Food and Agriculture
Organization of the
United Nations

Examples of PPR Episystems: North Africa and China-Mongolia-Central Asia

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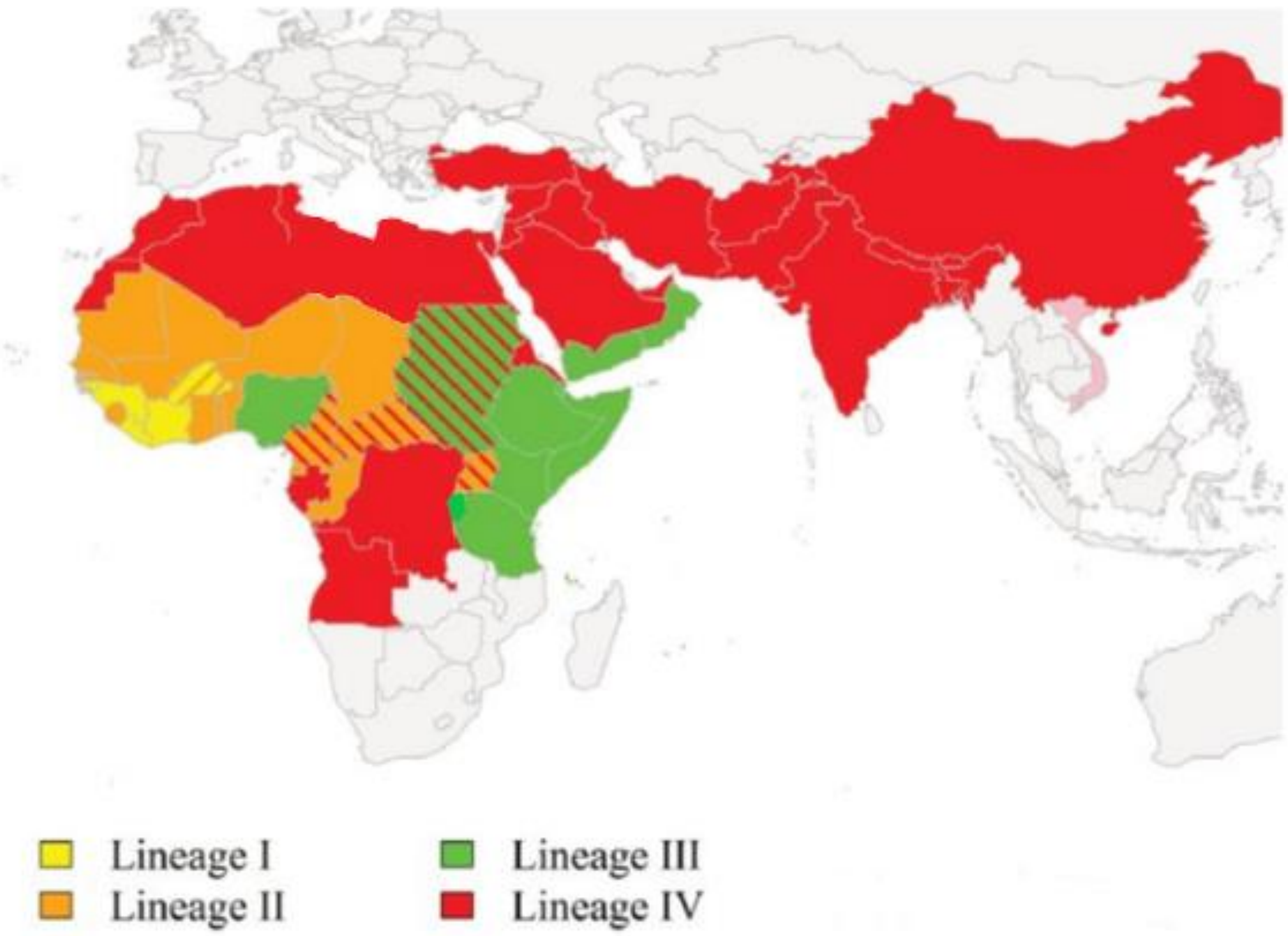
PPRV Lineage Distribution



PPR in North Africa, Morocco-2008

- **Morocco** experienced the first incursion of the disease in the little Maghreb in 2008 and the disease spread rapidly in the country mainly through animal trade

- Across outbreaks 2 833 sick animals were identified

- **257** outbreaks in **36** provinces were reported from 18 July 2008 to 5 November 2008

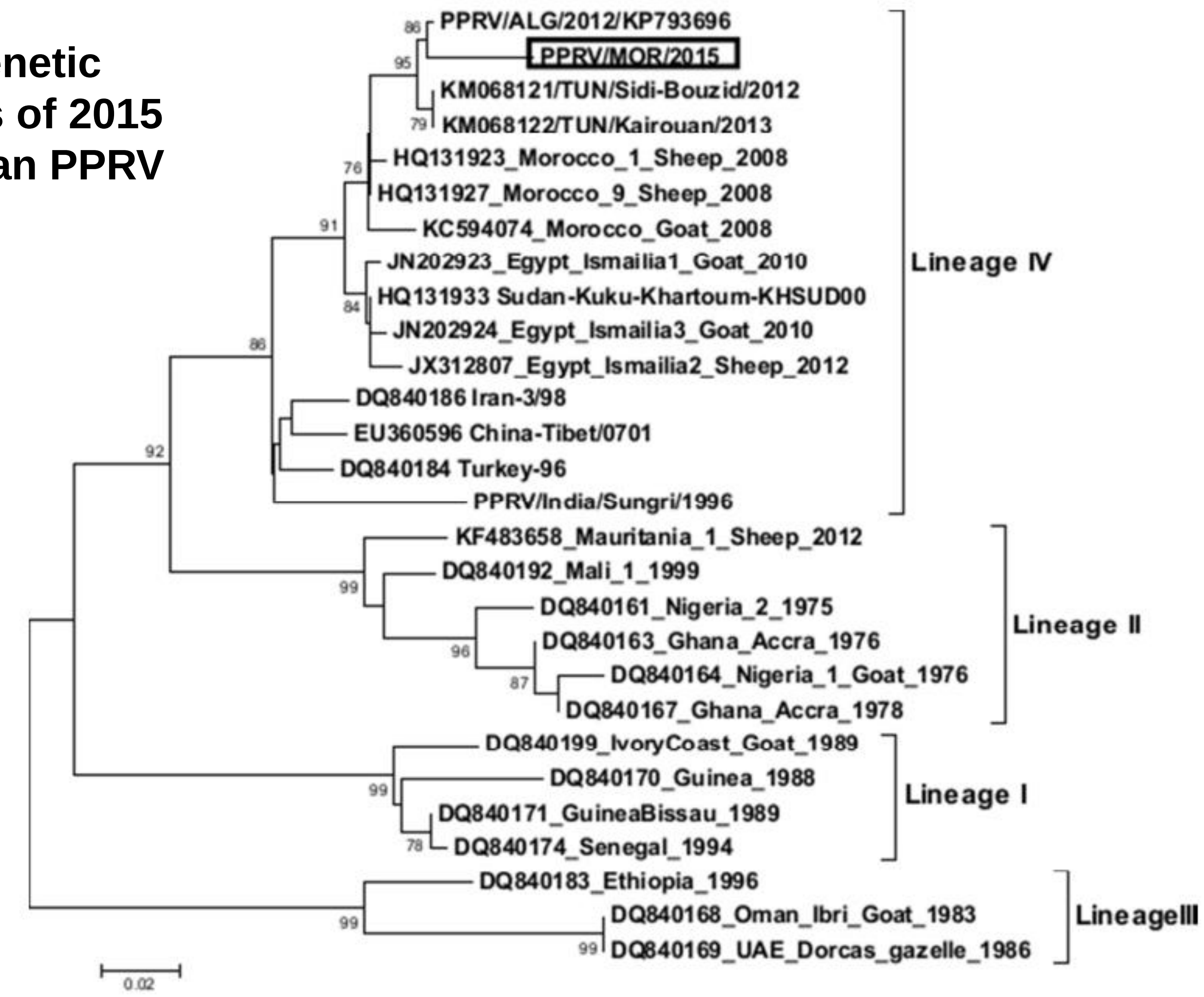
- Case fatality rates approached 50%

- Of the infected animals, 96% were sheep.

