

Ministry of Agriculture

Epidemiological situation and the measures regarding highly pathogenic avian influenza in Hungary



Meeting of the Standing Committee of Plants, Animals Food and Feed
26-27.02.2025.



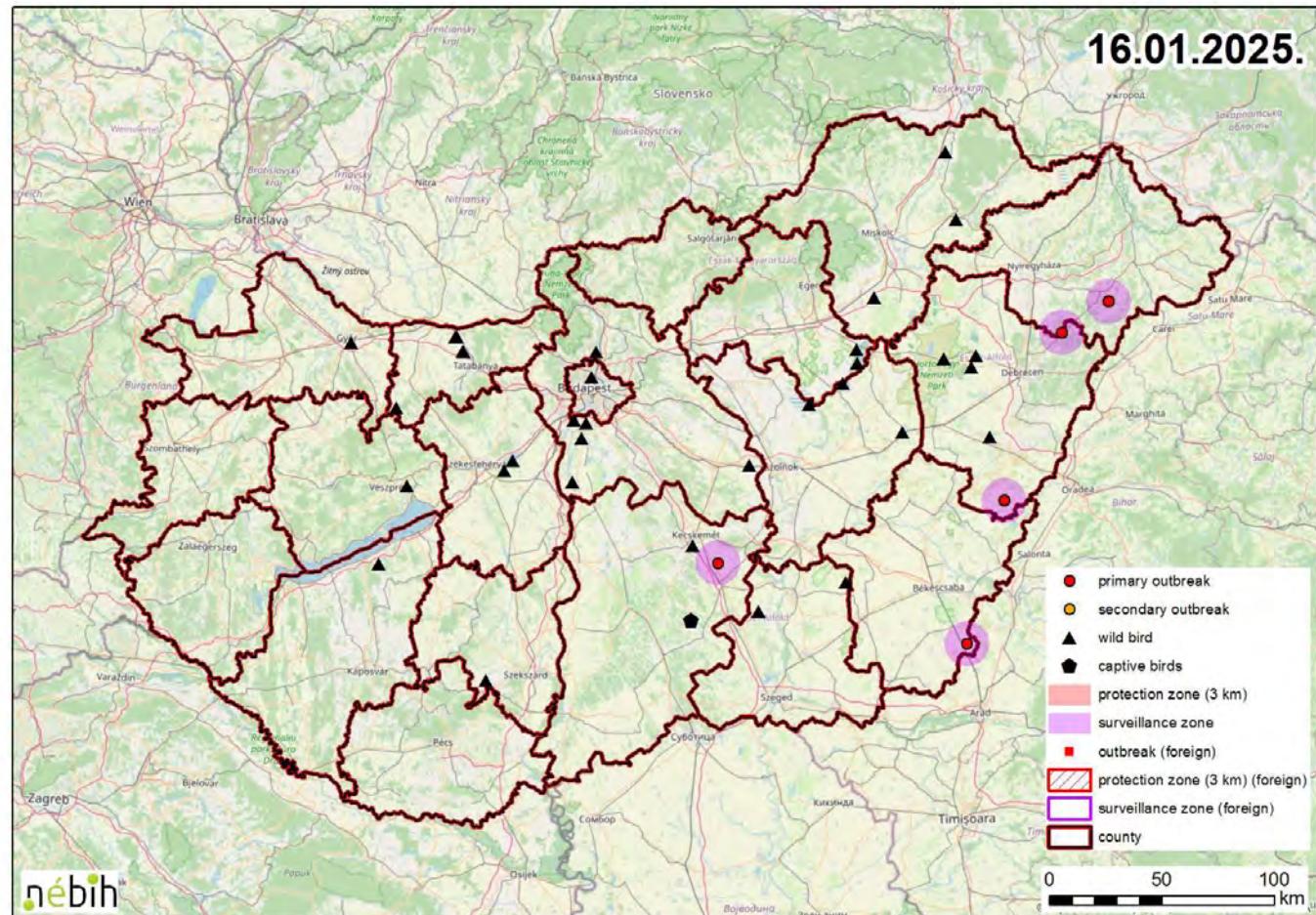
Timeline

20 January

Number of outbreaks: 191 –
37 primary – 154 secondary

Affected animals: 3 438 599
(including preventive
killings)

