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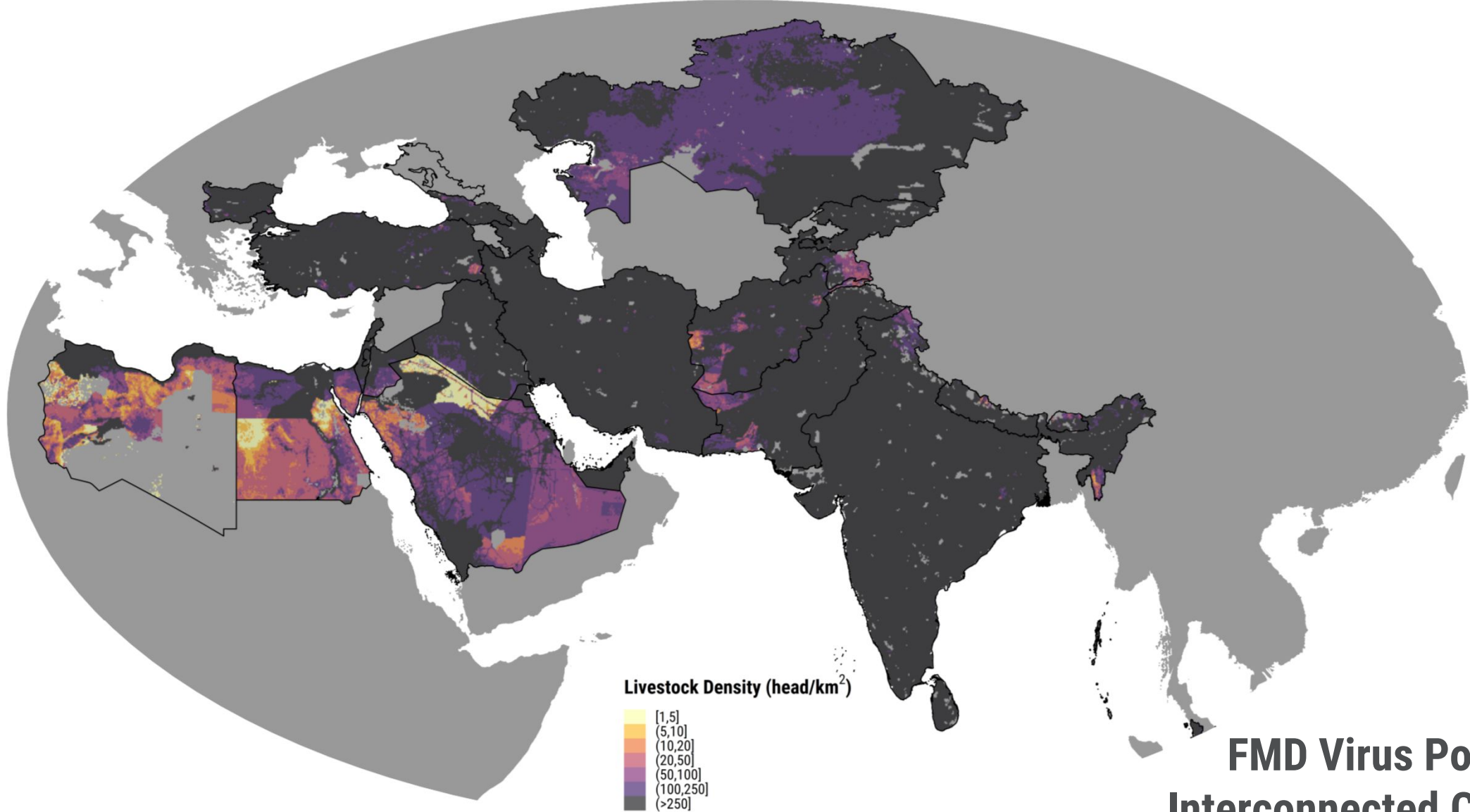
Evolutionary Competition Drives the Emergence and Extinction of FMDV Lineages

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Global FMD Research Alliance Conference, 29th – 31st October 2019, Bangkok, Thailand