PPR in Morocco-2015

Figure 1: 2015 Outbreak locations of PPRV in Northern Morocco. (Source: OIE, 2016)
104x54mm (100 x 100 DPI)

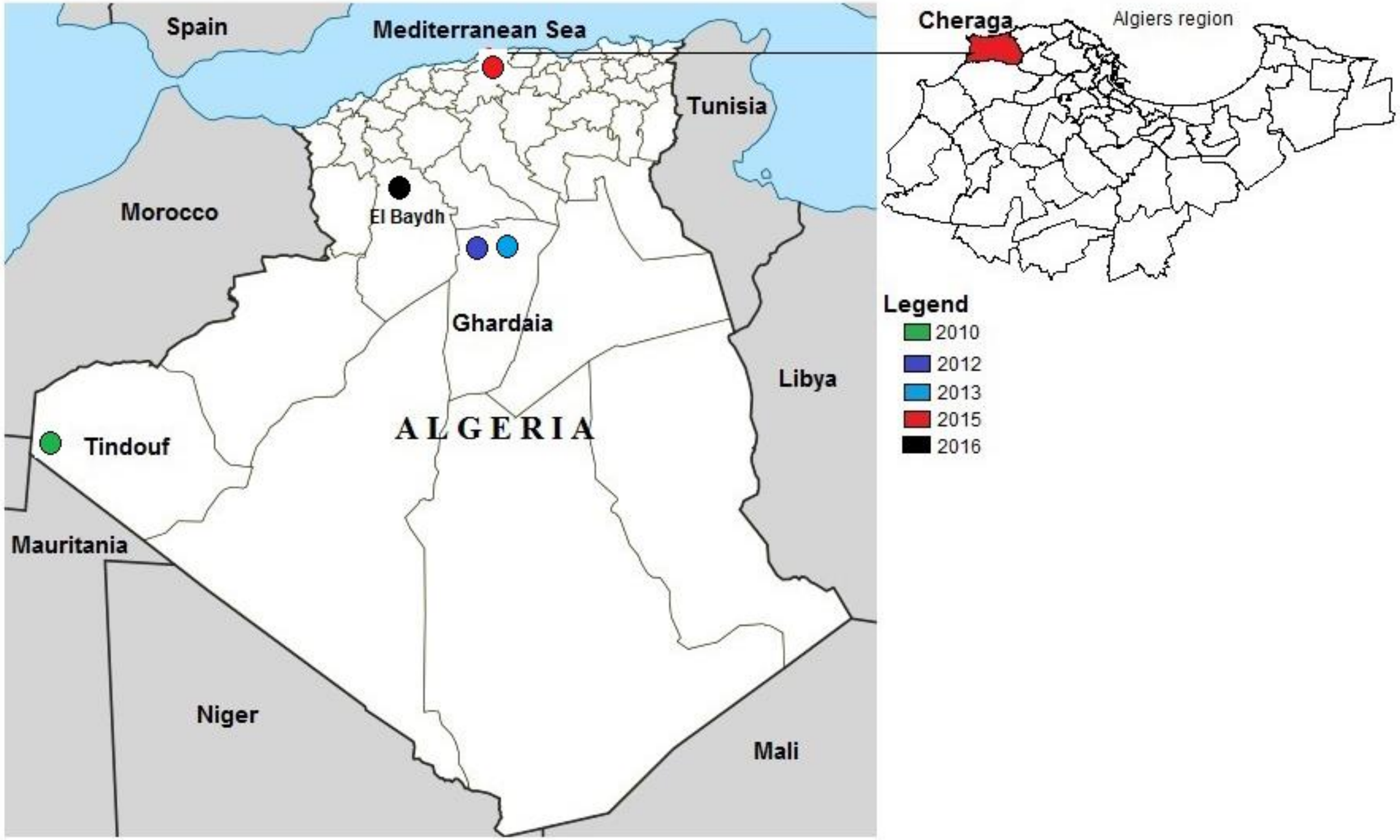
Phylogenetic analysis of 2015 Moroccan PPRV



4: Phylogenetic tree based on the nucleoprotein gene of peste des petits ruminants virus is
2015 Morocco outbreak (black rectangle) and selected comparison sequences from GenBank
-joining method was used for phylogenetic analysis; evolutionary distances were computed
Tamura 3-parameter using MEGA 6.0. The GenBank accession numbers are given against e
sequence. Scale bar indicates nucleotide substitutions per site.