1 captive wild bird
outbreak: 30 birds





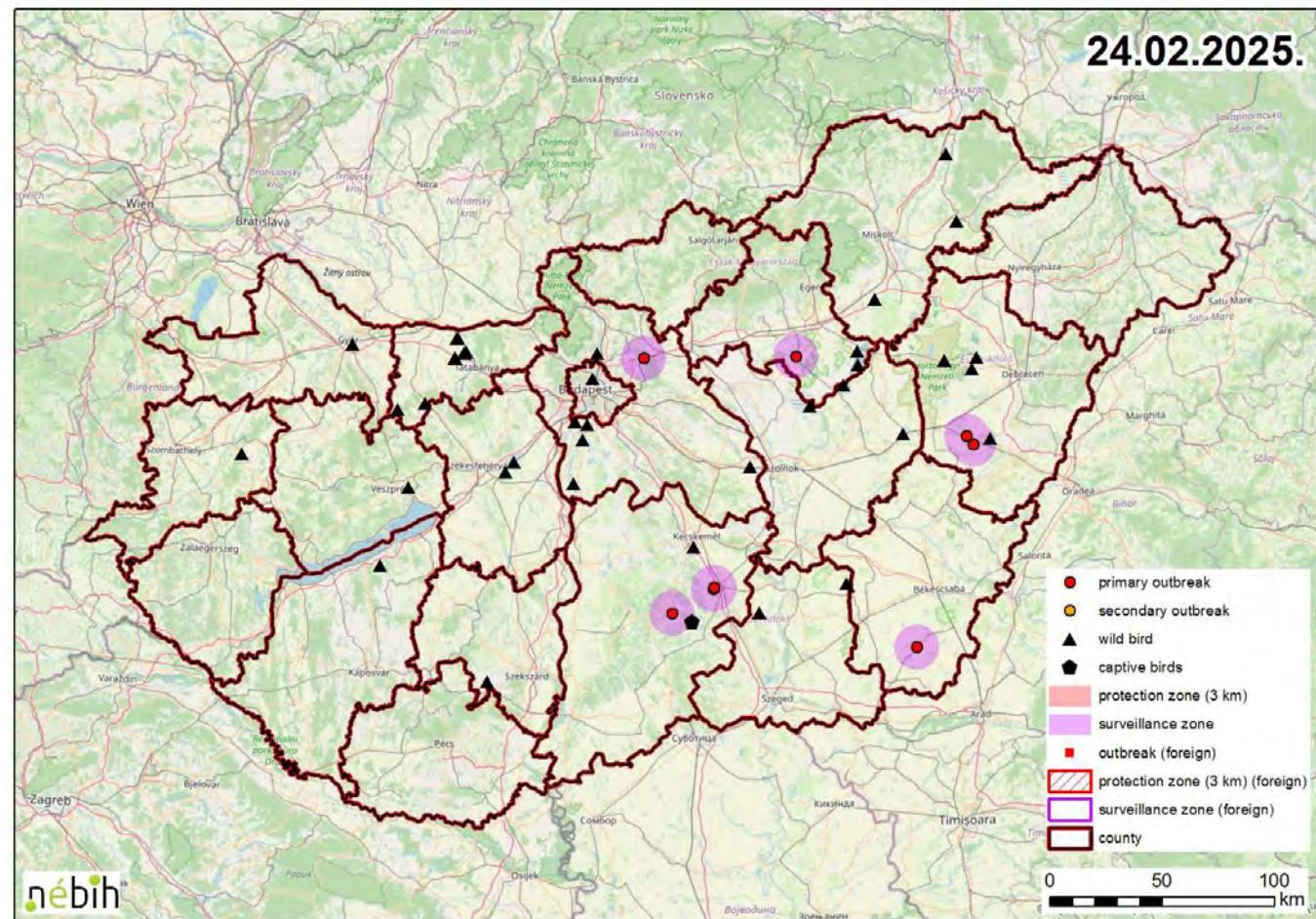
Timeline

25 February

Number of outbreaks: 201 –
44 primary – 157 secondary

Affected animals: 3 580 255
(including preventive
killings)