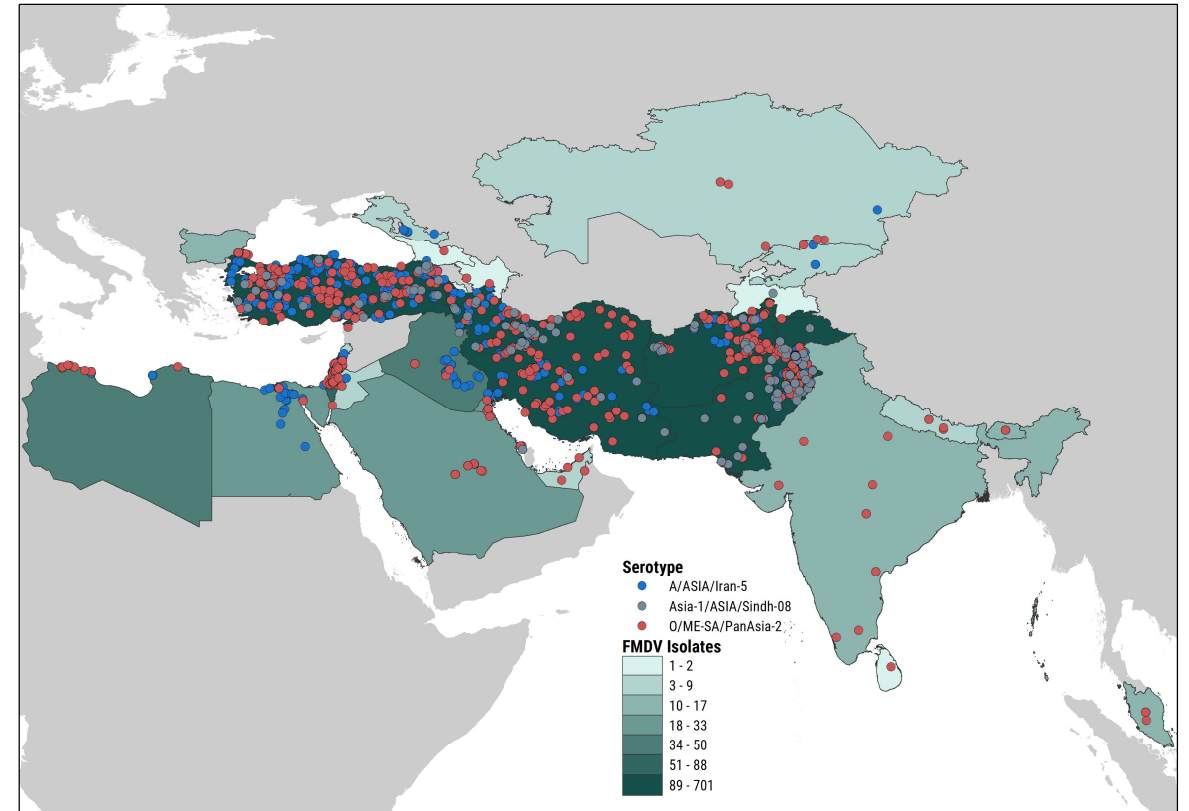
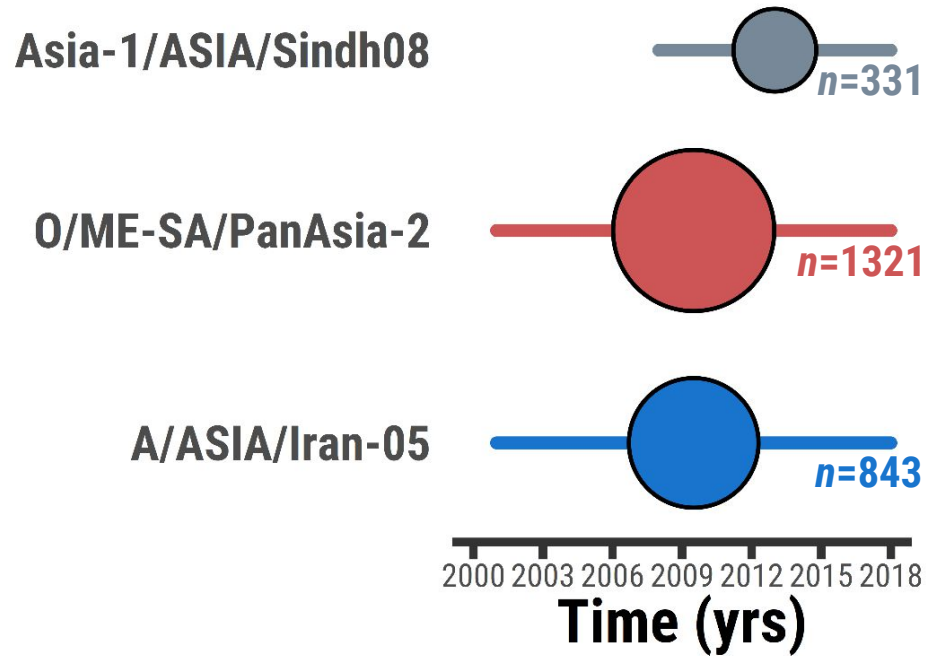
Study Region



FMD Virus Pool 3 & Interconnected Countries

Data Analysed

2495 FMDV VP1 coding sequences



Research Questions



- A.** How FMDV lineages **move** across the regions?
- B.** How FMDV lineages **interact** within the region?
- C.** How **host** species drive FMDV evolution?
- D.** What **drives** FMDV transmission in the region?

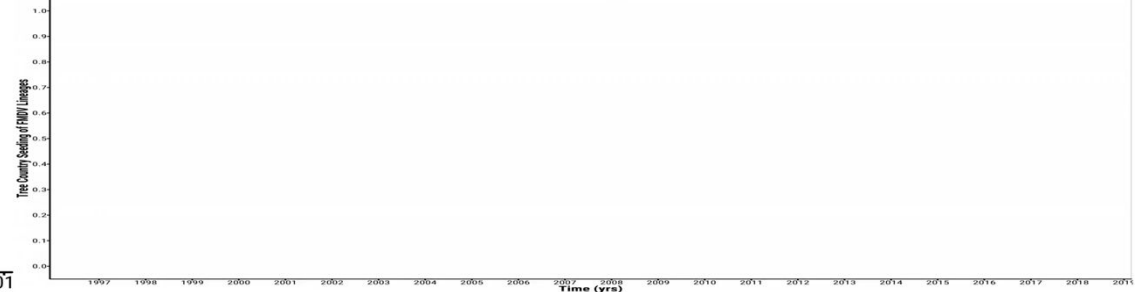
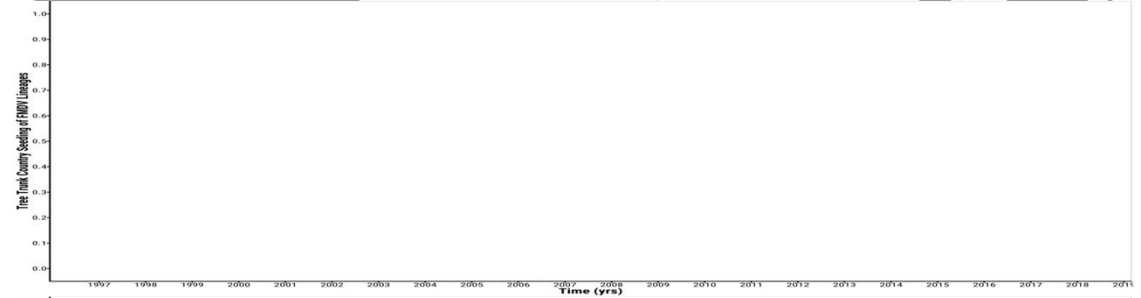
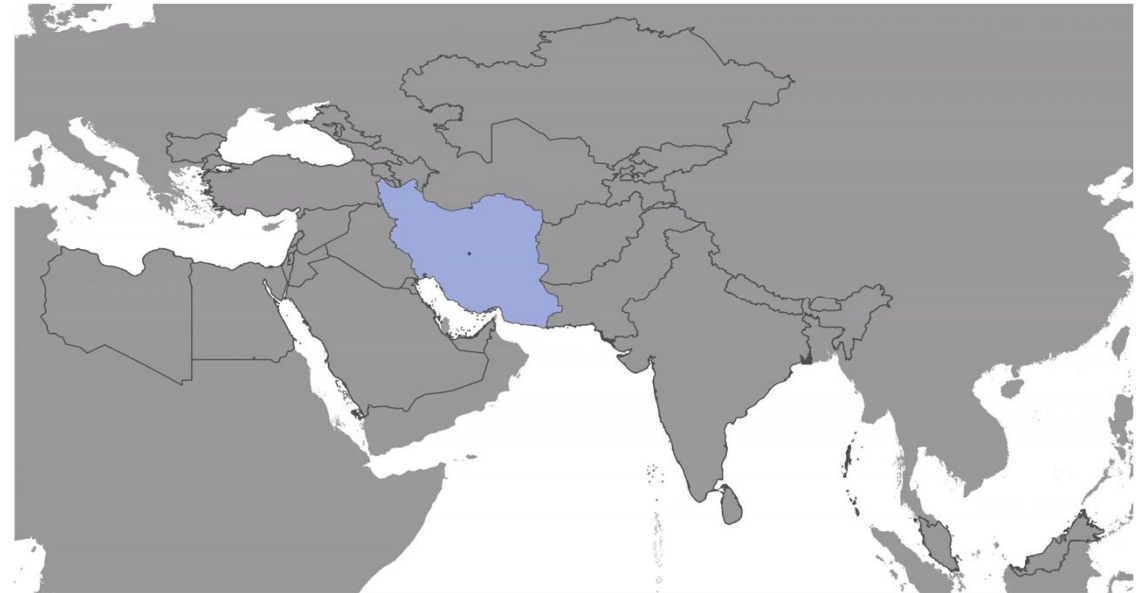
How FMDV lineages move across the regions?