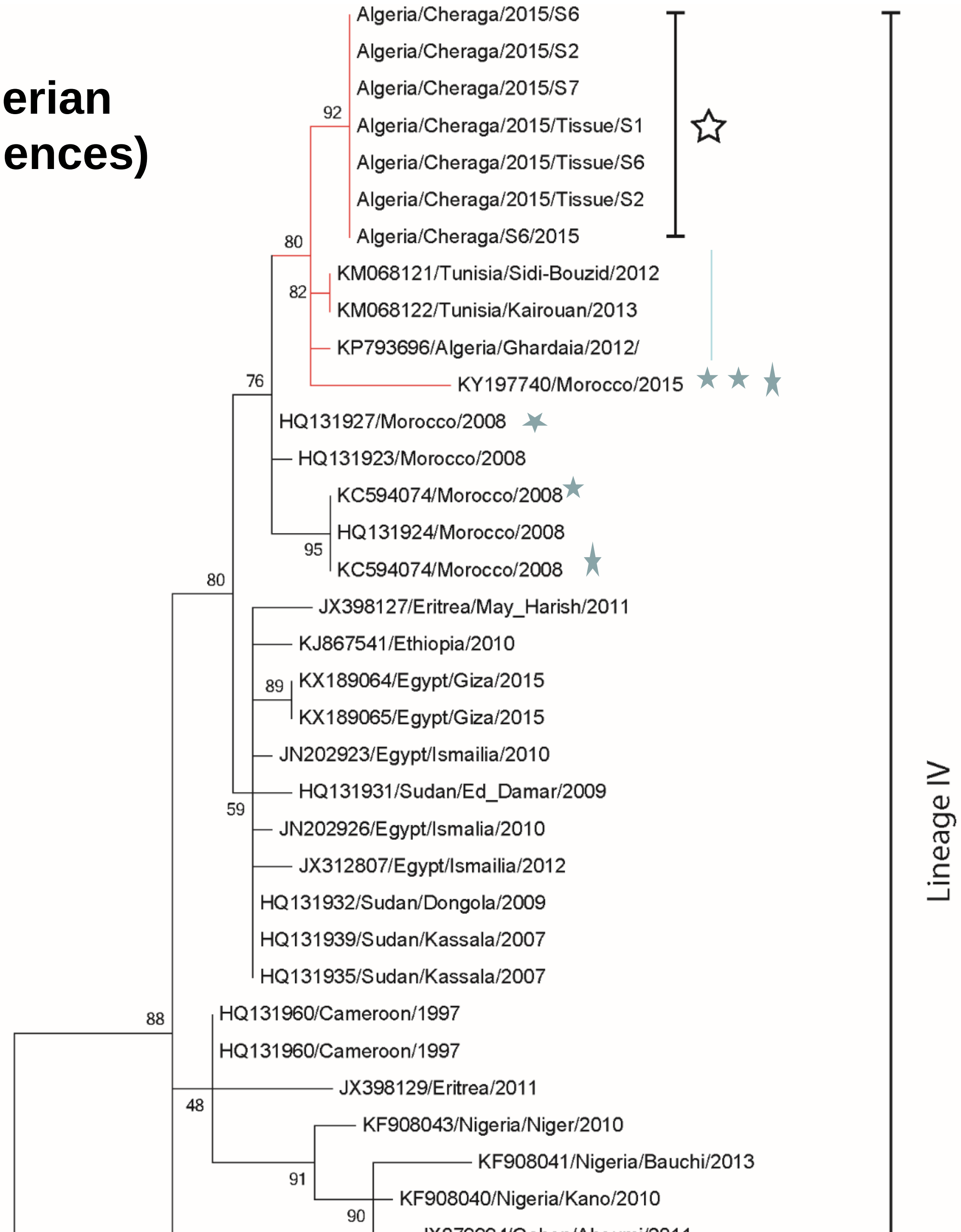
Fakir et al., 2016

PPR in Algeria-2010-2016



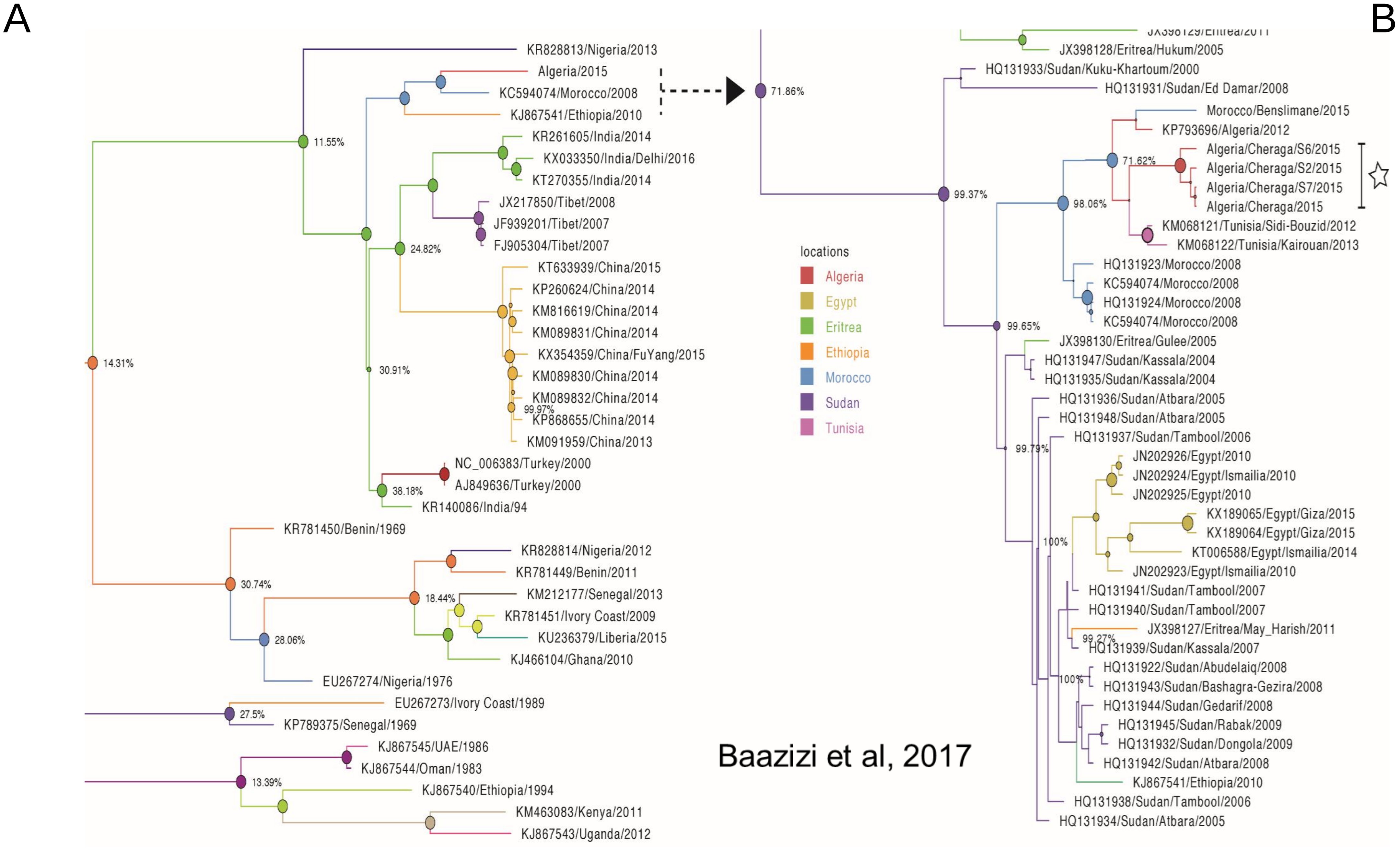
Baazizi et al, 2017

Phylogenetic analysis of 2015 Algerian and Moroccan PPRV (Partial sequences)