2 captive wild birds
outbreak: 135 birds





New outbreaks

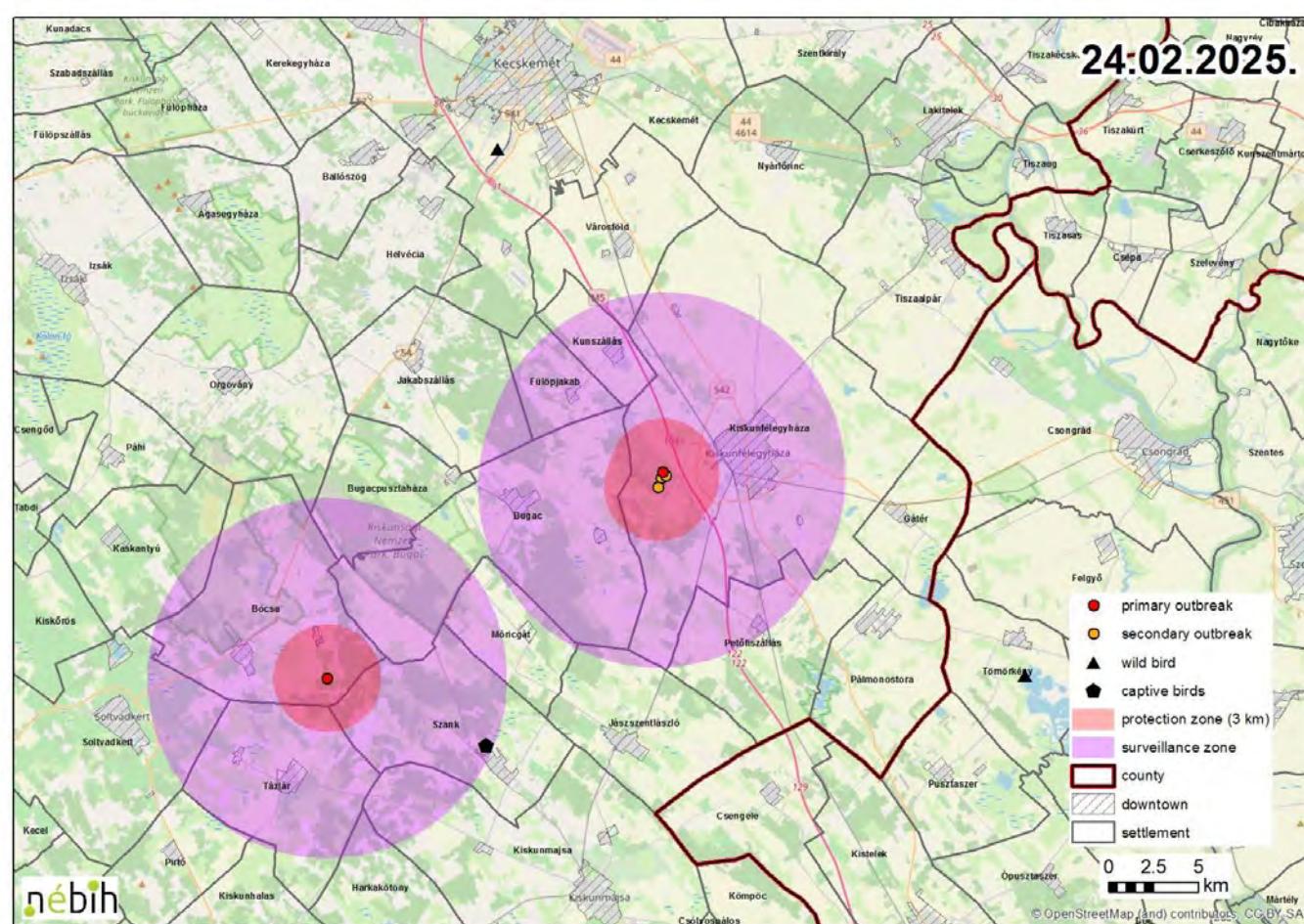
County	Outbreaks	No. of animals
Bács-Kiskun	5	15878
Békés	1	13300
Hajdú-Bihar	2	98931
Heves	1	2744
Pest	1	1845
Total	10	132698

Species	Type	Outbreaks	No. Of animals
duck	breeding	1	13300
goose	breeding	1	1845
	foie gras	5	5052
moulard	foie gras	1	13570
turkey	breeding	1	17853
<i>Gallus gallus</i>	laying	1	81078
Total		10	132698



