

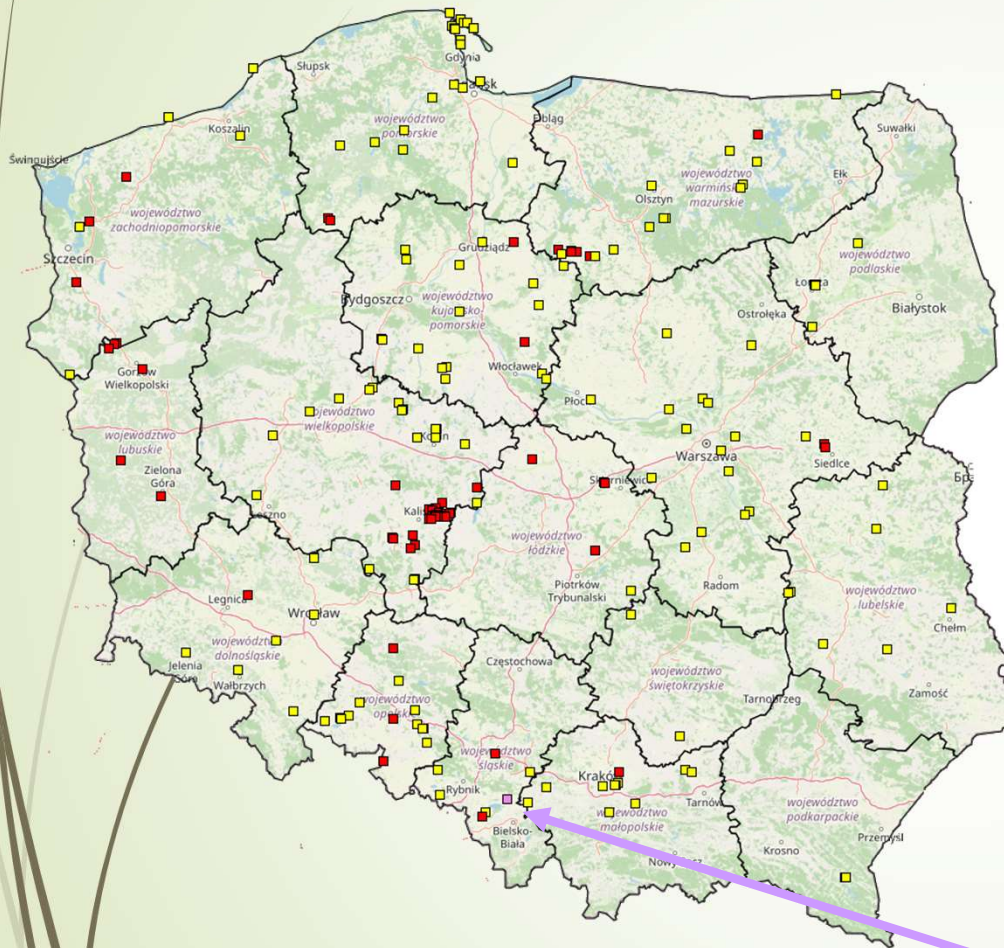
# Avian influenza

## *Epidemiological situation in Poland*



General Veterinary Inspectorate  
21 February 2024

# Epidemiological situation in 2023 (poultry & wild birds)



Poultry farms <span style="color: red;">■</span>	Number of outbreaks	Number of birds in outbreaks
<b>In total</b>	<b>68</b>	<b>1 289 465</b>

Wild birds <span style="color: yellow;">■</span>	Number of outbreaks in wild birds in 2023
<b>In total</b>	<b>141</b>

Captive birds <span style="color: purple;">■</span>	Number of outbreaks in in 2023
<b>In total</b>	<b>1</b>



# Epidemiological situation since 01.01.2024

## **1/01 – 22/01 (until last PAFF):**

- 4 outbreaks in poultry (102 210 birds in outbreaks)
- 4 outbreaks in wild birds

## **23/01 – 19/02 (since last PAFF):**

- 12 outbreaks in poultry (273 381 birds in outbreaks)
- 2 outbreaks in captive birds (103 birds in outbreaks)
- 4 outbreaks in wild birds

## **TOTAL 1/01 – 19/02 2024:**

- **Poultry: 16 outbreaks**
- **Captive birds: 2 outbreaks**
- **Wild birds: 8 outbreaks**



# Epidemiological situation 01.01.2024



captive

# WGS/HTS data for selected outbreaks

## 6/2024:

- genotype DI (1st time confirmed in December 2023 in Moldova and Poland);
- Close related to viruses confirmed in mute swan in **podkarpackie region** and other wild birds in Moldova and Czech Republic.