Spatial Diffusion and Phylogeography



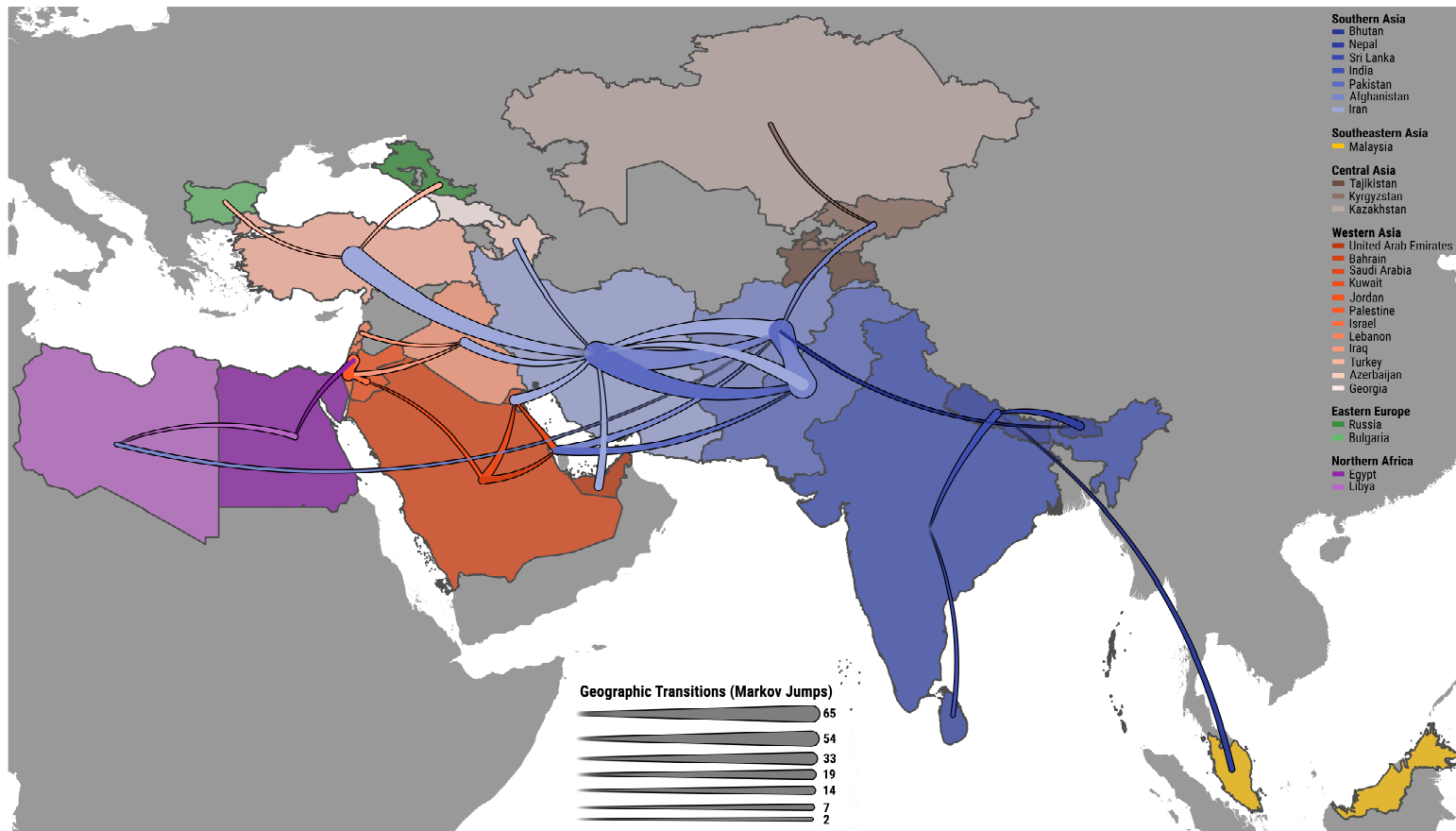
FMDV Transboundary Network

Date: 21 February 1997
Decimal Time: 1997.141



1997 1998 1999 2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019

FMDV Transboundary Network



FMDV transboundary movements:

- ✓ Spatial cluster of virus interchange identified in **Southern Asia** (i.e. between Pakistan, Afghanistan and Iran), likely constituting a single meta-population of FMDV persistence
- ✓ **Iran** as hub of virus diffusion to the West, acting as an habitat corridor for virus dispersal from Southern Asia
- ✓ High flow of unidirectional migration of viruses from Iran towards **Turkey**

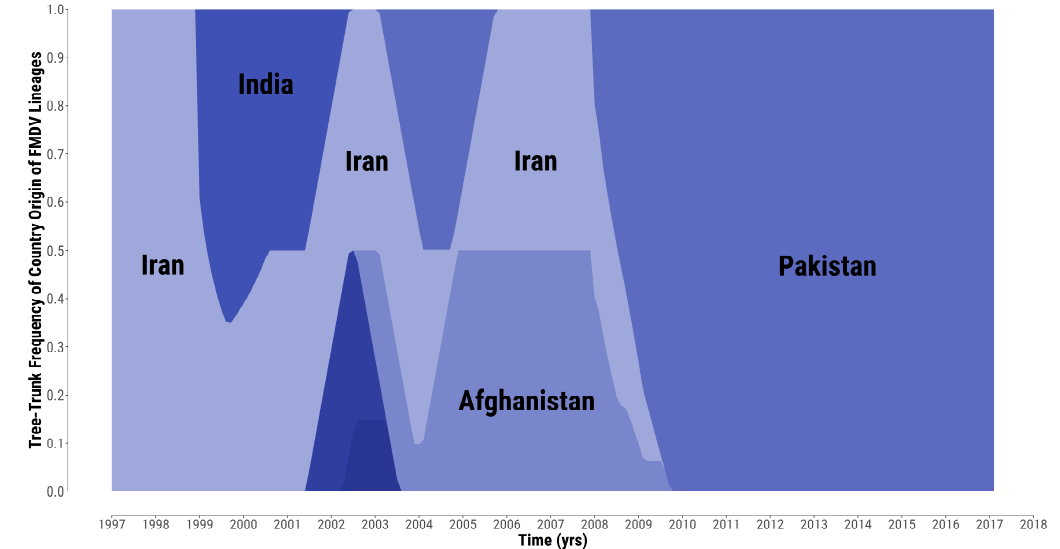
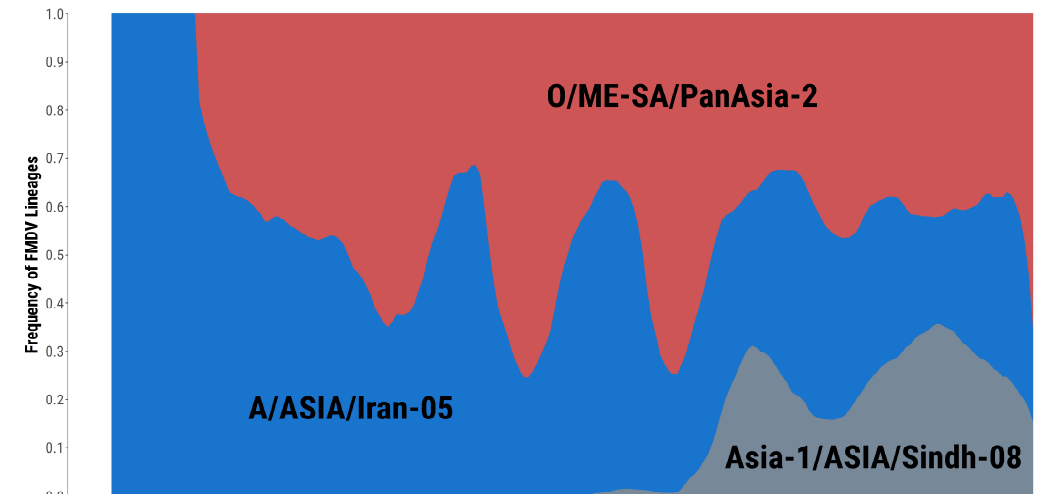
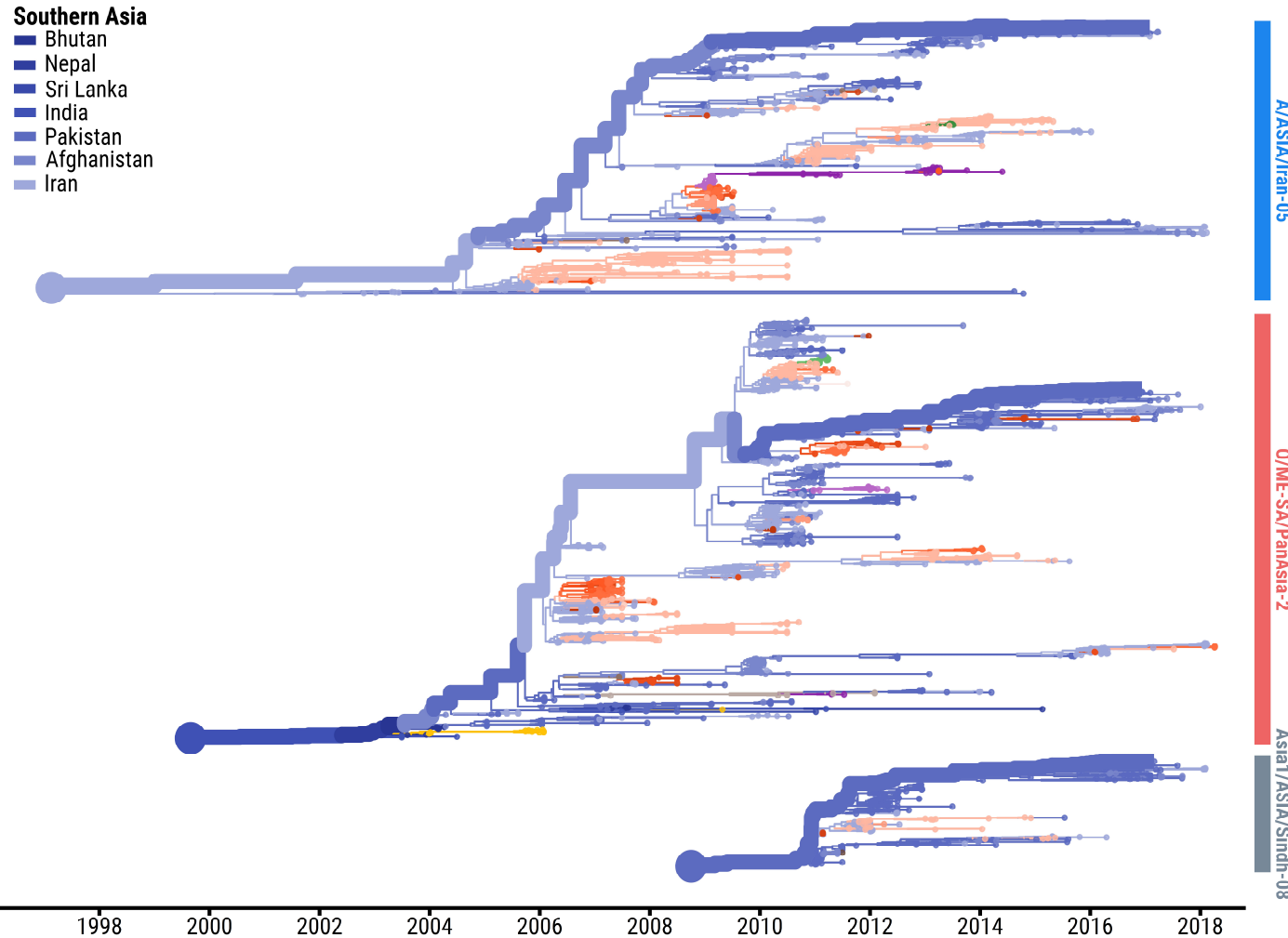
How FMDV lineages interact within the region?