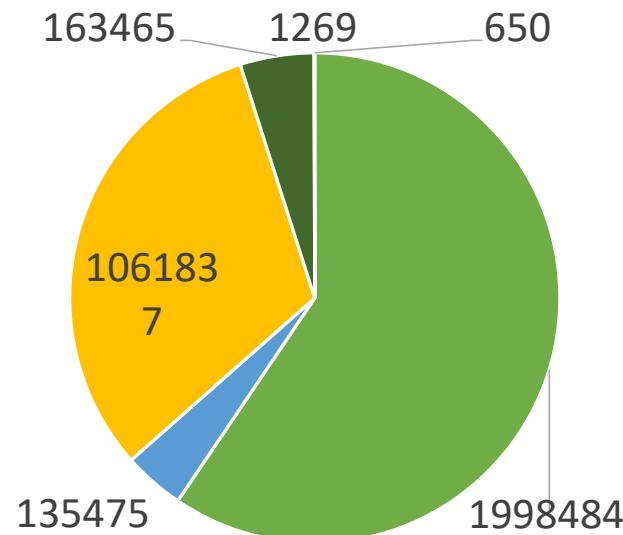
New outbreaks

ADNS	Species, type	No. of animals
13	foie gras moulard	13570
11	foie gras geese	810
10	foie gras geese	499
9	foie gras geese	499
8	foie gras geese	500