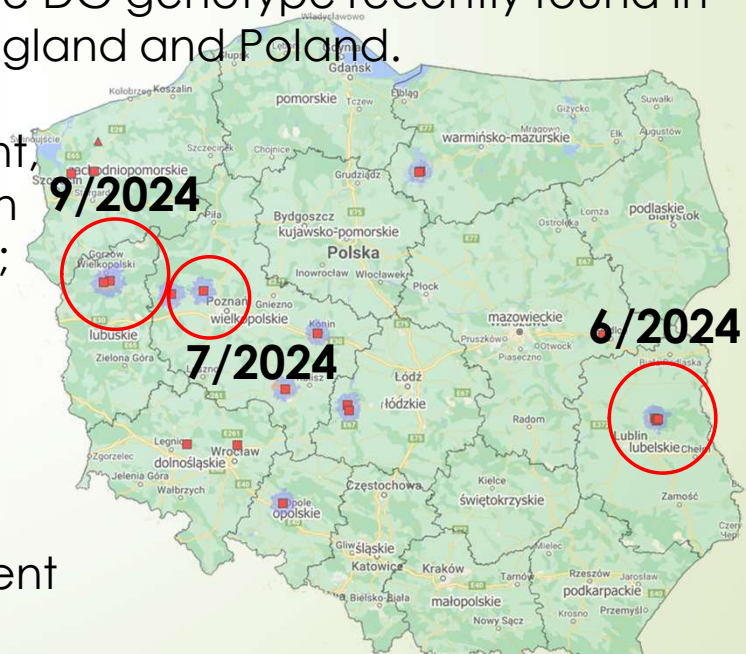
## 7/2024:

- virus from the outbreak 7/2024 belongs to the DG genotype, which was first detected in November 2023 in Belgium;
- virus groups with other strains belonging to the DG genotype recently found in wild birds and poultry in Belgium, Sweden, England and Poland.

## 9/2024:

- New genotype, not confirmed at this moment, which was created by reassortment between H5N1 virus and low pathogenicity virus (LPAI); Genes PB2, PB1, HA, NA, M and NS are closely related to H5N1 viruses belonging to the AB genotype, originating mainly from wild birds in Sweden. On the other hand, PA and NP genes group with LPAI viruses detected in wild birds in recent years in Europe.

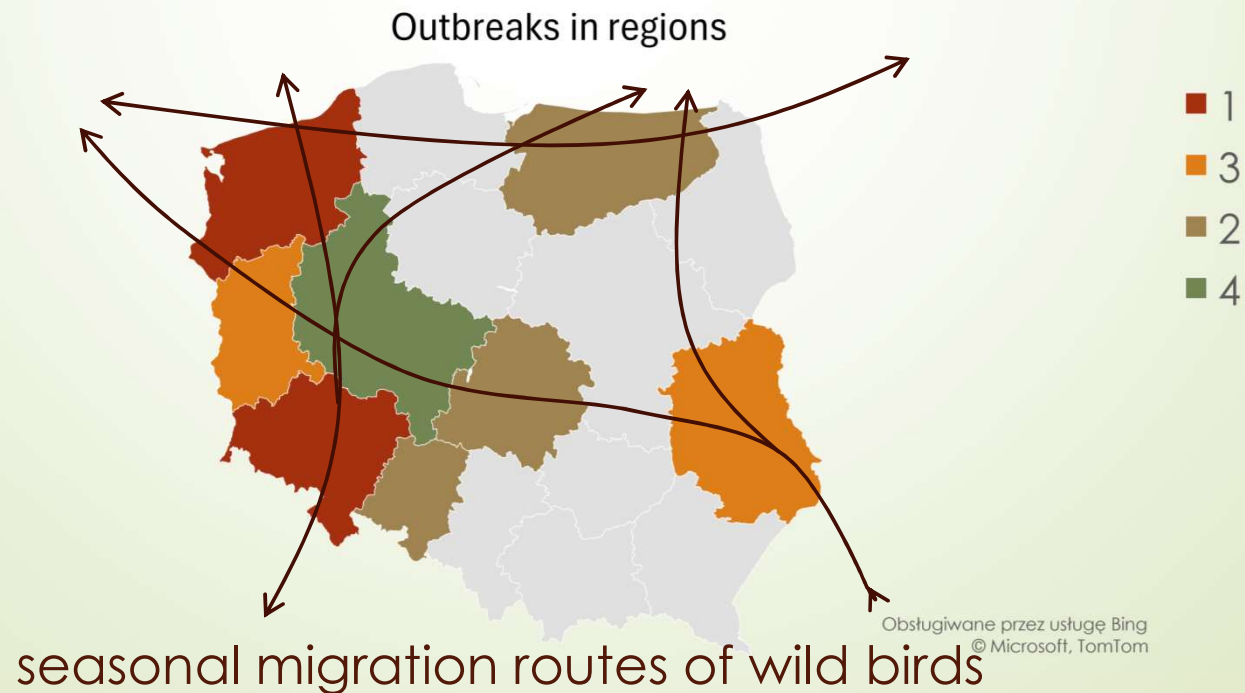
**Virus sequence H5N1 from outbreak 9 was sent to EURL in Padua, where it will be resequenced given an appropriate designation.**





