



Reporting on SARS-CoV-2 as per CID 2021/788

PAFF – Section Animal Health and Welfare

9-10 June 2022

Unit G2 – Animal Health

Reporting on:

- SARS-CoV-2 in minks and other animals of the family *Mustelidae* and in raccoon dogs
- CID 2021/788 adopted on 12 May 2021
- Four follow-up reports by Poland and Spain

Poland – update on previous outbreaks

- **4/2021 (voivodeship zachodniopomorskie)**

- On 17.03.2022 samples were taken for laboratory tests (I testing to exclude the disease on the 90th day of quarantine) with negative results.
- On 05.04.2022 samples were taken for laboratory tests (II testing to exclude the disease on the 104th day of quarantine) with negative results.
- **Outbreak was closed**

- **5/2021 (voivodeship zachodniopomorskie)**

- On 23.03.2022 samples were taken for laboratory tests (I testing to exclude the disease on the 90th day of quarantine) with negative results.
- On 07.04.2022 samples were taken for laboratory tests (II testing to exclude the disease on the 104th day of quarantine) with negative results.
- **Outbreak was closed**

Poland – update on previous outbreaks

- **6/2021 (voivodeship zachodniopomorskie)**

- On 22.03.2022 samples were taken for laboratory tests (I testing to exclude the disease on the 90th day of quarantine) with negative results.
- On 06.04.2022 samples were taken for laboratory tests (II testing to exclude the disease on the 104th day of quarantine) with negative results.
- **Outbreak was closed**

- **8/2021 (voivodeship podkarpackie)**

- On 22.03.2022 samples were taken for laboratory tests (I testing to exclude the disease on the 90th day of quarantine) with negative results.
- On 05.04.2022 samples were taken for laboratory tests (II testing to exclude the disease on the 104th day of quarantine) with negative results.
- **Outbreak was closed**

Poland – update on previous outbreaks

- **10/2021 (voivodeship lubelskie)**

- on 29.04.2022 samples were taken for laboratory tests (I testing to exclude the disease on the quarantine) with negative results.
- on 20.05.2022 samples were taken for laboratory tests (II testing to exclude the disease after 20 days from I testing) with negative results.
- **Outbreak was closed**

- **11/2021 (voivodeship pomorskie)**

- On 07.04.2022 samples were taken for laboratory tests (I testing to exclude the disease on the 90th day of quarantine) with negative results.
- On 21.04.2022 samples were taken for laboratory tests (II testing to exclude the disease on the 104th day of quarantine) with negative results.
- **Outbreak was closed**

Spain – CONCLUSIONS ON SEQUENCING OF SARS-CoV-2 VIRAL GENOME FROM OUTBREAKS IN MINK FARMS

- **Outbreak 2020/1** (Aragón Autonomous Community):
 1. In all sequences, **D614G** mutation was identified in the sequence codifying for the spike protein, mutation that defines the **predominant clade present in Spain and Europe** when the outbreak 1/2020 was detected.
 2. **Y453F mutation** described in cluster 5, as well as the rest of changes that define this cluster, that appeared in some of SARS-CoV-2 positive mink farms in Denmark, **was not present** in any of the analysed sequences.
 3. N501T mutation was present in all sequences. This site is related to an adaptation to the host and to antigenic drift that is under intensive study given that this position is part of the group of mutations identified in the United Kingdom variant (N501Y).
 4. In 22 out of the 38 sequences, two changes that always appear together were identified: F486V and D796H. These changes have not been identified in the GISAID database or in human or mink samples. The biological relevance of these changes is yet to be determined.

Spain – CONCLUSIONS ON SEQUENCING OF SARS-CoV-2 VIRAL GENOME FROM OUTBREAKS IN MINK FARMS

- **Outbreak 2021/1** (Galicia Autonomous Community):
 1. In all sequences, **D614G** mutation was identified in the sequence codifying the spike protein, mutation that defines the **predominant clade present in Spain and Europe** when the outbreak 1/2021 was detected.
 2. **Y453F** mutation described in cluster 5, as well as the rest of changes that define this cluster, that appeared in some of SARS-CoV-2 positive mink farms in Denmark, **was not present** in any of the analysed sequences.
 3. N501T mutation was present in 1 out of the 4 sequences related to the spike gene analysed. This site is related to an adaptation to the host and to antigenic drift that is under intensive study given that this position is part of the group of mutations identified in UK viral variant VOC 202012/01 (N501Y).