Baazizi et al, 2017

Full genome (**A**) and Partial genome (**B**) analysis of Lineage IV PPRV



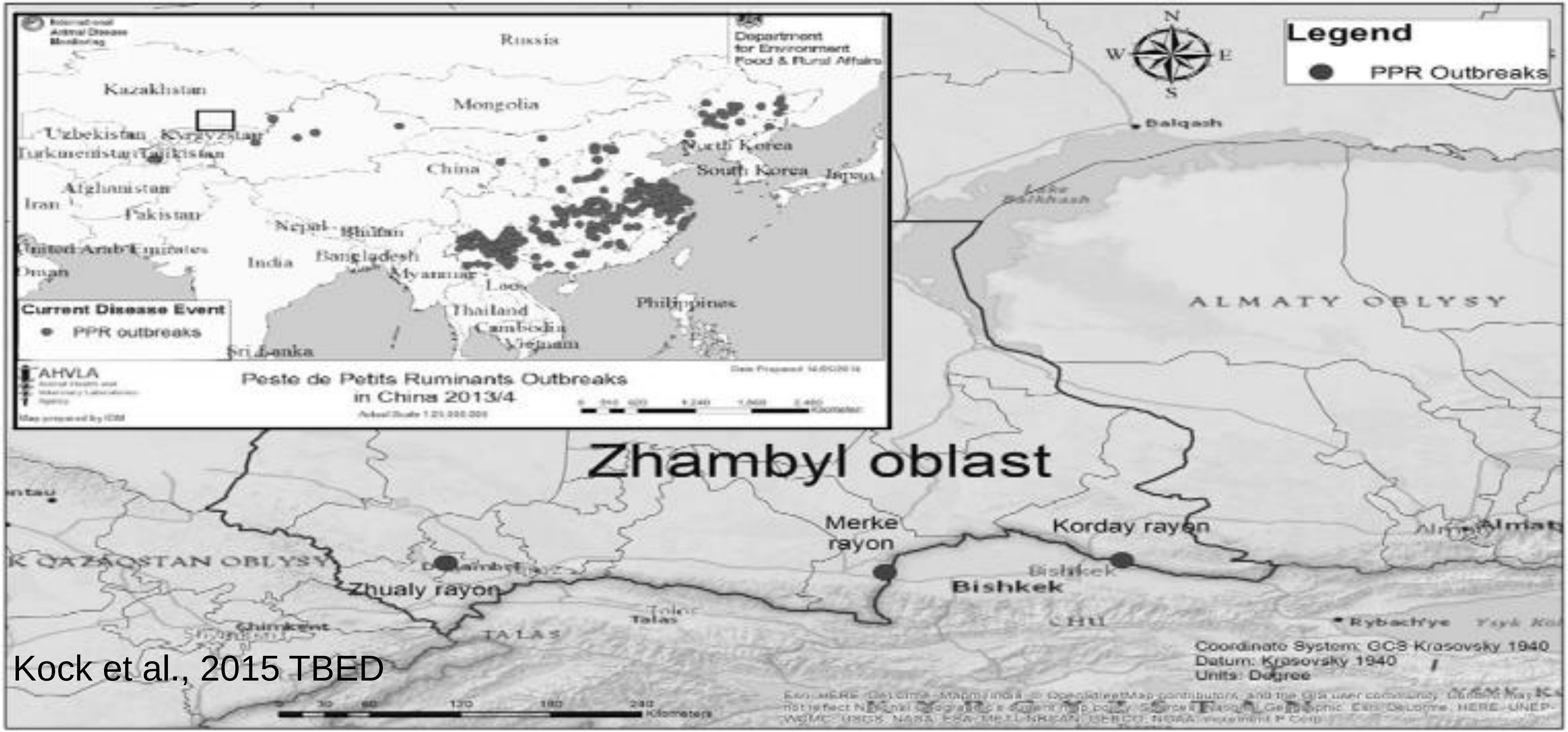
Baazizi et al, 2017

Animal movement correlates with PPRV lineage circulation

Baazizi et al, 2017

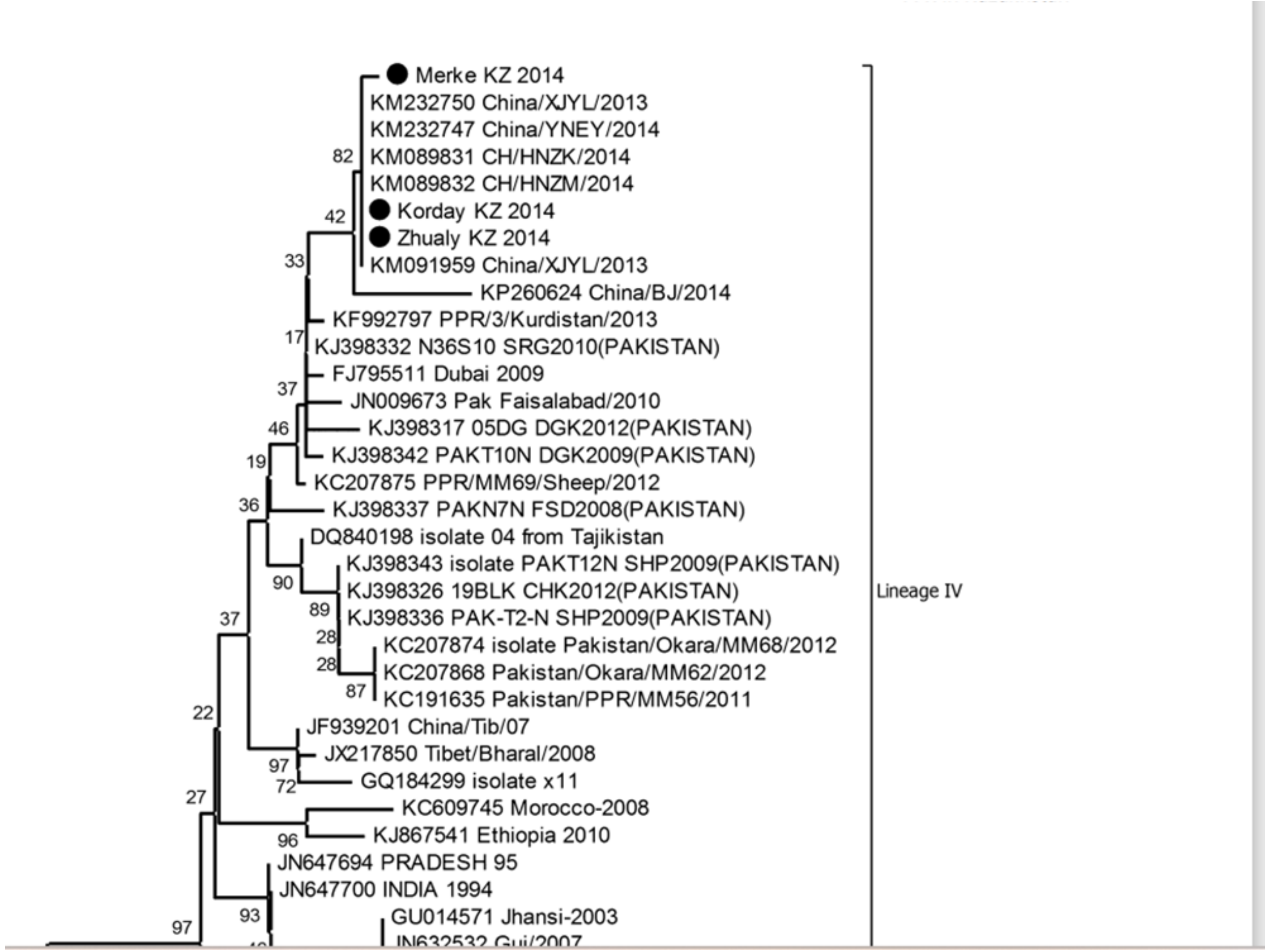
Modified figure from FAO web

PPR outbreaks in Kajakstan 2014



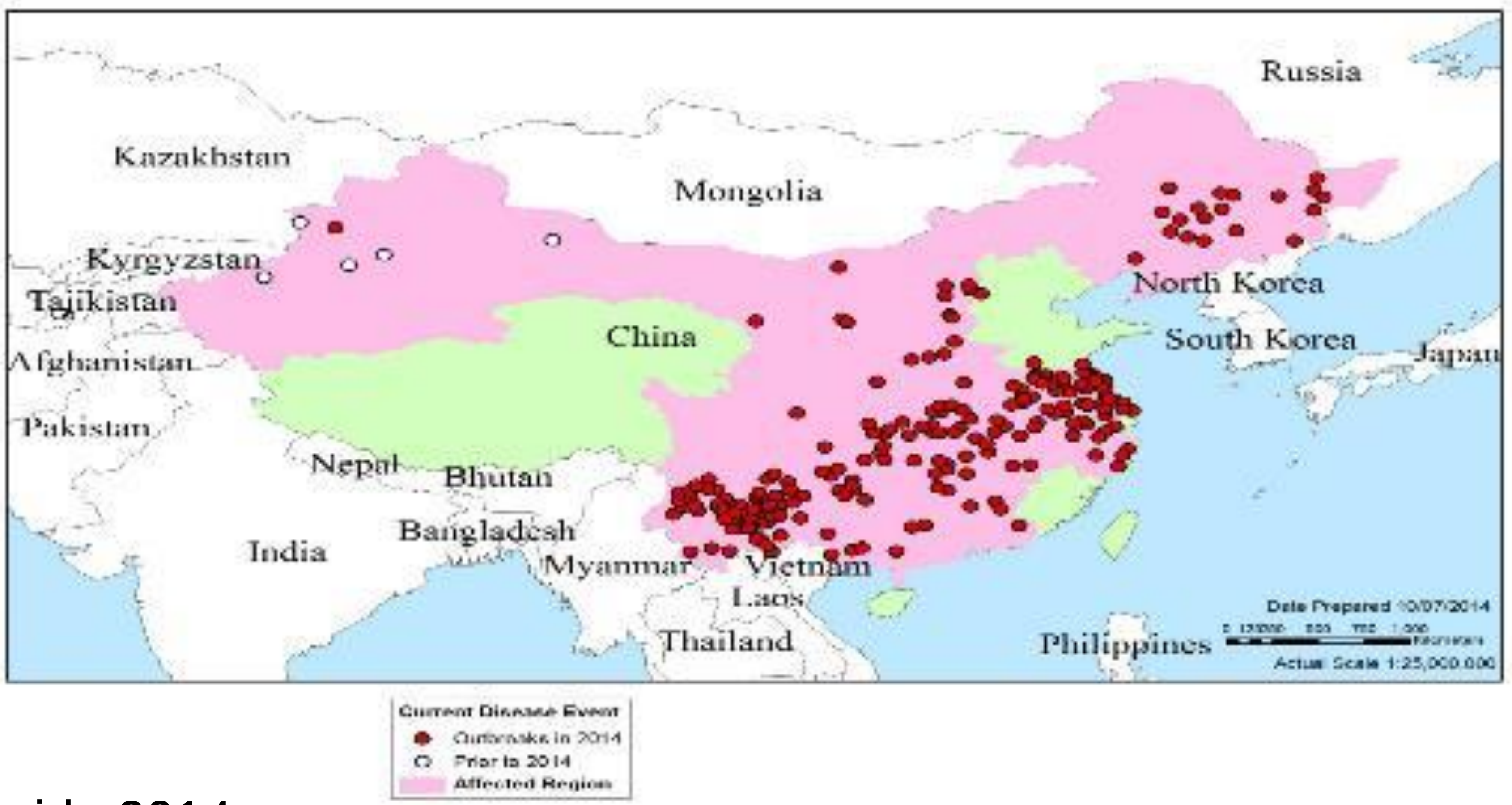
