



# UPDATE ON NEWCASTLE DISEASE IN RUSSIA

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# Background on the current ND situation in Russia

Viruses are regularly detected during monitoring:

- APMV-1 viruses of genotype I class II and class I mainly among wild birds;
- virulent viruses of genotype VI and its derivatives (XXI/Vlg) in pigeons;
- vaccine strains of genotypes II (LaSota, B1, Clone 30) and I (V4, Bor 74) are mainly from chickens.

Virulent viruses from chickens (most often genotype VII and its derivatives) are sporadically isolated, usually having similar isolates in the neighboring countries/regions.

A set of methods for laboratory diagnostics is required!!!



# APMV-1 detected in the monitoring process

Isolate name, 2017	Collection date	Phylogenetic group
Pigeon/Kostroma/3606	19.09.17	VIg
Chicken/Primorje/1688	18.07.17	II .B1
Chicken/Primorje/1689	18.07.17	II B1
Chicken/Kostroma/2890	19.09.17	Ic Bor-74
Chicken/Kostroma/2908	19.09.17	Ic Bor-74
Mallard/Amurskaya/3077 (a total of 9 viruses in population)	23.11.17	Ib
Gadwall/Amurskaya/3158	23.11.17	Ib

Isolate name, 2018	Collectio n date	Phylogenetic group
pigeon/Vladimir/1141	14.06.18	VIg
pigeon/Vladimir/1142	14.06.18	VIg
chicken/Vladimir/3963	07.02.18	Ic Bor-74
turkey/Penza/3964	07.02.18	Ia V4
chicken/Krasnoyarsk/11 20	23.05.18	II LaSota
wildduck/Vladimir/1849	12.07.18	Ib
wildduck/Vladimir/1848	12.07.18	Ib

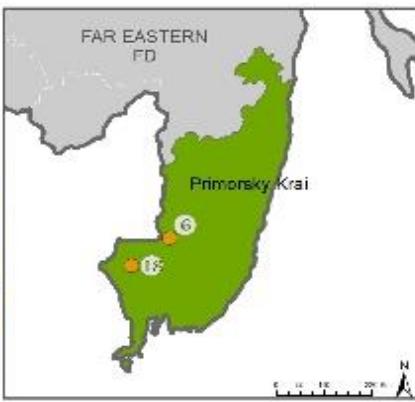
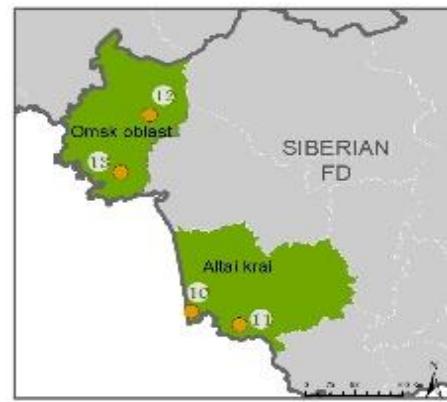
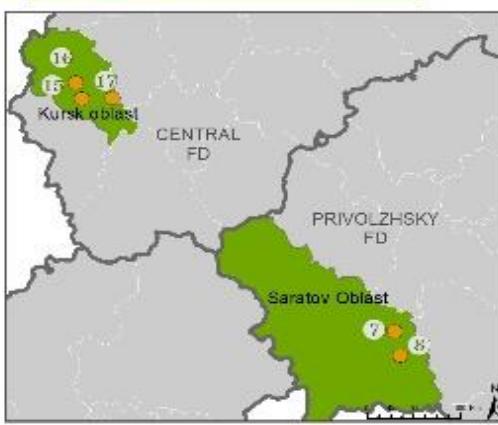
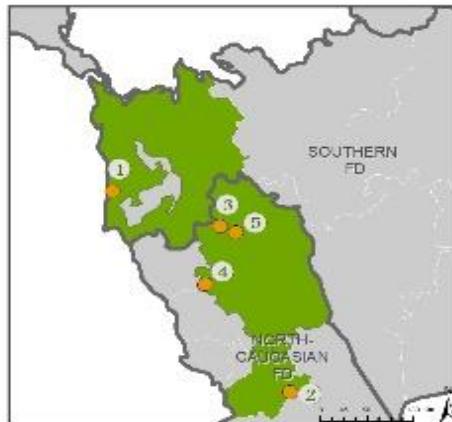
live vaccines are used in poultry industry, and PCR screening may not be sufficient