# Outbreaks analysis data 2024

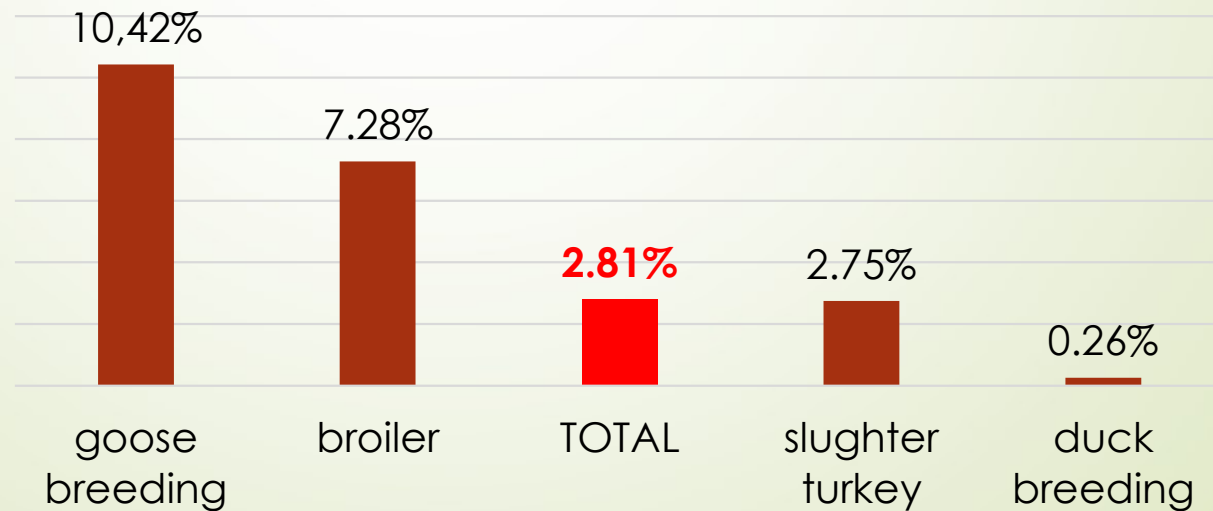
Voivoidship	Outbreaks	Birds in Ob.	Death birds	Mortality	% Obs. In Poland
dolnośląskie	1	38 805	91	0,23%	6,25%
lubelskie	3	61 269	1 166	1,90%	18,75%
lubuskie	3	50 031	2 675	5,36%	12,50%
opolskie	2	43 419	295	0,68%	6,25%
warmińsko-mazurskie	2	51 400	2 997	5,83%	12,50%
wielkopolskie	4	35 770	2 798	7,82%	25,00%
zachodniopomorskie	1	34 950	180	0,52%	6,25%
łódzkie	2	61 644	415	0,67%	12,50%
<b>Suma</b>	<b>16+2=18</b>	<b>377 185 + 103</b>	<b>10 617</b>	<b>2,81%</b>	<b>100,00%</b>