Kock et al., 2015 TBED

PPR virus circulation in Central Asia and China



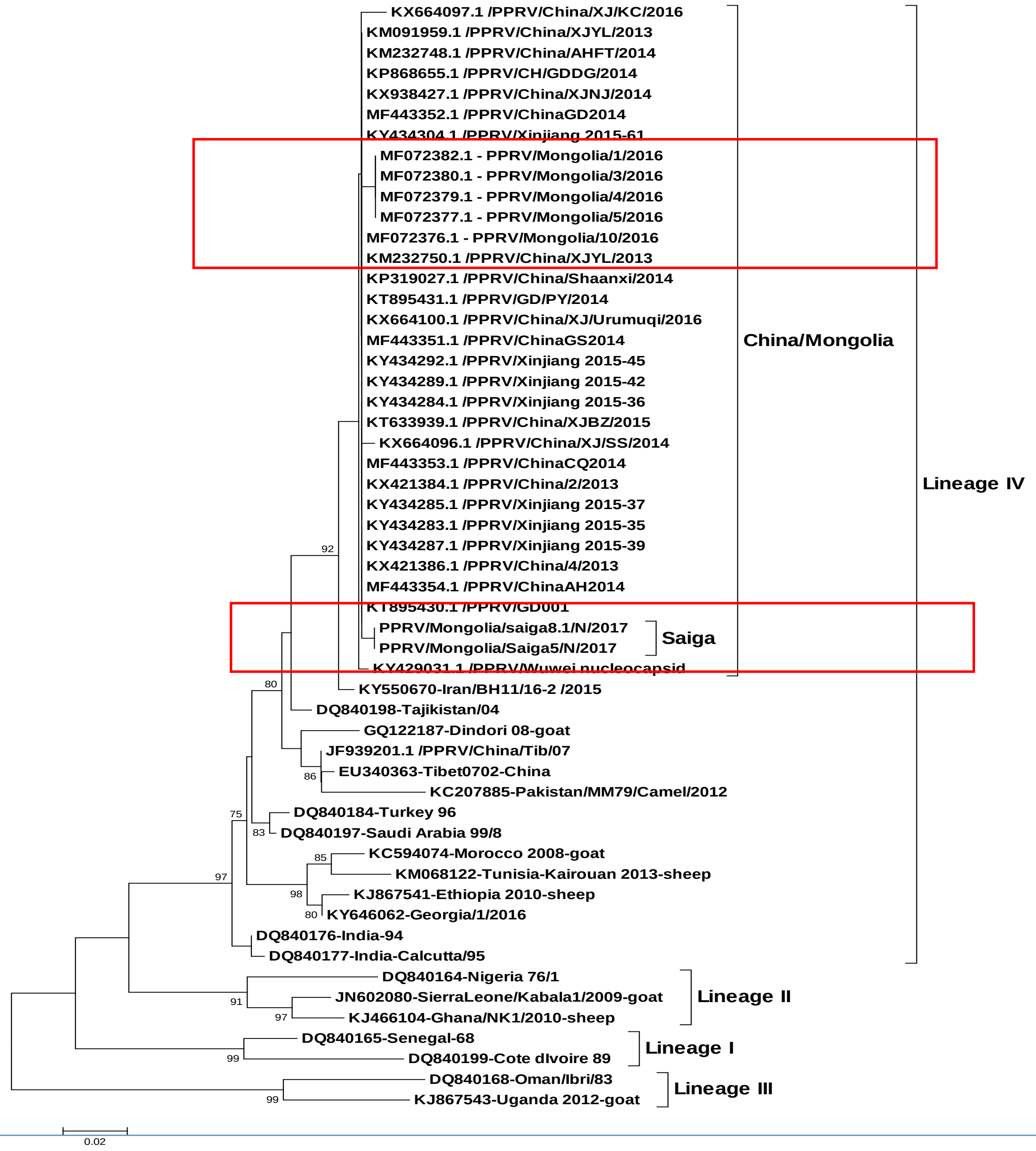
Kock et al , 2015 TBED

2013-2014 outbreaks in China



Banyard and Parida 2014

Outbreaks in Saiga in Mongolia



Pruvot et al., 2020

PPRV – Georgia 2016

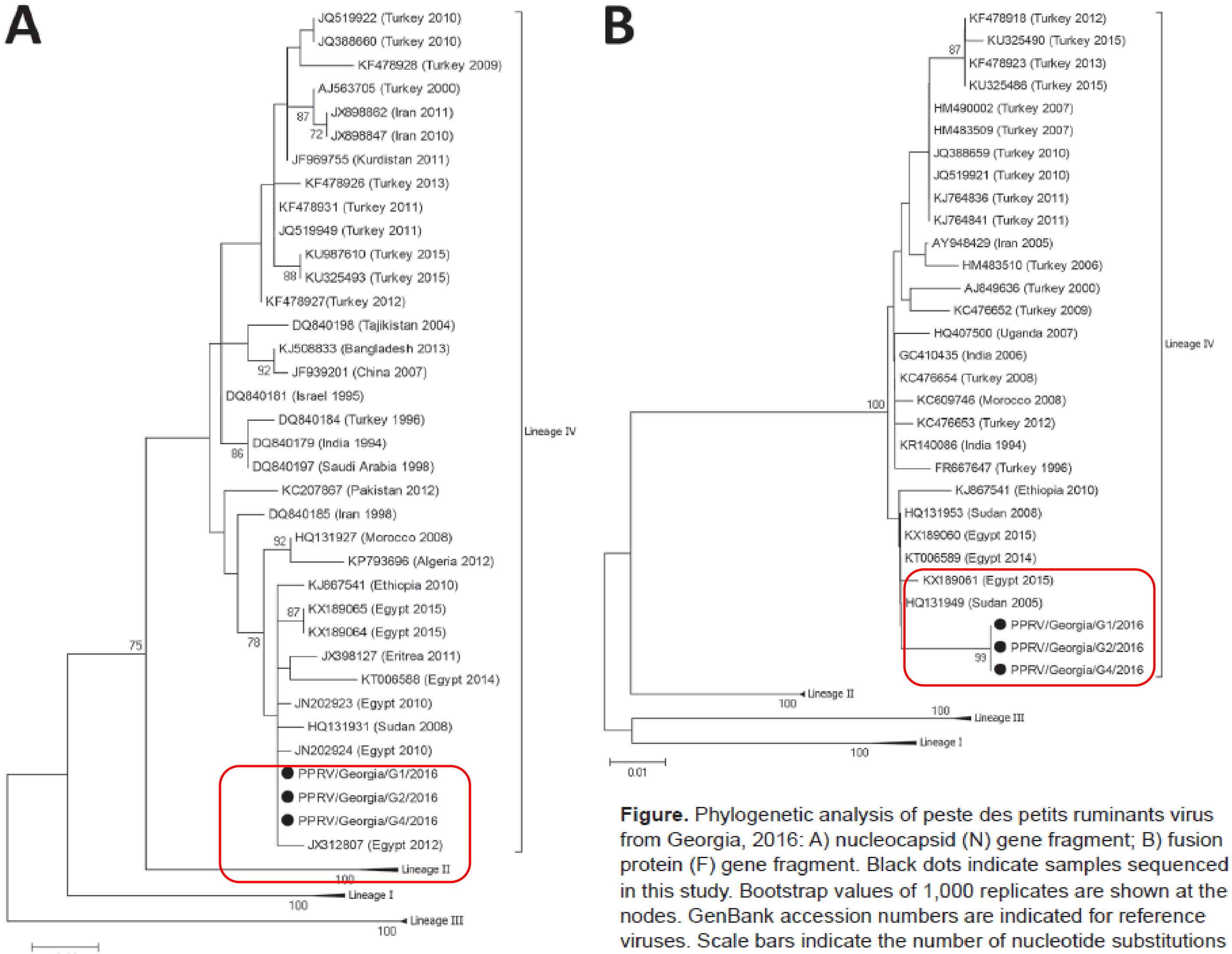
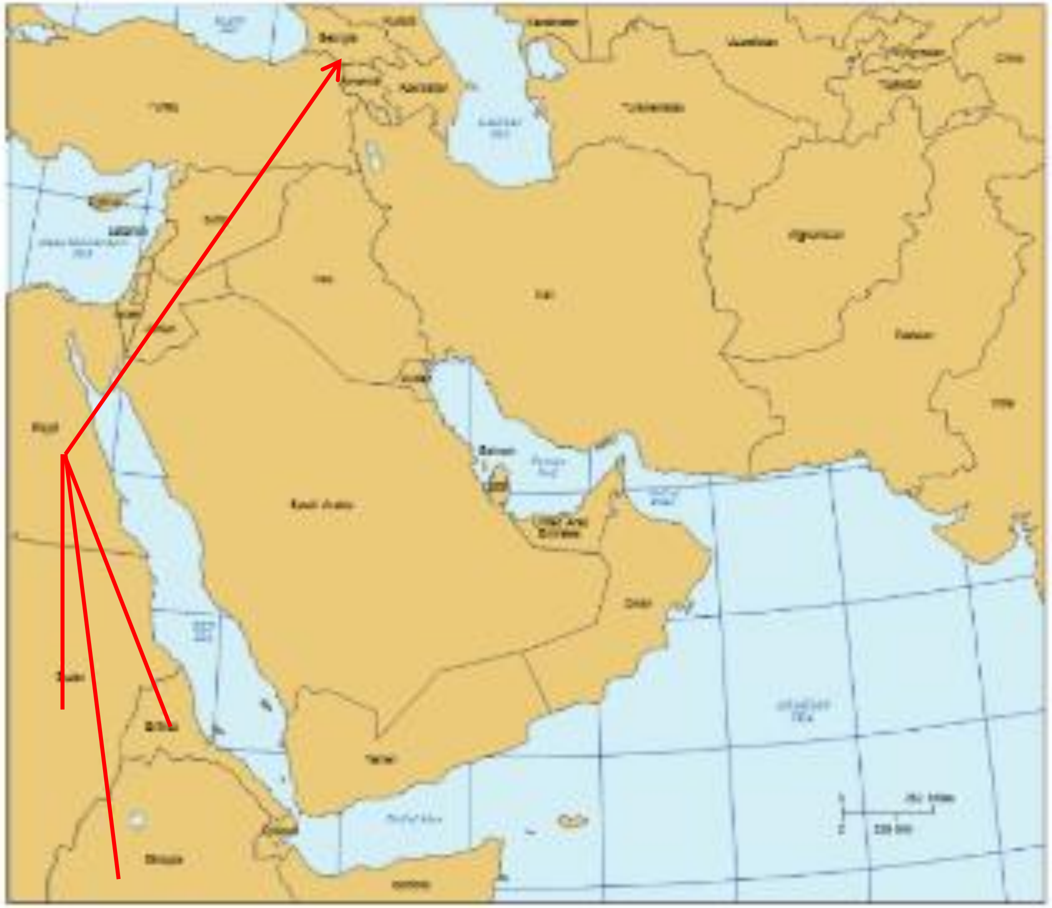
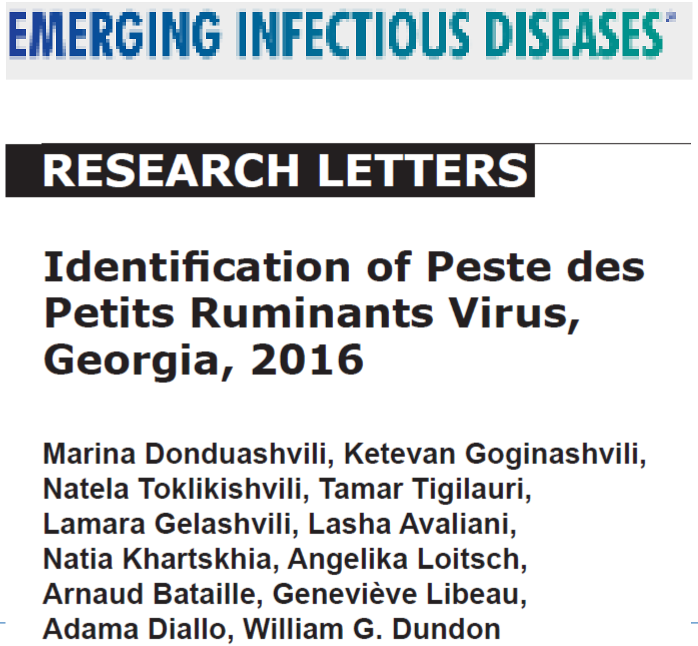


Figure. Phylogenetic analysis of peste des petits ruminants virus from Georgia, 2016: A) nucleocapsid (N) gene fragment; B) fusion protein (F) gene fragment. Black dots indicate samples sequenced in this study. Bootstrap values of 1,000 replicates are shown at the nodes. GenBank accession numbers are indicated for reference viruses. Scale bars indicate the number of nucleotide substitutions per site.