- The most important event in 2019-2020 in the field of control of Newcastle disease and the study of its causative agent was a large-scale outbreak of the disease caused by subtype VII-L virus.
- The virus was detected in eight regions of six federal districts of the Russian Federation: the North Caucasus (Chechnya, Stavropol Krai), Southern (Krasnodar Krai), Central (Kursk and Vladimir Oblasts), Volga (Saratov Oblast), Siberian (Zabaykalsky Krai, Omsk Oblast), and Far Eastern (Primorsky Krai).
- In some regions, outbreaks were reported repeatedly, in various regions: Kursk, Saratov, Omsk and Vladimir Oblasts, Zabaykalsky and Primorsky Krais.
- The outbreak began in February 2019 and appears to be continuing up to now. The group of isolates from Iran named subtype VII-L is the closest to the Russian isolates in 2019 (97-98% for the F gene) (Mayahi, Esmaelizad, 2017; Esmaelizad et al., 2017; Molouki et al., 2019).



## Newcastle disease-affected regions of the Russian Federation 2019

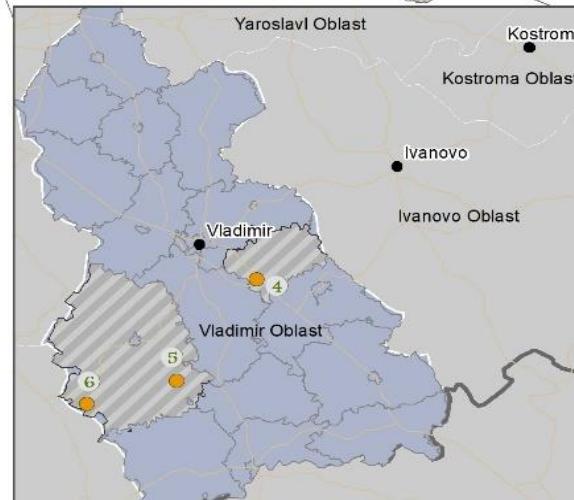
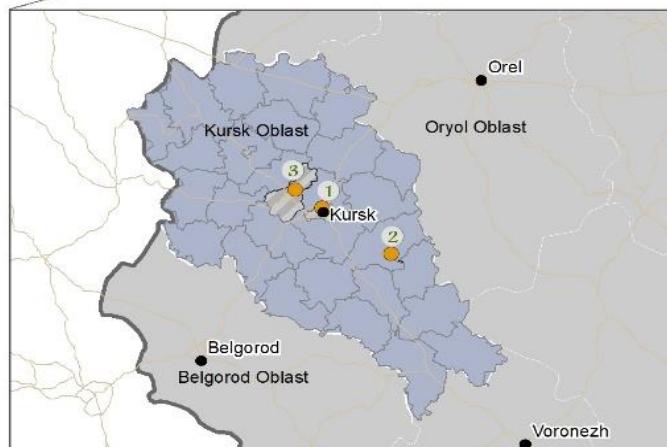