Spain – CONCLUSIONS ON SEQUENCING OF SARS-CoV-2 VIRAL GENOME FROM OUTBREAKS IN MINK FARMS

- **Outbreak 2021/2** (Castilla y León Autonomous Community):
 1. In all sequences, **D614G** mutation was identified in the sequence codifying the spike protein, mutation that defines the predominant clade present in Spain and Europe when the outbreak 2/2021 was detected.
 2. **A222V** mutation was identified in the spike protein that defines the B.1.177 lineage and that **was circulating widely in Spain, Europe** and the rest of the world, being **characteristic of the human cases**.
 3. **Y453F** mutation described in cluster 5, as well as the rest of changes that define this cluster, that appeared in some of SARS-CoV-2 positive mink farms in Denmark, **was not present** in any of the analysed sequences.
 4. Mutations that define the variants of interest were not detected (VOC 202012/01,501Y.V2 or B.1.1.248).

Spain – CONCLUSIONS ON SEQUENCING OF SARS-CoV-2 VIRAL GENOME FROM OUTBREAKS IN MINK FARMS

- **Outbreak 2021/3** (Galicia Autonomous Community):
 1. In all sequences, **D614G** and **A222V** mutations were identified in relation to the spike protein, mutations that define the **predominant clade in Spain** B.1.177, and **Europe** when the outbreak 3/2021 was detected.
 2. **Y453F** mutation described in Cluster 5 that appeared in some of the SARS-CoV-2 positive mink farms in Denmark **is present in 6 of the analysed sequences, but not the rest of the substitutions and deletions that define this cluster.**
 3. Mutations that define the British variant VOC 202012/01 or the South African variant 501Y.V2, or the one related to the Brazilian Amazon of the P.1 lineage were not detected.

Spain – CONCLUSIONS ON SEQUENCING OF SARS-CoV-2 VIRAL GENOME FROM OUTBREAKS IN MINK FARMS

- **Outbreaks 2021/4, 2021/5 and 2021/6** (Galicia Autonomous Community):
 1. The **Alpha variant** corresponding to lineage B.1.1.7 was identified in all sequences.
 2. For 2021/4 and 2021/5, no mutations other than lineage-defining mutations have been identified.
- **Outbreak 2021/7** (Galicia Autonomous Community):
 1. The virus obtained is **Alpha variant** corresponding to lineage B.1.1.7.
 2. No mutations other than lineage-defining mutations have been identified.
- **Outbreaks 2021/8, 2021/9, 2021/13 and 2021/15** (Galicia Autonomous Community):
 1. In all samples analysed from these outbreaks, it was not possible to obtain the complete sequence making sequencing not possible.

Spain – CONCLUSIONS ON SEQUENCING OF SARS-CoV-2 VIRAL GENOME FROM OUTBREAKS IN MINK FARMS

- **Outbreak 2021/10, 2021/11 and 2021/11** (Galicia Autonomous Community):
 1. For 2021/10, the 2 viruses are **Delta variant** corresponding to lineage B.1.617.2.
 2. For 2021/11 and 2021/12, the 2 viruses are **Alpha variant** corresponding to lineage B.1.1.7.
 3. No mutations other than those defining lineage have been identified.
- **Outbreak 2021/16** (Valencia Autonomous Community):
 1. The virus is **Delta variant** corresponding to lineage AY.98.1.
 2. No mutations other than those defining lineage have been identified.
- **Outbreak 2021/17**(Galicia Autonomous Community):
 1. The 2 viruses are **Delta variant** corresponding to lineage B.1.617.2.
 2. No mutations other than those defining lineage have been identified.

Thank you



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