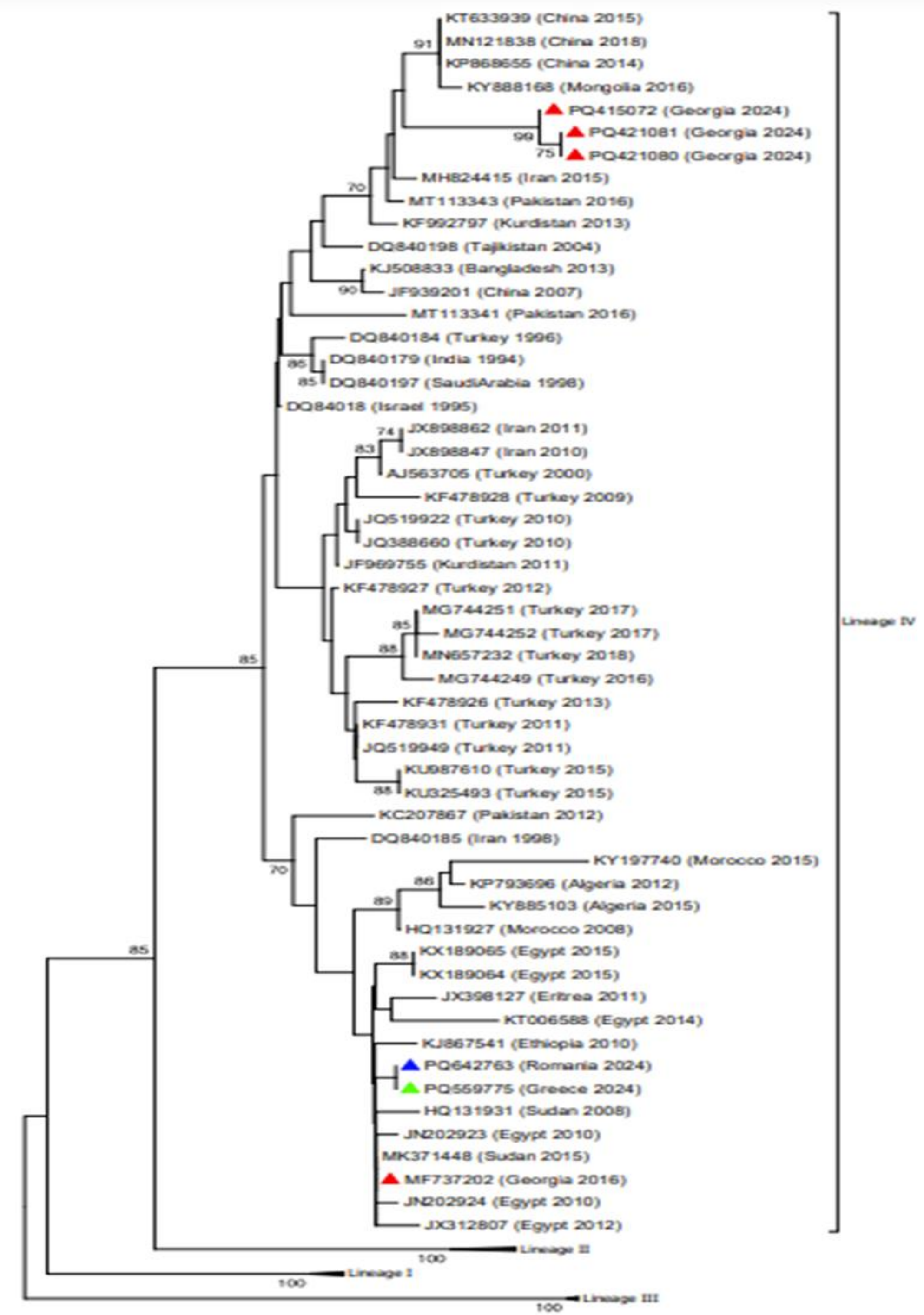

EMERGING INFECTIOUS DISEASES®

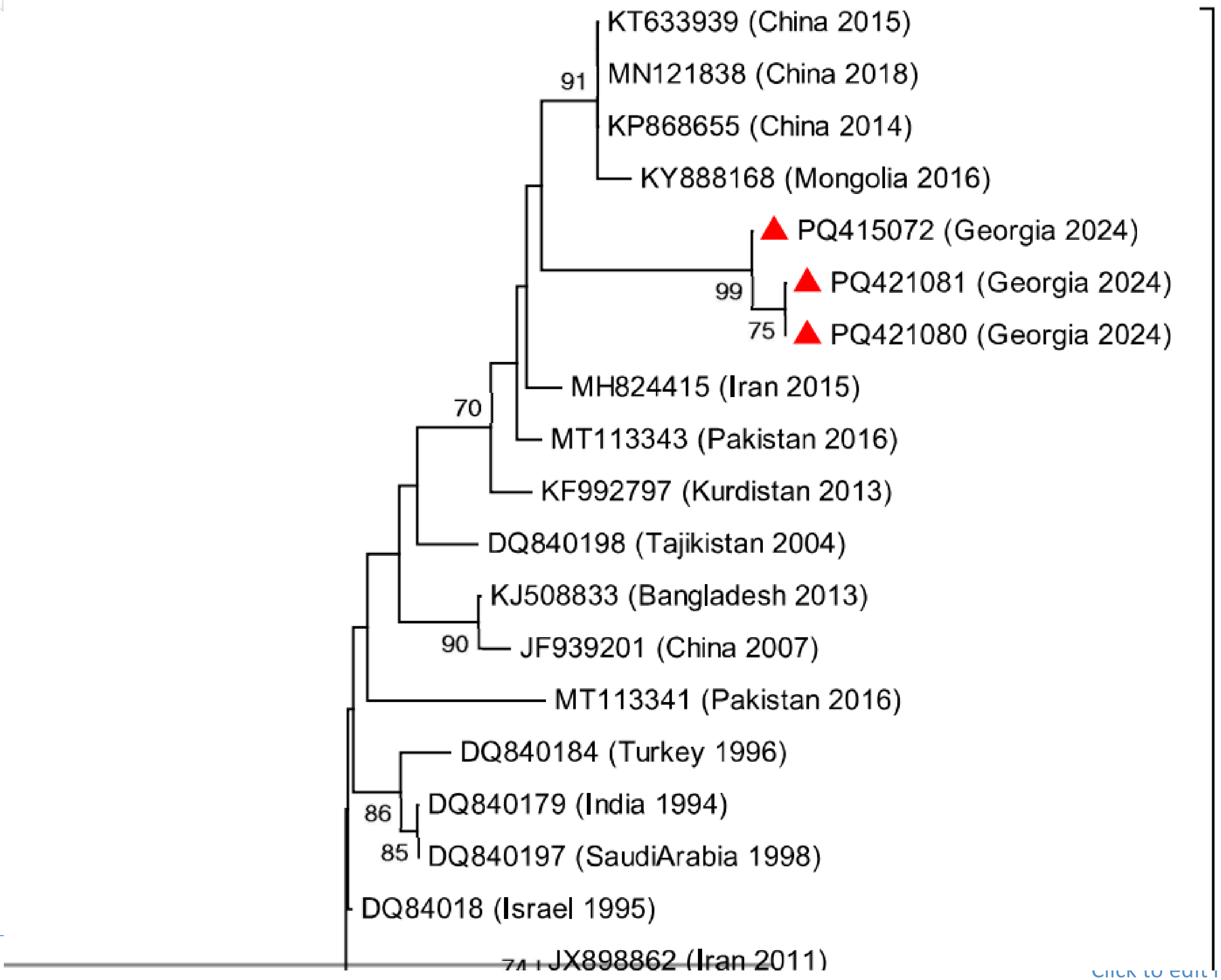
RESEARCH LETTERS

Identification of Peste des Petits Ruminants Virus, Georgia, 2016

Marina Donduashvili, Ketevan Goginashvili,
Natela Toklikishvili, Tamar Tigilauri,
Lamara Gelashvili, Lasha Avaliani,
Natia Khartskhia, Angelika Loitsch,
Arnaud Bataille, Geneviève Libeau,
Adama Diallo, William G. Dundon

