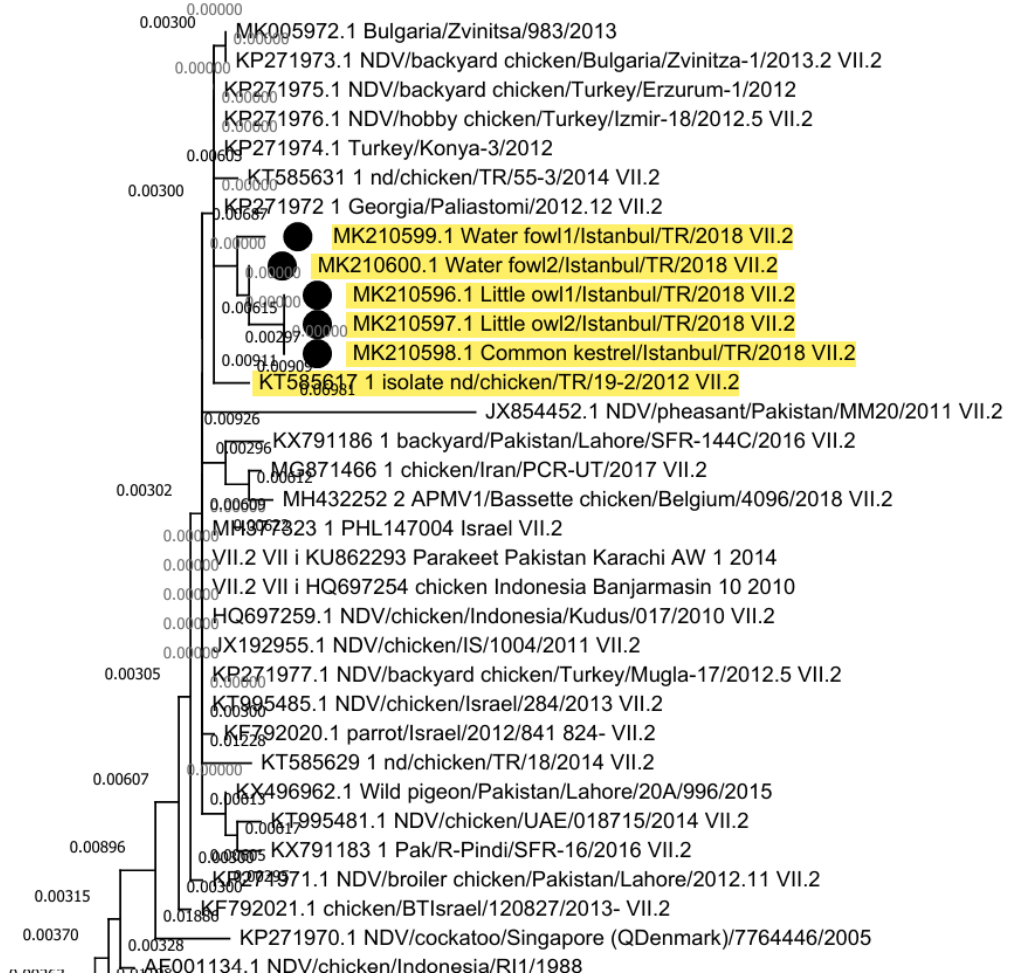
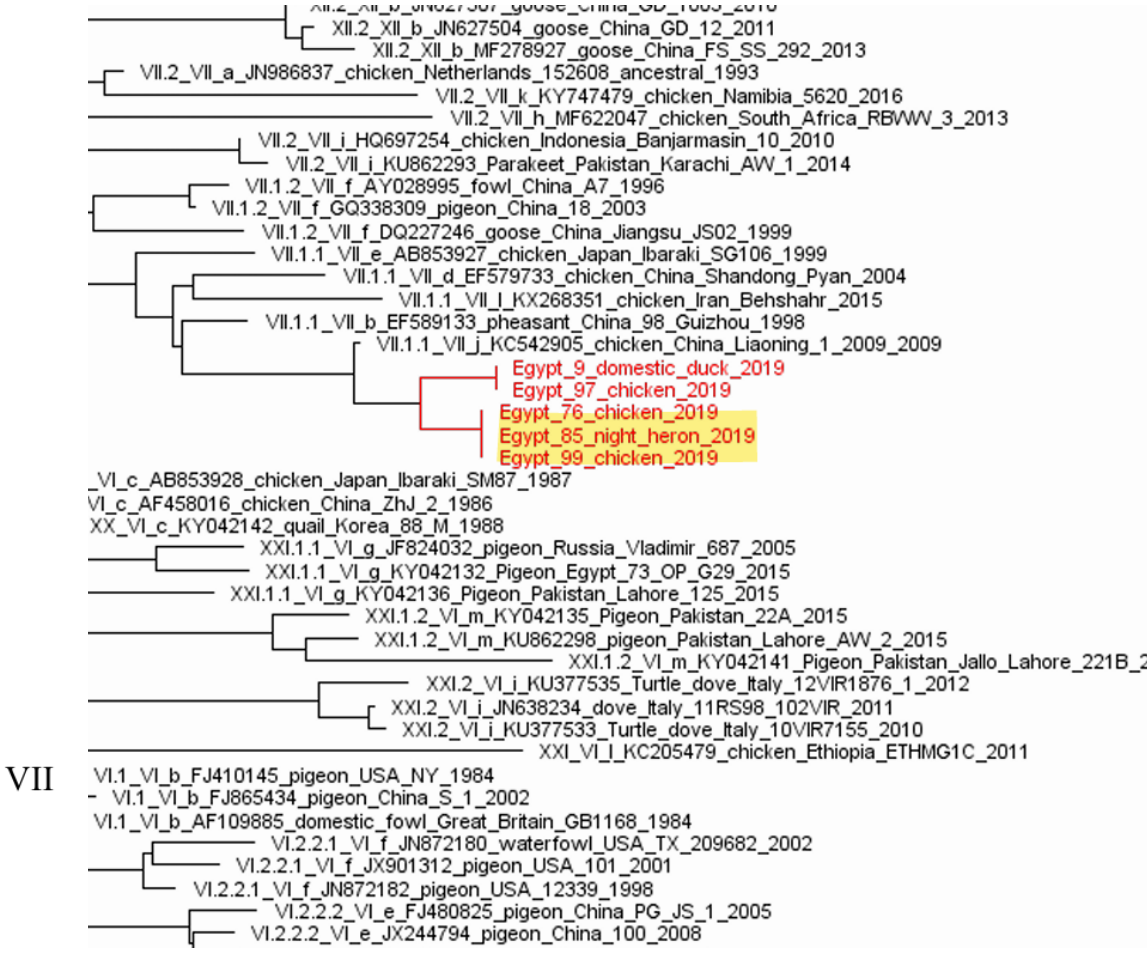
ABSTRACT: Avian paramyxoviruses type 1 or Newcastle disease viruses (NDV) are frequently recovered from wild birds and such isolates are most frequently of low virulence. Velogenic NDV are usually recovered from poultry and only occasionally from wild birds. Five NDV isolates were obtained from carcasses of four wild bird species during 2007 in Serbia: Mallard (*Anas platyrhynchos*), Eurasian Sparrowhawk (*Accipiter nisus*), feral Rock Pigeon (*Columba livia*), and Eurasian Collared Dove (*Streptopelia decaocto*). All the isolates have a typical fusion protein cleavage site motif of velogenic viruses (^{112}R-R-Q-K-R-F^{117}). The highest homology (99%) for the nucleotide sequences spanning the M and F gene of the studied isolates was with the genotype VII NDV isolate Muscovy duck/China(Fujian)/FP1/02. Phylogenetic analysis based on a partial F gene sequence showed that the isolates from wild birds cluster together with concurrent isolates from poultry in Serbia within the subgenotype VIId, which is the predominant pathogen involved currently in Newcastle disease outbreaks in poultry worldwide. It is unlikely that the wild birds