## Isolates from ND outbreak of 2019

Isolate name	Region	Host	Date	Virus subtype
Ck/Krasnodar/9/19	Krasnodar	Chicken	01.02.19	VII-L
Ck/Krasnodar/10/19	Krasnodar	Chicken	01.02.19	VII-L
Ck/Chechnya/431/19	Chechen Republic	Chicken	12.04.19	VII-L
Ck/Stavropol/509/19	Stavropol	Chicken	23.04.19	VII-L
Ck/Stavropol/888/19	Stavropol	Chicken	26.04.19	VII-L
Ck/ Stavropol/1190/19	Stavropol	Geese	15.05.19	VII-L
Ck/Primorsky/1284/19	Pimorsky Krai	Chicken	22.05.19	VII-L
Ck/Saratov/4521-1/19	Saratov	Chicken	20.06.19	VII-L
Ck/Saratov/3122/19	Saratov	Chicken	27.08.19	VII-L
Ck/Zabaikalsky/3915/19	Zabaykalsky Krai	Chicken	3-4.10.19	VII-L
Ck/Omsk/3941-4/19	Omsk	Chicken	10.10.19	VII-L
Ck/Zabaikalsky/4635/19	Zabaykalsky Krai	Chicken	21.10.19	VII-L
Ck/Omsk/2677/19	Omsk	Chicken	8.11.19	VII-L
Ck/Kursk/2819/19	Kursk	Domestic birds	18.11.19	VII-L
Ck/Kursk/2949_1/19	Kursk	Chicken	03.12.19	VII-L
Ck/Primorsky/3087_1/19	Primorsky Krai	Chicken	19.12.19	VII-L