Evolution and Ecosystem

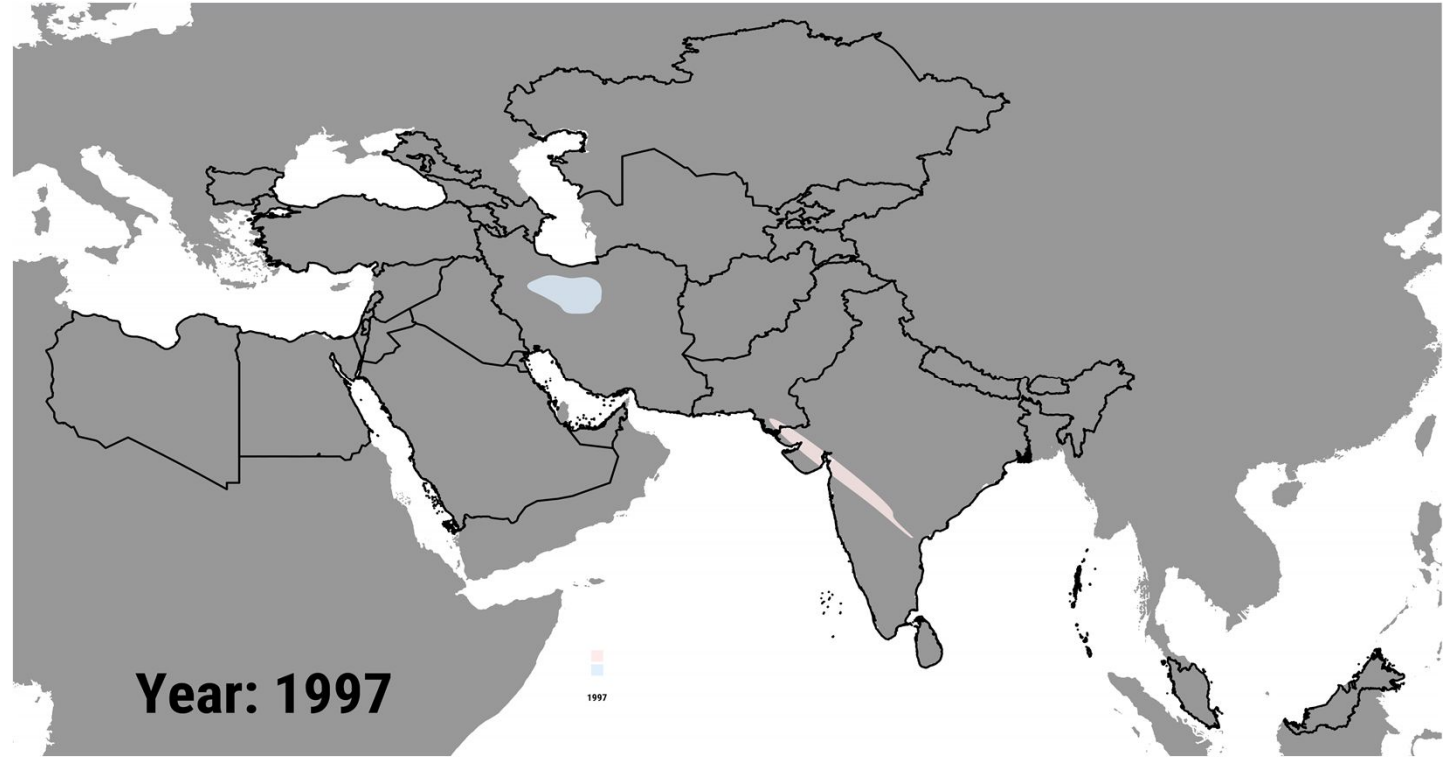
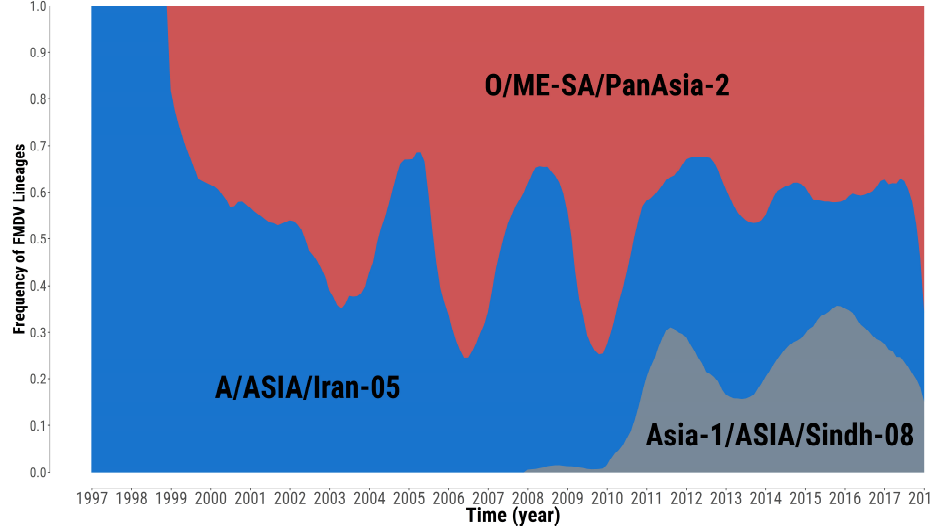
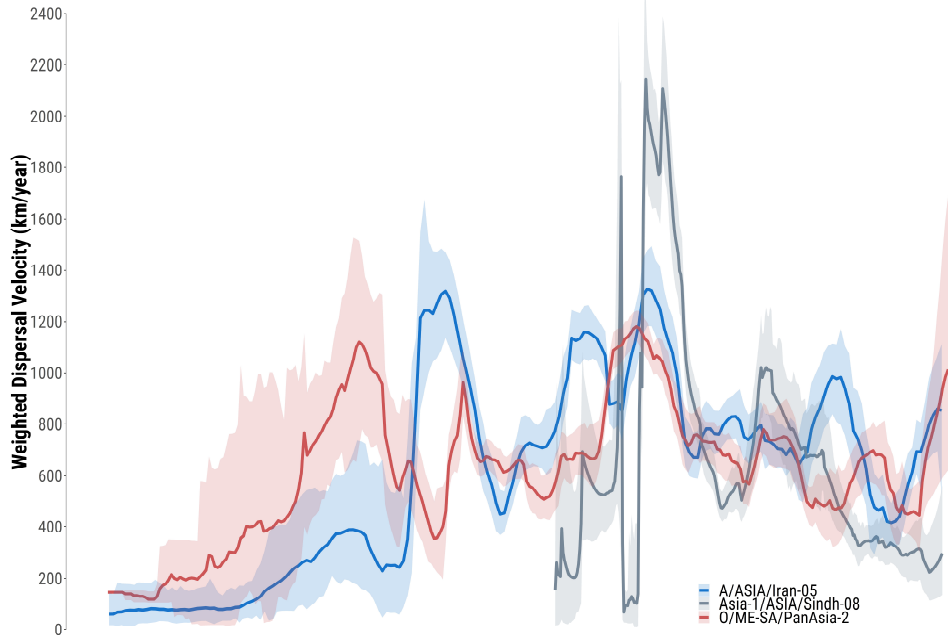