PPRV – Georgia 2024

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MN121838 (China 2018)
91
KP868655 (China 2014)
KY888168 (Mongolia 2016)
PQ415072 (Georgia 2024)
PQ421081 (Georgia 2024)
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75
PQ421080 (Georgia 2024)
MH824415 (Iran 2015)
70
MT113343 (Pakistan 2016)
KF992797 (Kurdistan 2013)
DQ840198 (Tajikistan 2004)
KJ508833 (Bangladesh 2013)
90
JF939201 (China 2007)
MT113341 (Pakistan 2016)
DQ840184 (Turkey 1996)
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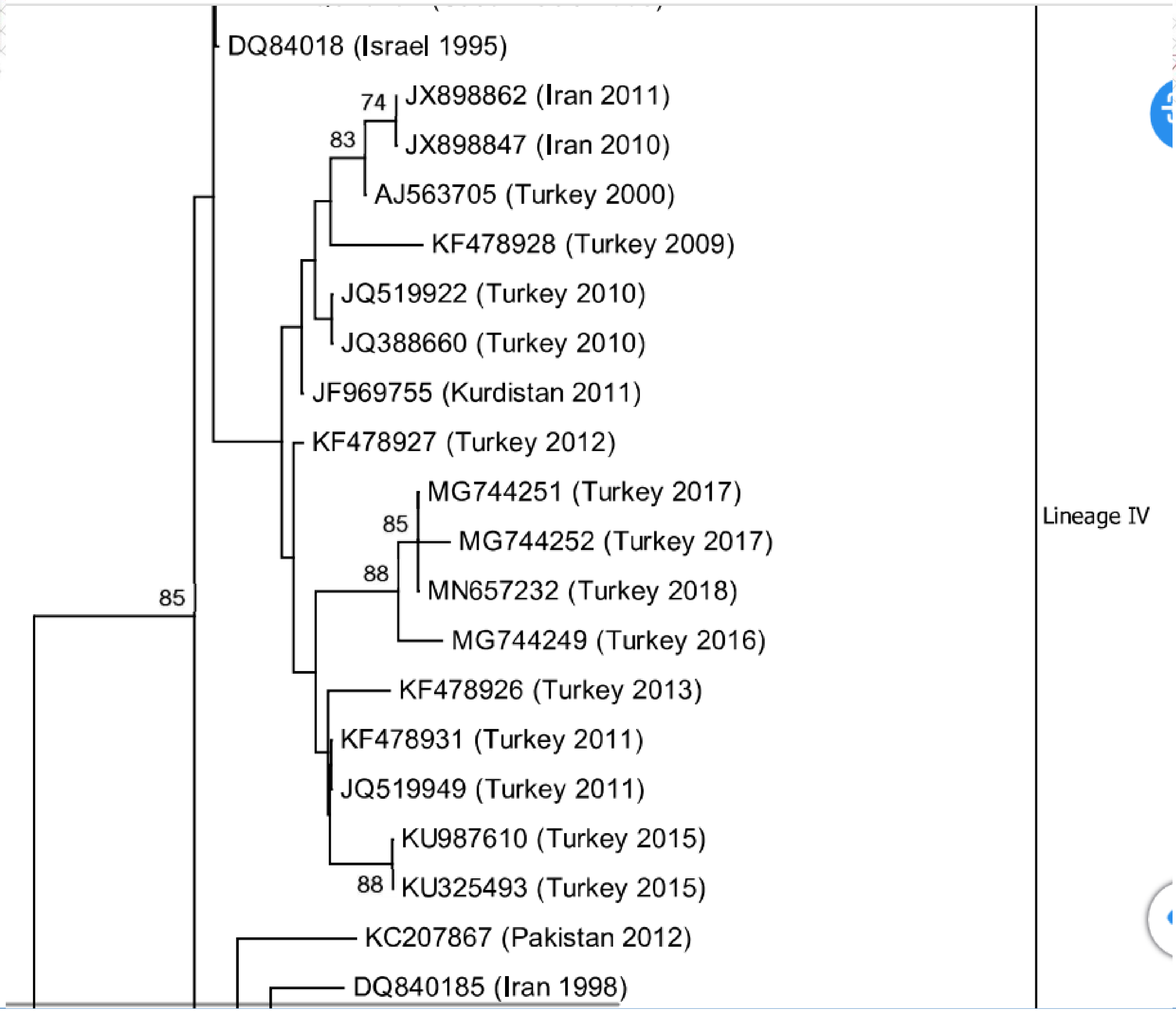
DQ840179 (India 1994)
85
DQ840197 (SaudiArabia 1998)
DQ84018 (Israel 1995)
74
JX898862 (Iran 2011)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MG744251 (Turkey 2017)
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MG744252 (Turkey 2017)
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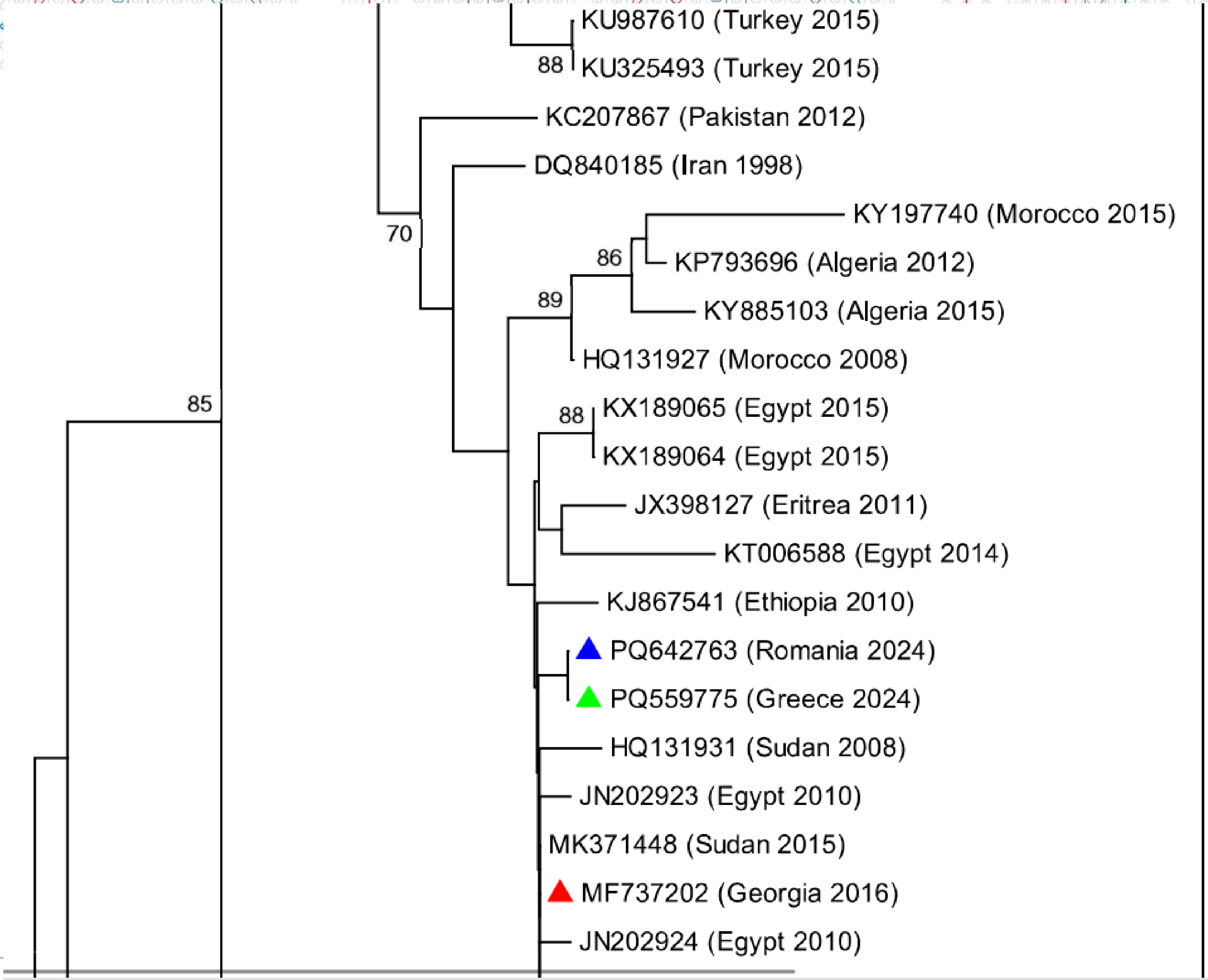
DQ840185 (Iran 1998)
Lineage IV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KU325493 (Turkey 2015)
KC207867 (Pakistan 2012)
DQ840185 (Iran 1998)
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KY197740 (Morocco 2015)
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KP793696 (Algeria 2012)
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KY885103 (Algeria 2015)
HQ131927 (Morocco 2008)
85
88
KX189065 (Egypt 2015)
KX189064 (Egypt 2015)
JX398127 (Eritrea 2011)
KT006588 (Egypt 2014)
KJ867541 (Ethiopia 2010)
▲ PQ642763 (Romania 2024)
▲ PQ559775 (Greece 2024)
HQ131931 (Sudan 2008)
JN202923 (Egypt 2010)
MK371448 (Sudan 2015)
▲ MF737202 (Georgia 2016)
JN202924 (Egypt 2010)

Take home messages

Establishment of an Episystem in North Africa that is connected to East Africa

Existence of an episystem in China, Mongolia, and Central Asia

We need to break these episystems for PPR eradication

Thank you