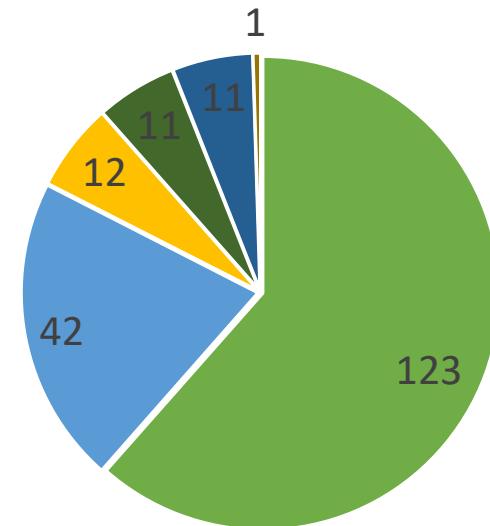


Affected poultry



**Number of birds
in outbreaks**

- Duck
- Goose
- Gallus gallus
- Turkey
- Backyard
- Pheasant



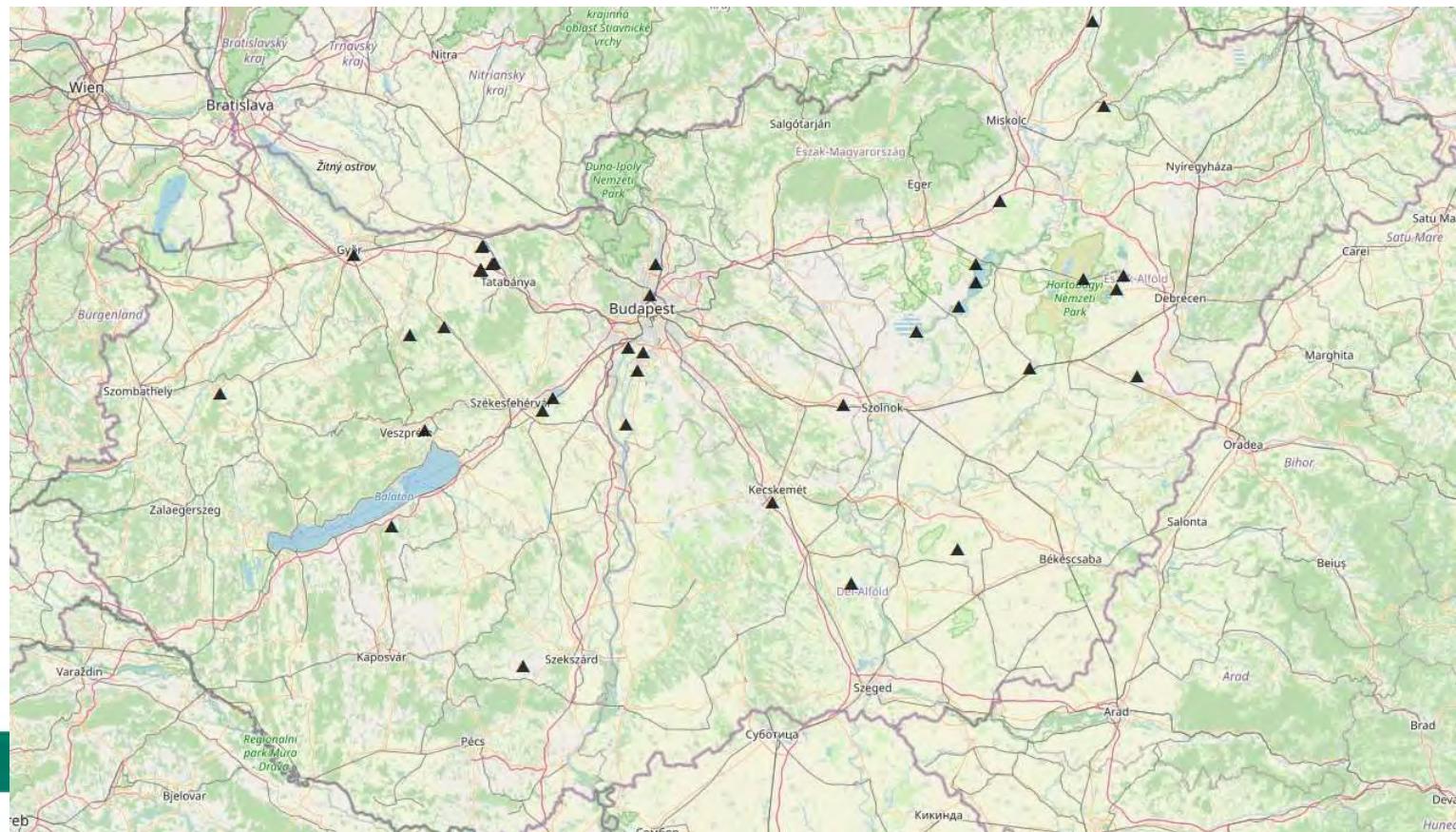
**Number of
outbreaks**



83 wild birds (45 outbreaks)

- Greylag goose
(*Anser anser*) - 13
- Mute swan
(*Cygnus olor*) - 17
- Black-headed gull
(*Chroicocephalus ridibundus*) - 4
- Eurasian blackcap
(*Sylvia atricapilla*) - 1
- Mallard
(*Anas platyrhynchos*) - 1
- Eurasian collared dove
(*Streptopelia decaocto*) - 1
- Peregrin falcon
(*Falco peregrinus*) - 1
- Common buzzard
(*Buteo buteo*) - 41
- Yellow-legged gull
(*Larus michahelis*) - 1

Wild birds



Measures

- Stamping out
- Epidemiological investigation
- Phylogenetic examination
- Wild birds
- Awareness-raising and information-spreading
- Sampling when transport
- Stocking and restocking





Phylogenetic analysis – by the EURL

The 7 HPAI H5N1 viruses belong to the clade 2.3.4.4b., to the **EA-2024-DI** genotype (1, 2), the most frequent and widespread genotype in Europe. All the 7 viruses from Hungary belong to the DI.2 subgroup.

Topology of the phylogenetic trees indicate the occurrence of multiple virus introductions into the country. All the viruses cluster separately, except for two viruses collected in January 2025 (A/goose/Hungary/1871_25VIR1318-8/2024 and A/goose/Hungary/2544_25VIR1318-9/2025), which are identical to each other, suggesting a possible spillover event.



Laboratory examinations (from 01.09.2024)

County	Carcass	Swab	Total
Bács-Kiskun	1970	83607	85577
Baranya	135	786	921
Békés	388	26320	26708
Borsod-Abaúj-Zemplén	105	460	565
Csongrád-Csanád	197	19183	19380
Fejér	39	1147	1186
Győr-Moson-Sopron	40	2152	2192
Hajdú-Bihar	557	12796	13353
Heves	24	973	997
Jász-Nagykun-Szolnok	171	4432	4603
Komárom-Esztergom	139	3744	3883
Nógrád	13	186	199
Pest	85	2064	2149
Somogy	61	357	418
Szabolcs-Szatmár-Bereg	272	4631	4903
Tolna	23	293	316
Vas	17	60	77
Veszprém	54	973	1027
Zala	12	232	244
Total	4302	164396	168698

Thank you for your attention!



Photo: Zoltán Máthé, MTI