FMDV Lineages Competition

From 2002 onwards when A/Iran-05 and O/PanAsia-2 were evolutionary adapted to form cocirculation patterns within the region, evolutionary trajectories of FMDV populations reveal **cyclical dynamics of transmissions** (periodicity in lineages upsurge of ~3yrs)



FMDV Lineages Competition

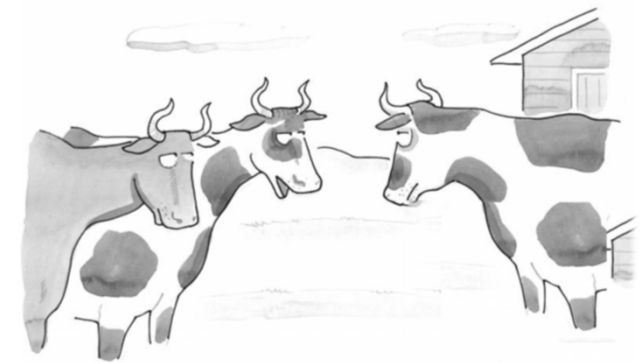


FMDV lineages competition and spatial dynamics:

- ✓ Following emergence and increasing incidence, FMDV lineages **rapidly move** across the region
- ✓ Spatial diffusion wavefront of ~ 730 km/year

How host species drive FMDV evolution?

Virus Fitness Within- and Between- Host



* WE USED TO LIVE IN CONNECTICUT
BUT THEN WE MOVED TO VERMONT. I HAVE NO IDEA WHY. "

Geoffrey

Virus-Host Interface

FMDV persistence in different host species varies according to the transmitting serotype:

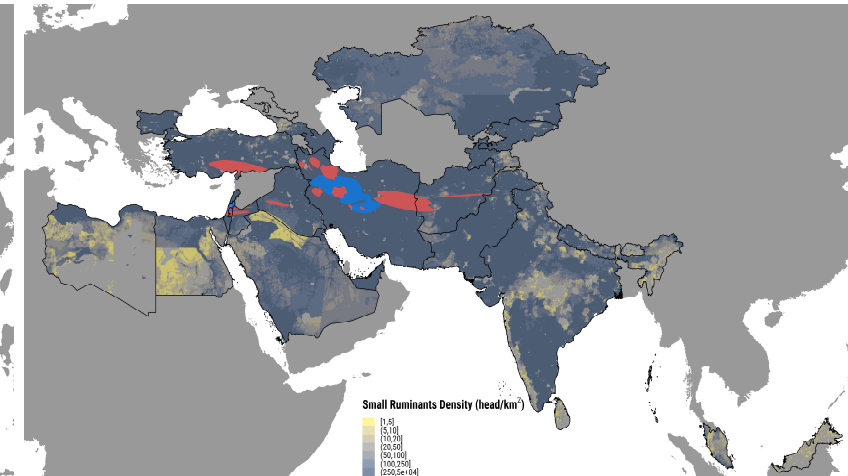
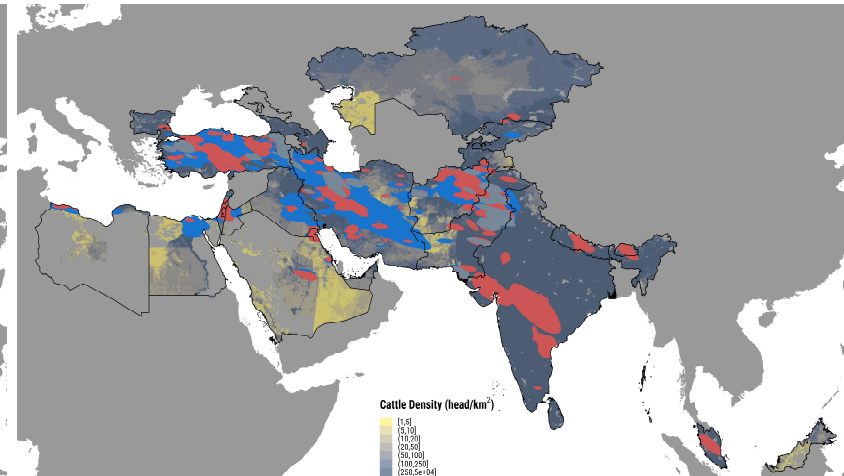
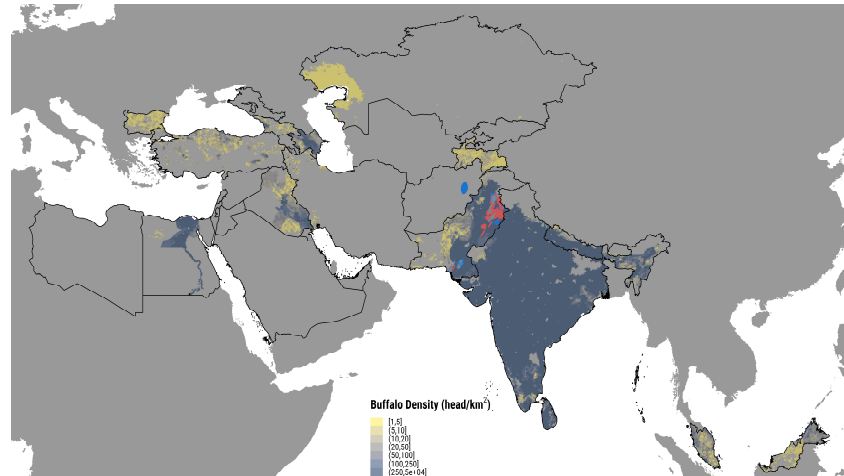
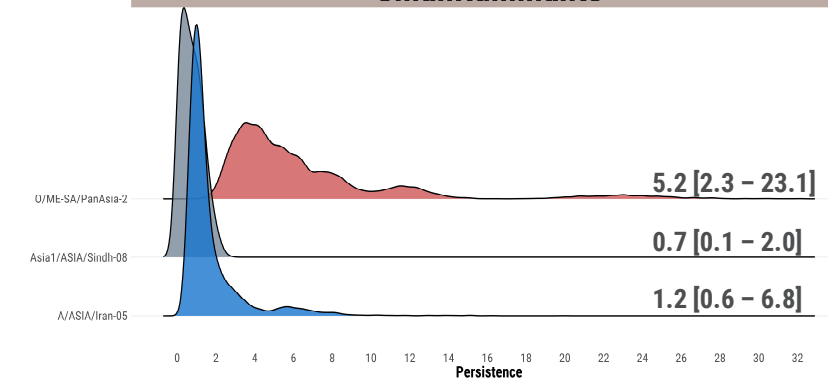
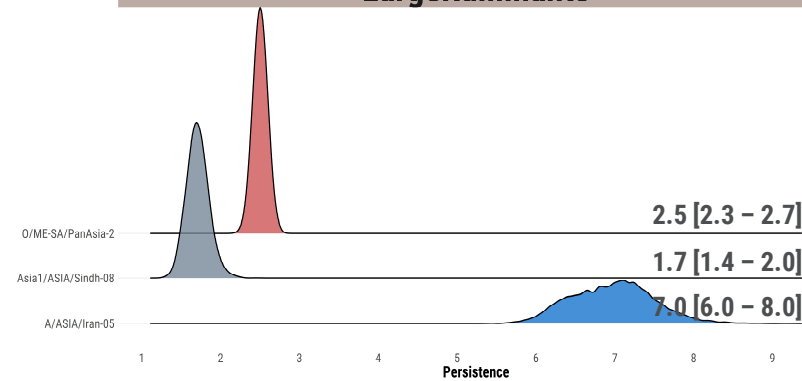
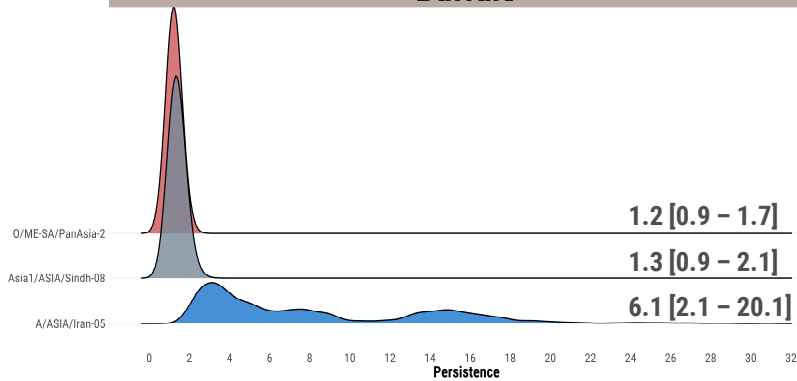
Cattle: longer within A/Iran-05 infected populations, differently O/PanAsia-2 lineage shows markedly short durations

Small Ruminants: duration of virus persistence is longer in populations infected by O/PanAsia-2 as compared with A/Iran-05

