Virus characterisation results from the PPR outbreaks of Bulgaria

Report from the EU Reference Laboratory for peste des petits ruminants (EURL-PPR)

PAFF Committee, 22-23 January 2025

EURL-PPR activities

- To ensure availability and use of high quality methods and high quality performance by NRLs

  Including distribution of Standard Operating Procedures and reference material, and organization of Proficiency Tests

- To provide scientific and technical assistance to NRLs

- To provide scientific and technical assistance to the European Commission and other organisations

  Including active assistance in the diagnosis of PPR outbreaks

EU Reference laboratory for Peste des Petits Ruminants

Funded by
the European Union

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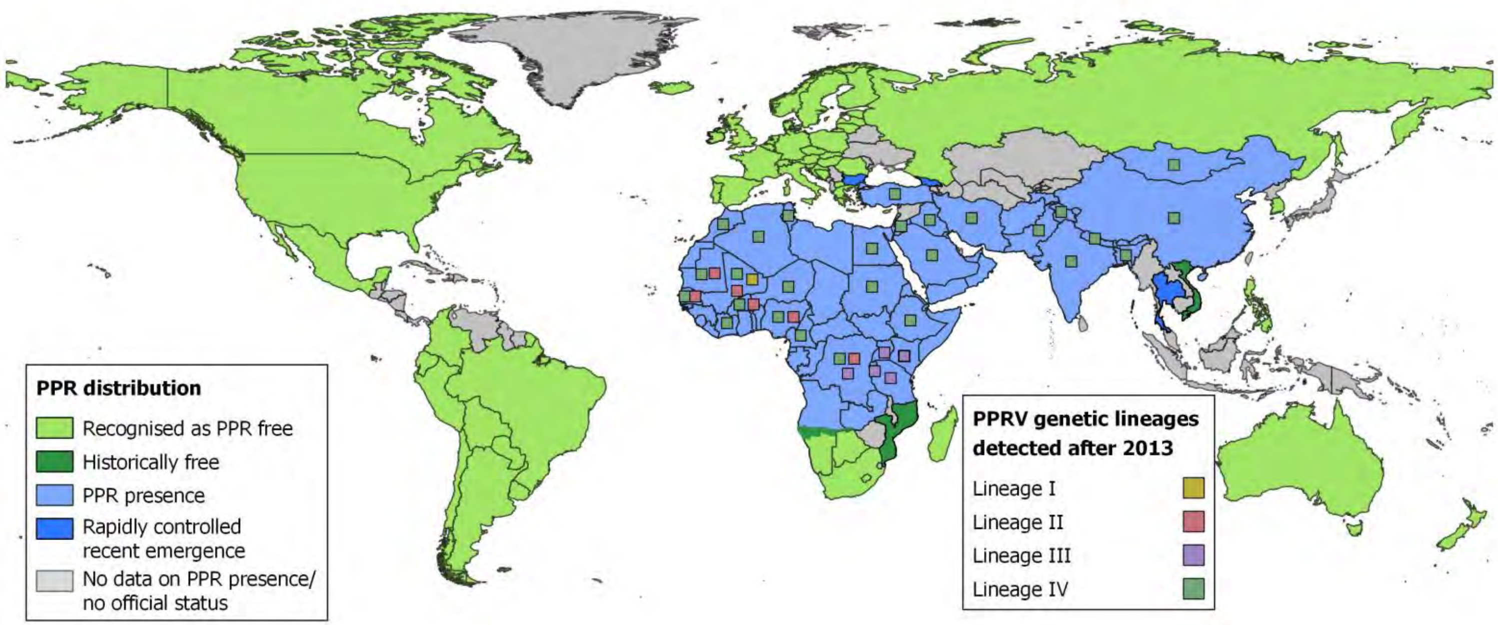
Key information regarding PPR virus

- *Morbillivirus with small RNA genome (16kb) coding for 8 proteins*
- *Four genetic lineages, with lineage IV most widely distributed across Africa, Middle East, Asia*
- *One serotype (vaccine protects against all strains)*



Samples received from NRL of Bulgaria

Reception on 06/12/2024:

- 25 blood samples
- 25 ocular swabs

From 25 animals sampled at ADIS-1

- 20 serum samples

From 20 animals sampled at ADIS-1

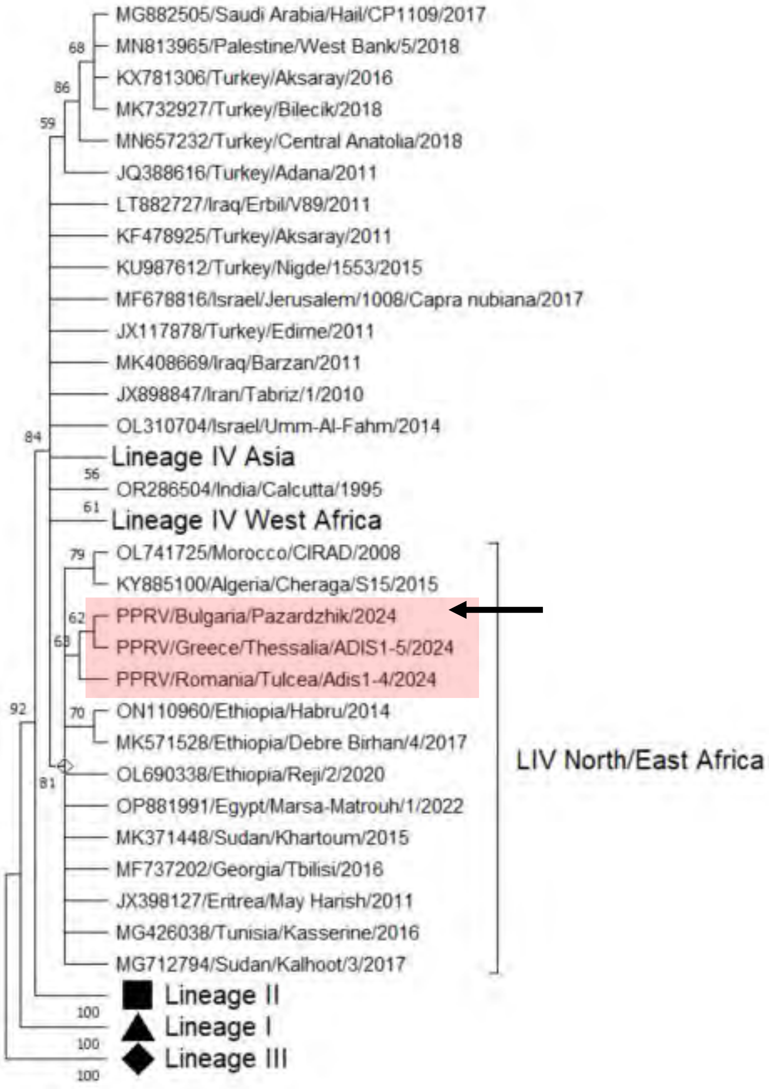
ELISA assay on serum samples *(cELISA for the detection of antibodies against PPR agent)* and real-time quantitative PCR on all other samples

Positive results obtained for all samples, confirming results obtained by NRLs (reports sent to NRLs and EC)

NRL of Bulgaria tested blood and swab samples in pools of 5 while the EURL-PPR tested every sample individually. Our results suggest that a higher sensitivity is obtained with individual swabs.