# Newcastle disease-affected regions of the Russian Federation 2020



## Условные обозначения

■ Infected raions where outbreaks notified to the OIE in 2020 are located

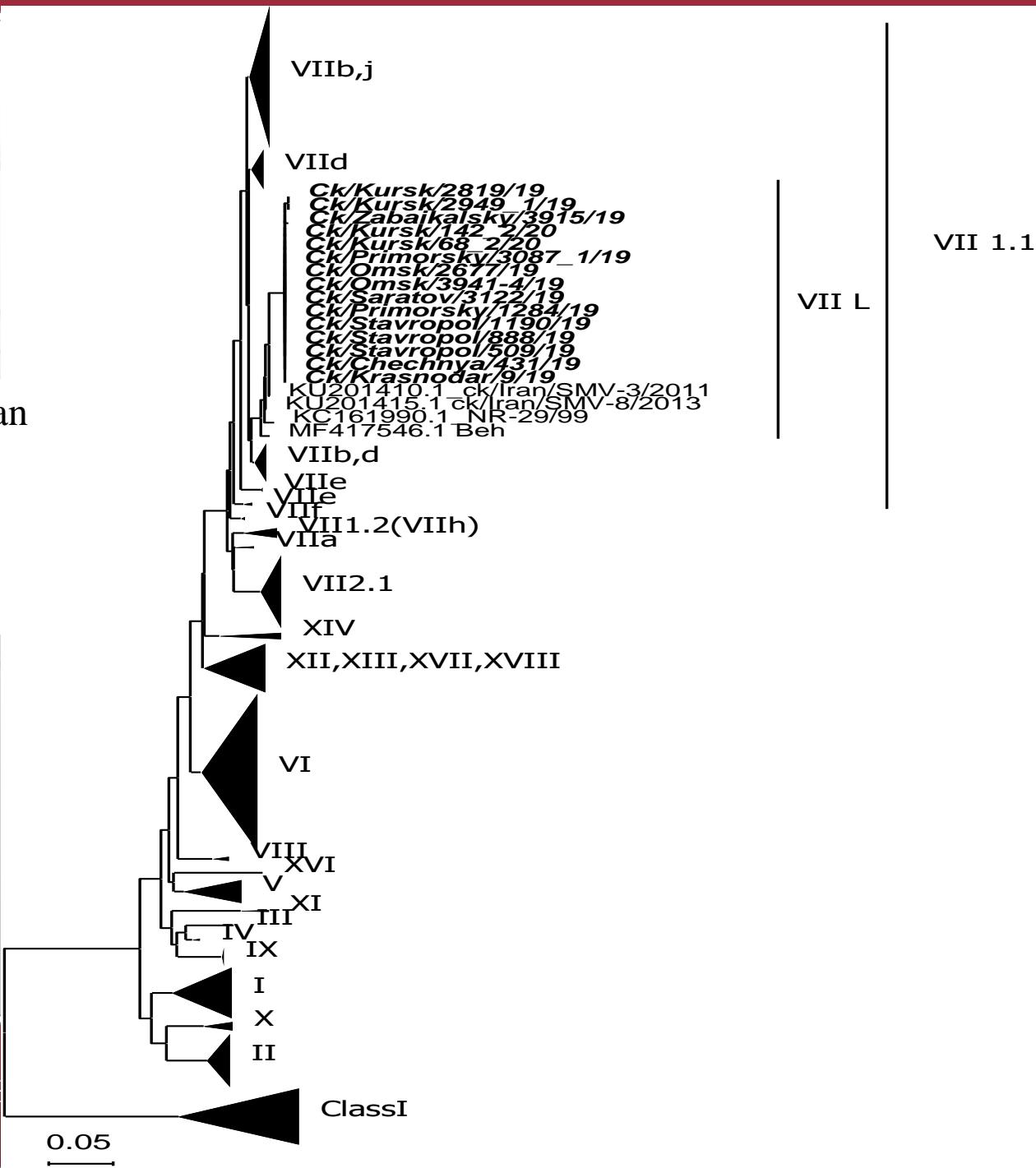
— Main road

● Main city

0 315 630 1 260 Km



Phylogenetic position of Russian isolates VIII  
(gene F fragment 20-420, NJ  
method in  
MEGA 6.06)



- Nucleotide sequences of the F gene for 9 isolates and complete genome sequences for 7 of them were determined.
- When comparing the sequences of Russian isolates and earlier isolates from Iran, the possibility of repeated introduction (isolate from Chechnya and all the others) of the virus is shown.
- In total, Russian isolates have 48 substitutions in the F gene, including 10 significant and 5 non-conservative ones.
- Comparison of complete genomes showed that the most variable, as in other cases, is the P (phosphoprotein) gene. The variability of other genes is approximately at the same level.
- The ck/Chechnya/431/19 isolate is the most remote from the rest of the Russian isolates.



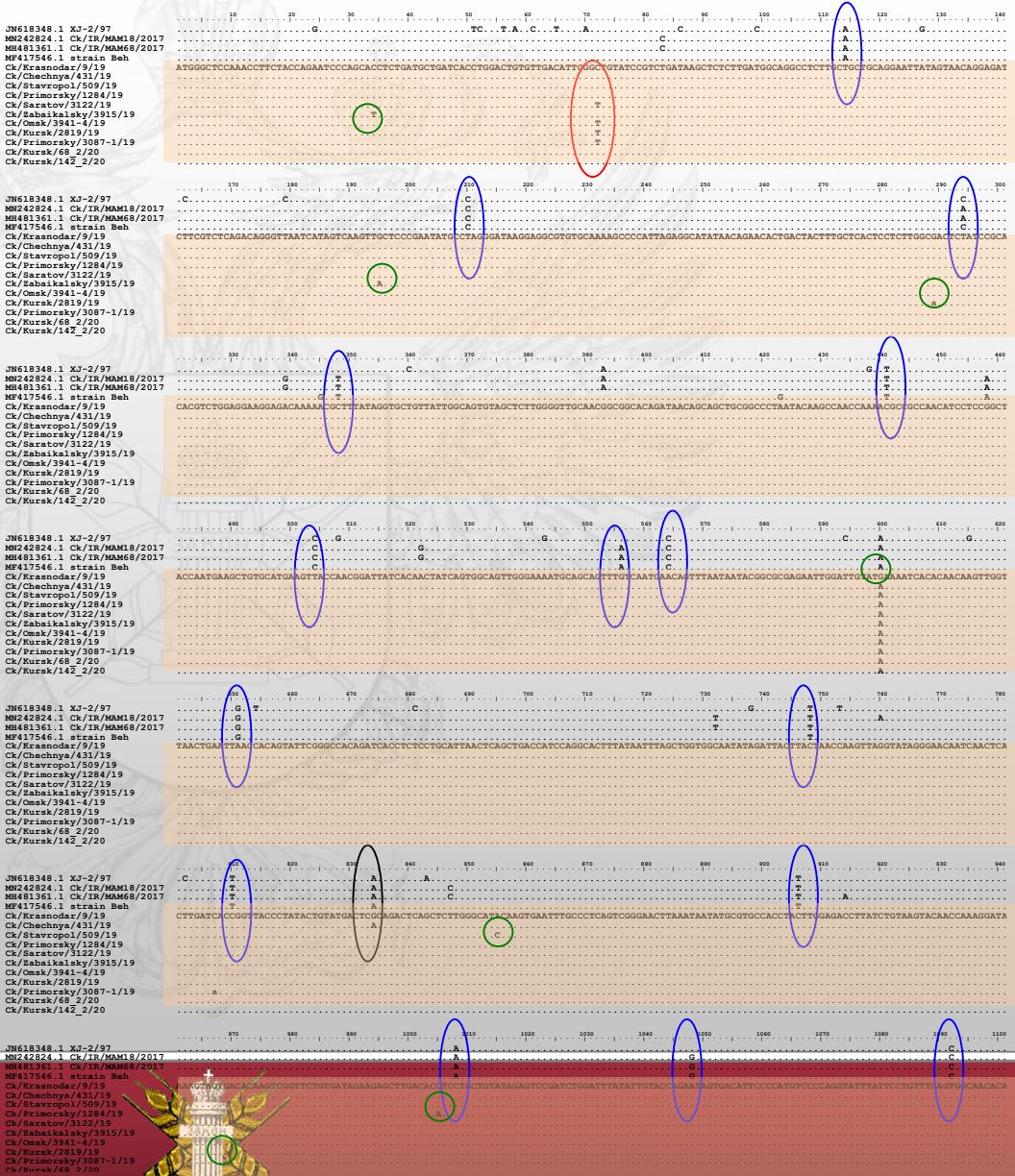
# Alignment of nine gene F nucleotide sequences of Russian isolates and four sequences of subgenotypes VIIl and VIId