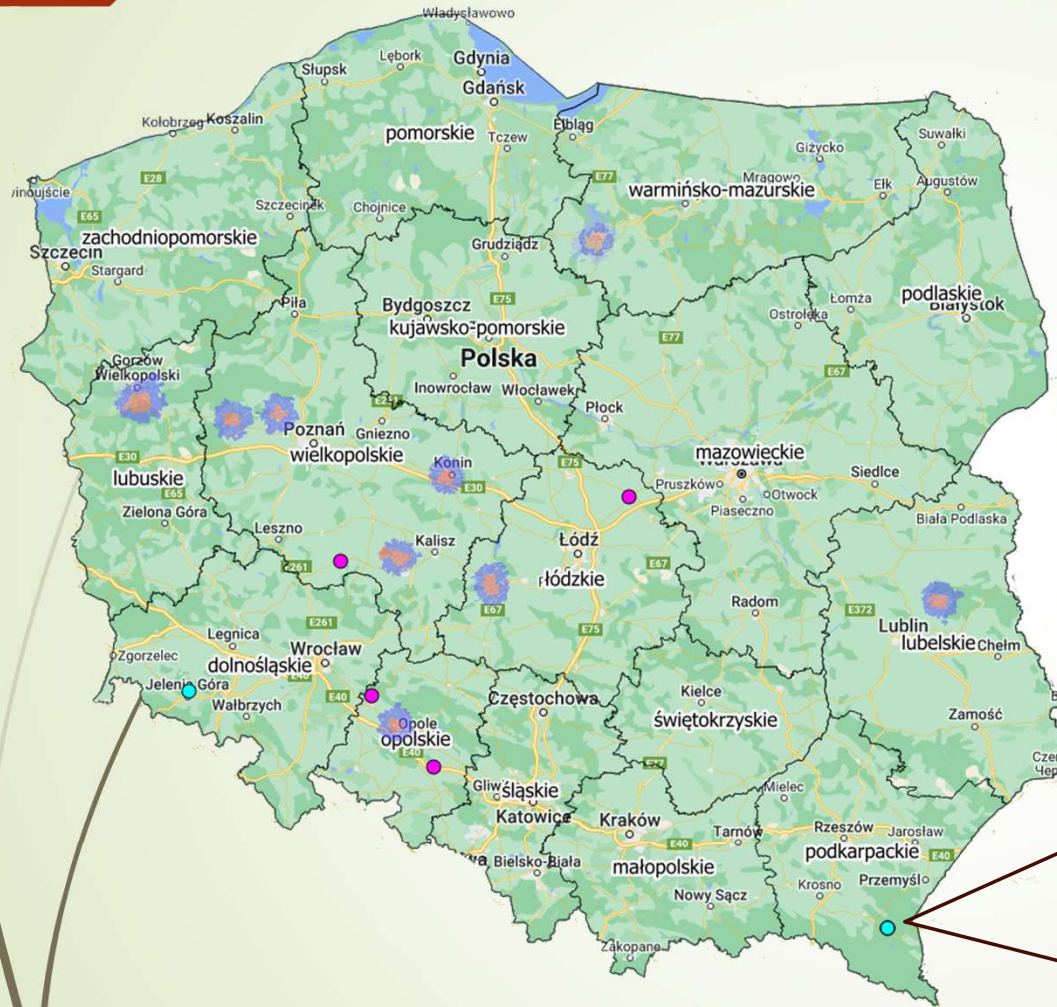
# Outbreaks analysis data 2024

Species	Outbreaks (poultry & captive)	Mortality
goose breeding	1	10.42%
slughter turkey	9	2.75%
breeding duck	3	0.26%
duck slaughter	2	0.5%
broiler	2	7.28%

## Mortality



# Outbreaks in wild birds in 2024



- Outbreak(H5N1)in wild birds: 8
  - 1 Greyllag goose *Anser anser*
  - 14 Mute swan *Cygnus olor*

➤ last confirmed outbreak  
8.02.2024



3 outbreaks in 2024

(next slide)



# Outbreaks in wild birds in 2024

## WGS/HTS data

Outbreaks in wild birds (H5N1)

Mute swan *Cygnus olor* in Podkarpackie Voivoidship, leski district, Solina community, Hydroelectric Power Plant Complex Solina-Myczkowce in Myczkowce at the top of the dam

Phylogenetic analysis of all genome segments showed that **the viruses** detected belong to a new genotype, **not yet detected in Europe**. EU Laboratory The Avian Influenza Reference Authority has assigned this **genotype a DI** designation. PA, HA, NP genes NA, M and NS of the analyzed viruses show close relatedness to HPAI H5N1 viruses DA genotype detected in the current season in wild birds and poultry **in Europe**, and PB2 and PB1 genes most likely come from low pathogenicity viruses (LPAIV) occurring in wild birds. **The results indicate that the DI genotype arose from reassortment between the HPAI virus H5N1 and LPAI virus of unknown subtype.**

**Detecting so much genetic diversity** in the viral population on this area in just one year indicates numerous introductions **of HPAI viruses**, most likely coming from different geographical directions, and **makes this area particularly important** from an epidemiological point of view, not only on a national scale, but **also Europe (mainly due to the detection of genotypes earlier in our unidentified continent).**





Thank you