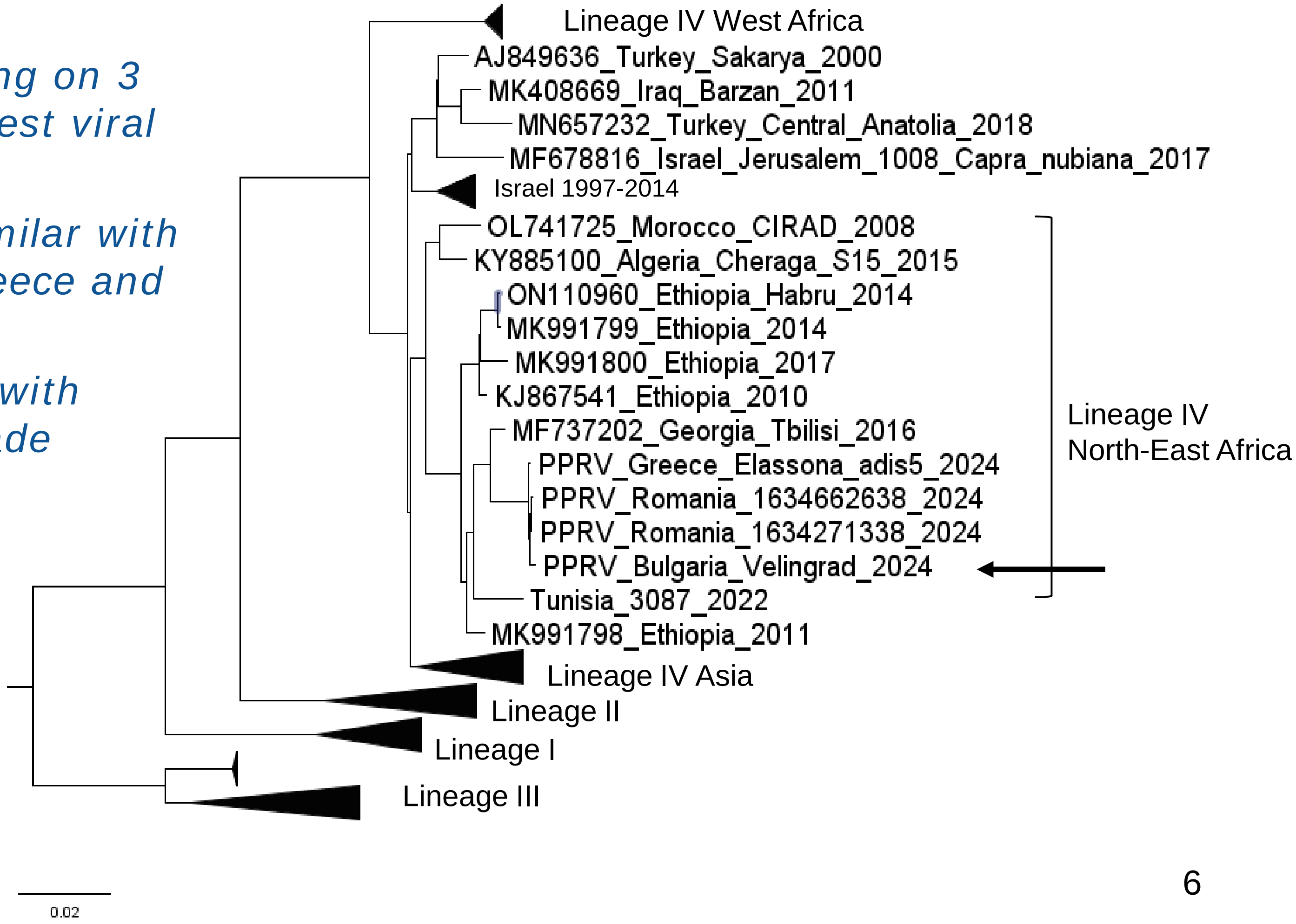
Partial genome sequence

- *Conventional RT-PCR targeting portion of nucleoprotein (255bp) followed by Sanger sequencing*
- *Identical sequence obtained from all samples*
- *99.7% similar to sequence from Romania*
- *Phylogenetic analyses place sequence with sequences from Romania and Greece within lineage IV, sub-clade grouping strains from North and East Africa*



Genome sequencing and phylogenomic analysis

- *High-throughput sequencing focusing on 3 samples with highest viral load*
- *Genome highly similar with genomes from Greece and Romania*
- *Confirm grouping with Lineage IV sub-clade North-East Africa*



Conclusions

- *The NRL has performed excellent diagnostic work to confirm PCR infections from samples received. The EURL-PPR continues its support with advise on protocols, provision of reference material*

- *Genomic data confirms that emergence of PPR in Bulgaria has a common origin with the emergence in Romania and Greece*
- *Additional sequencing from infected farms in Greece and Romania would help investigation into the origin of the PPR outbreak*

Thanks to

The EURL-PPR team

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The NRL-PPR in Bulgaria

Bulgarian Food Safety Agency