○ Substitutions specific for all Russian isolates (28 in F gene)

○ Substitutions specific for all Russian isolates except Ck/Chechnya/431/19 (1 in F and 2 in HN)

○ Substitutions specific for group of Russian isolates (only one)

○ Substitutions specific for individual Russian isolates (1-2 for isolate, 15 total)



# Genetic Variability of Russian NDV isolates of VII genotype

Genome fragment	Genetic distance (%)	
	Beh (MF417546) vs. Russian isolates	Russian isolates vs. each other
NP	1.79 – 2.02	0.00 – 0.56
P	3.52 – 4.32	0.01 – 1.25
M	1.63 – 1.87	0.08 – 0.57
F	1.92 – 2.15	0.06 – 0.28
HN	1.74 – 1.94	0.00 – 0.49
L	1.62 – 1.74	0.02 – 0.45
Complete genome	1.93 – 2.01	0.05 – 0.46



- On a broader time scale, the emergence and evolution of viruses of the VIII<sub>L</sub> subgenotype appears to be a continuation of the epidemic process associated with the VII<sub>d</sub> subgenotype, a derivative of which is probably the VIII<sub>L</sub> subgenotype.
- The spread of the virus over 5-6 thousand km in a short time seems to indicate the involvement of an anthropogenic factor.
- It is possible that there are unidentified endemic zones, primarily in wild bird populations, and this requires further study.



<b>Species and groups of birds studied in 2019</b>	<b>APMV-1</b>	<b>Samples</b>
Anseriformes		1098
1. Wild duck (species not known)	-	515
2. Mallard	1	259
3. Wild geese (species not known)	1	173
4. Teal	-	93
5. Wild duck (11 species)	-	58
Wild birds and waterfowl (species not known)	3	324
Synanthropic birds		325
1. Pigeon	-	177
2. Family Corvidae (crow, rook, jackdaw, raven, magpie, sparrow)	-	95
3. Unspecified birds	1	28
4. Sparrow	-	25
Charadriiformes		211
1. Woodcock	-	102
2. Gull	1	62
3. Others (grebe, coot and 9 others)	-	47
Forest birds (capercaillie, black grouse, thrush, jay and 5 other species)	-	57
Total:	7	2015





Федеральное государственное бюджетное учреждение  
«Федеральный центр охраны здоровья животных» (ФГБУ «ВНИИЗЖ»)



*Thank you!*