Source of introductions for virulent APMV-1 viruses





Spill-over to wild birds or new reservoir?

Take home messages

- The incremented number of outbreaks related to multiple introduction events might be a signal of increased epidemiological pressure (most of outbreaks appears to be at the EU borders) particularly from viruses belonging to genotype VII viruses;
- Exception represented by northern European areas (Norway and Sweden) where genotype XIII.1.1 is detected with a relative frequency;
- Control of ND still appears to be a challenge, as outbreaks can take years to resolve;
- An adequate vaccination plan against NDV is necessary to protect domestic birds from highly virulent ND viruses currently circulating in Europe;
- Role of wild birds remains unknown but evidences might suggest the need to do further investigations;
- Genetic characterisation of NDV is essential to track NDV spread in Europe, identify associated risk factors and select the best vaccination strategy.

Acknowledgements

European National Reference Laboratories for AI

Mieke Steensels and Steven Van Borm (Belgium); Emiliya Ivanova and Alexandra Rangelova (Bulgaria); Vasiliki Christodoulou (Cyprus); Alexander Nagy (Czechia); Charlotte Kristiane Hjulsager, Yuan Liang (Denmark); Armend Cana (Kosovo); Igor Dzadzovski, Aleksandar Dodovski (North Macedonia); Susan Chircop and Audrey Pullicino (Malta); Britt Gjerset (Norway); Anna Pikula, Katarzyna Domańska-Blicharz, Krzysztof Śmietanka and Edyta Swieton (Poland); Iuliana Onita and Adriana Neicut (Romania); Brigita Slavec and Uros Krapež (Slovenia); Montserrat Agüero García, María Teresa Barrios Zambrano and Azucena Sánchez (Spain); Siamak Zohari (Sweden);

European Union Reference Laboratory (EURL) for Avian Influenza and Newcastle Disease

IZSVe, EURL

Alice Fusaro, Ilaria Zambon, Lara Cavicchio, Bianca Zecchin, Marta Dianati, Edoardo Giussani, Silvia Ormelli, Angela Salomoni, Annalisa Salviato, Alessandro Sartori, Alessia Schivo, Enrico Savegnago, Maria Varotto, Gianpiero Zamperin, Bianca Zecchin, Alessandra Drago, Sofia Leardini, Beatrice Barbuto, Calogero Terregino

The authors, originating and submitting laboratories of the sequences from GISAID's EpiFlu™ Database