Buffalo

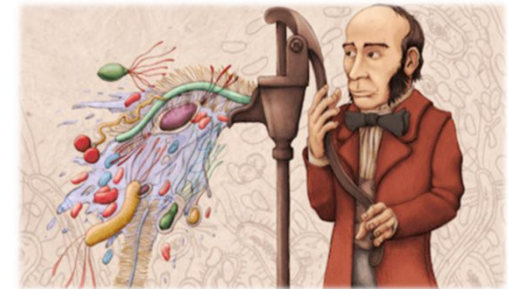
LargeRuminants

SmallRuminants



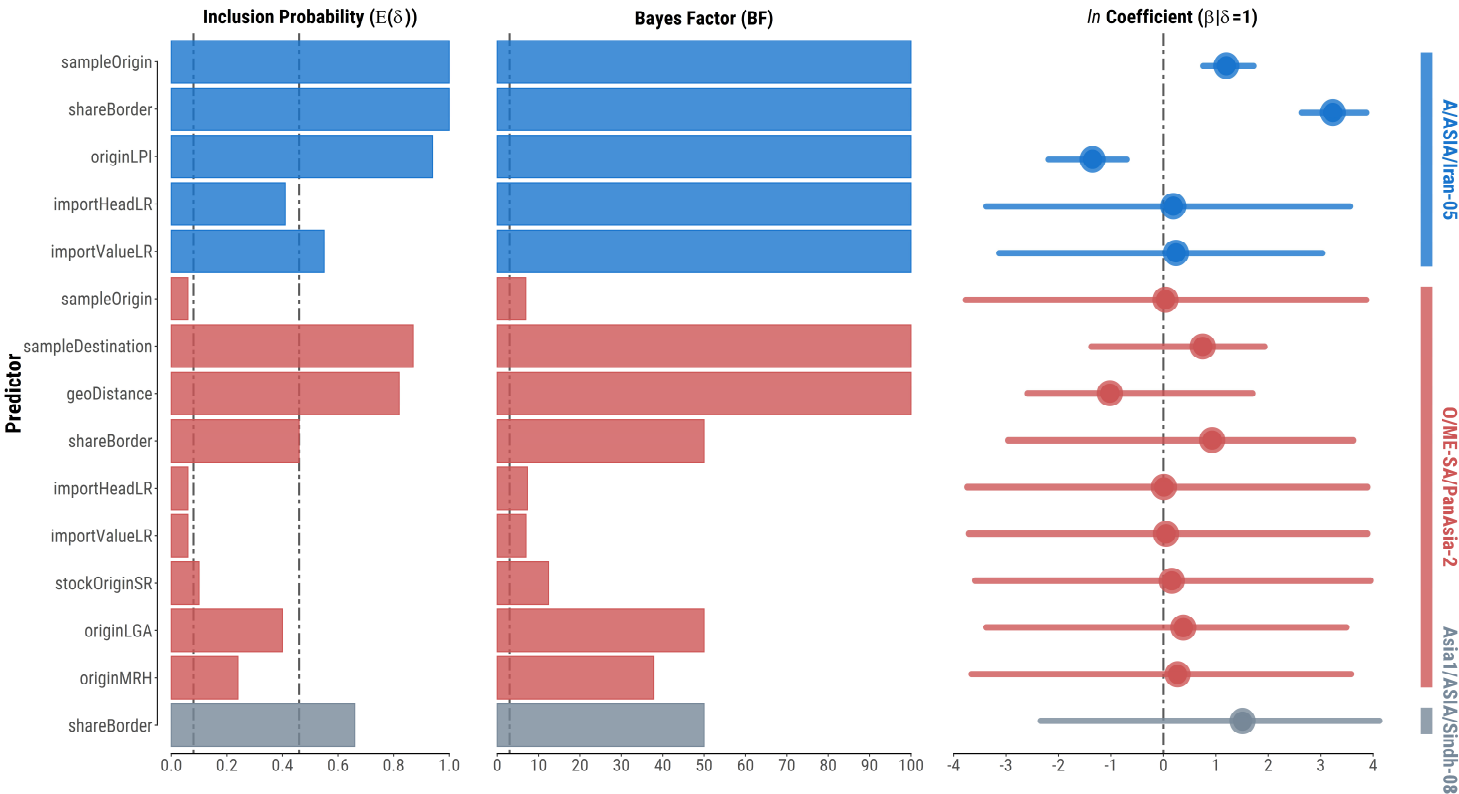
What drives FMDV transmission in the region?

Covariates of Virus Diffusion



Drivers of Virus Diffusion

Epidemiological factors associated with FMDV dispersal identified by Phylogenetic GLM



- ✓ FMDV is more likely to **move directly across borders**
- ✓ Livestock movements (i.e. **cattle import**) drives infections
- ✓ Presence of **large populations of small ruminants** might increase endemicity
- ✓ Virus diffusion might be eased within **livestock production** of:
 - Arid and semi-arid tropics and sub-tropics grassland-based system (LGA)
 - Humid and sub-humid tropics and sub-tropics rain-fed system (MRH)

Discussion



FMDV evolutionary dynamics in Western, Central and Southern Asia regions is defined as a complex process of competition between spatially structured FMDV populations evolving within an epidemiologically balanced ecosystem of coexistence between different FMDV serotypes

Findings:

- ✓ FMDV diffuse across the entire regions along well-defined transmission routes, with movements of viruses in a westerly direction accounting for 60% of the full geographic transitions reconstructed
- ✓ Southern Asia (Pakistan, Afghanistan and Iran) identified as having a key role in the regional diffusion of viruses
- ✓ Evolutionary trajectories of FMDV populations revealed cyclical dynamics of transmissions by alternating serotypes, with infections sustained by single lineages predominating at time intervals (~3yrs)
- ✓ Evidence of relative fitness of FMDV lineages (serotypes) on host populations
- ✓ Geographic, host population, economic and trade factors that likely contribute to the spread of FMDV at a regional level and beyond have been identified

Problems:

- ✓ Sampling bias due to poor epidemiological resolution in some countries/areas
- ✓ VP1 only...analysis of WGS biased by recombination: whole FMDV capsid (P1) sequences?

Acknowledgments

Countries submitting samples to the WRLFMD

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