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Evolution of antigenic and genetic characteristics of foot-and-mouth disease virus serotype A circulating in Thailand, 2007–2019

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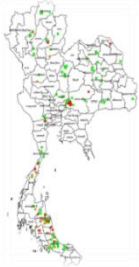
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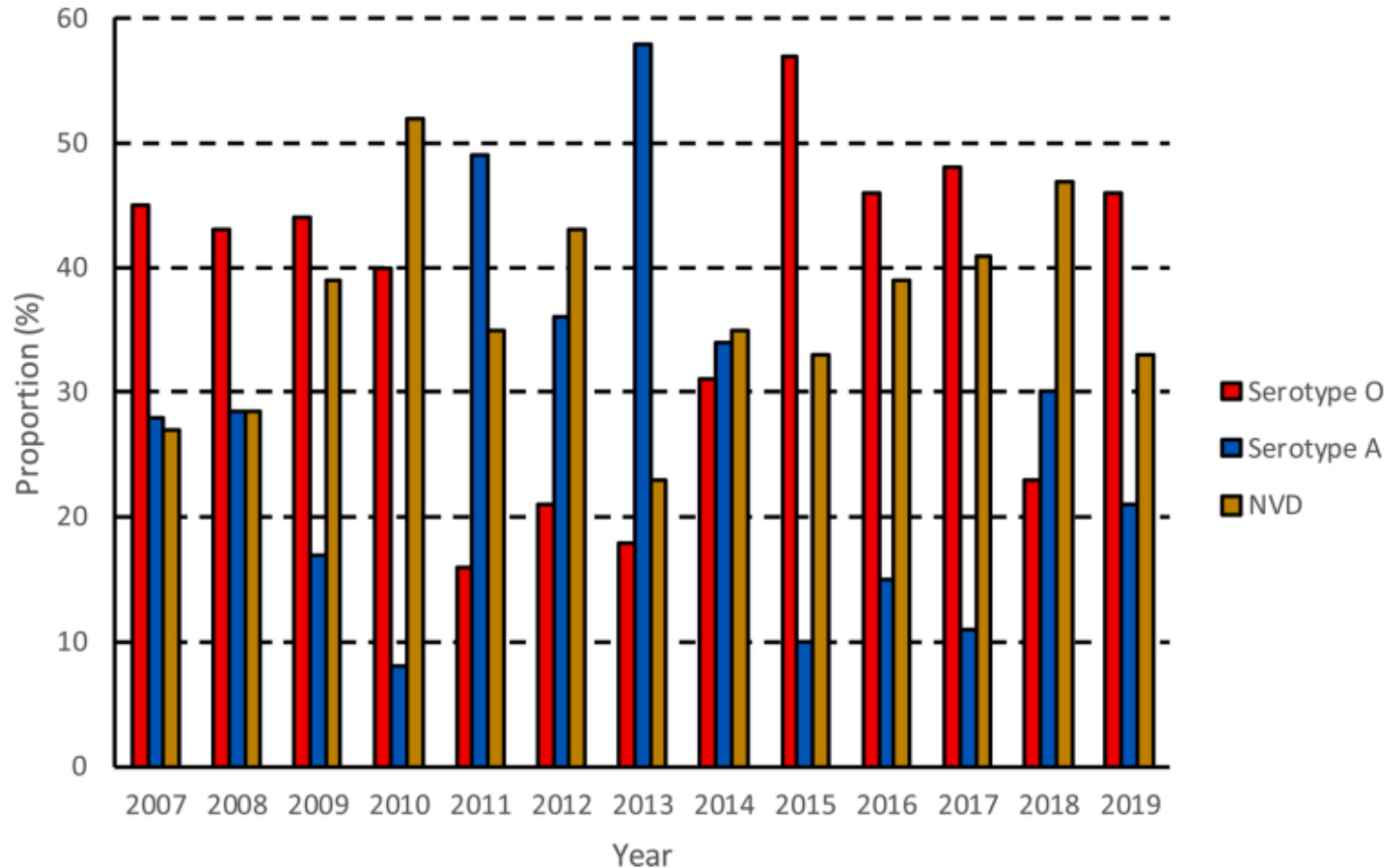
Reported by Regional Reference Laboratory For FMD in SEA, Pakchong, Nakhonratchasima, Thailand



- Thailand has occurred FMD detected more than 60 years ago that is a significant economic concern for livestock productivity. The impacts from outbreaks of FMD have resulted in the slaughter of millions of animals and make constraints to international trade in livestock and livestock product.

[illegible]

Frequencies of FMDV detection in tissue samples collected in the field in Thailand during 2007–2019.



OBJECTIVE

To generate information on the antigenic and genetic variations of FMDV serotype A and its prevalence in Thailand from 2007 to 2019

Basis of virus transmission.

Facilitate the development of planning control strategies

Selection of appropriate vaccine strains for effective control of FMD

METHOD

Antigenic Study

- **Vaccine Matching (r-value)**
 - The serotypes of specimens from field outbreaks in Thailand during from 2007 to 2019 were identified using an ELISA.

Genomic Study

- Nucleotide sequence and phylogenetic analyses of the VP1 region
- Whole L-fragment genome sequencing

RESULTS

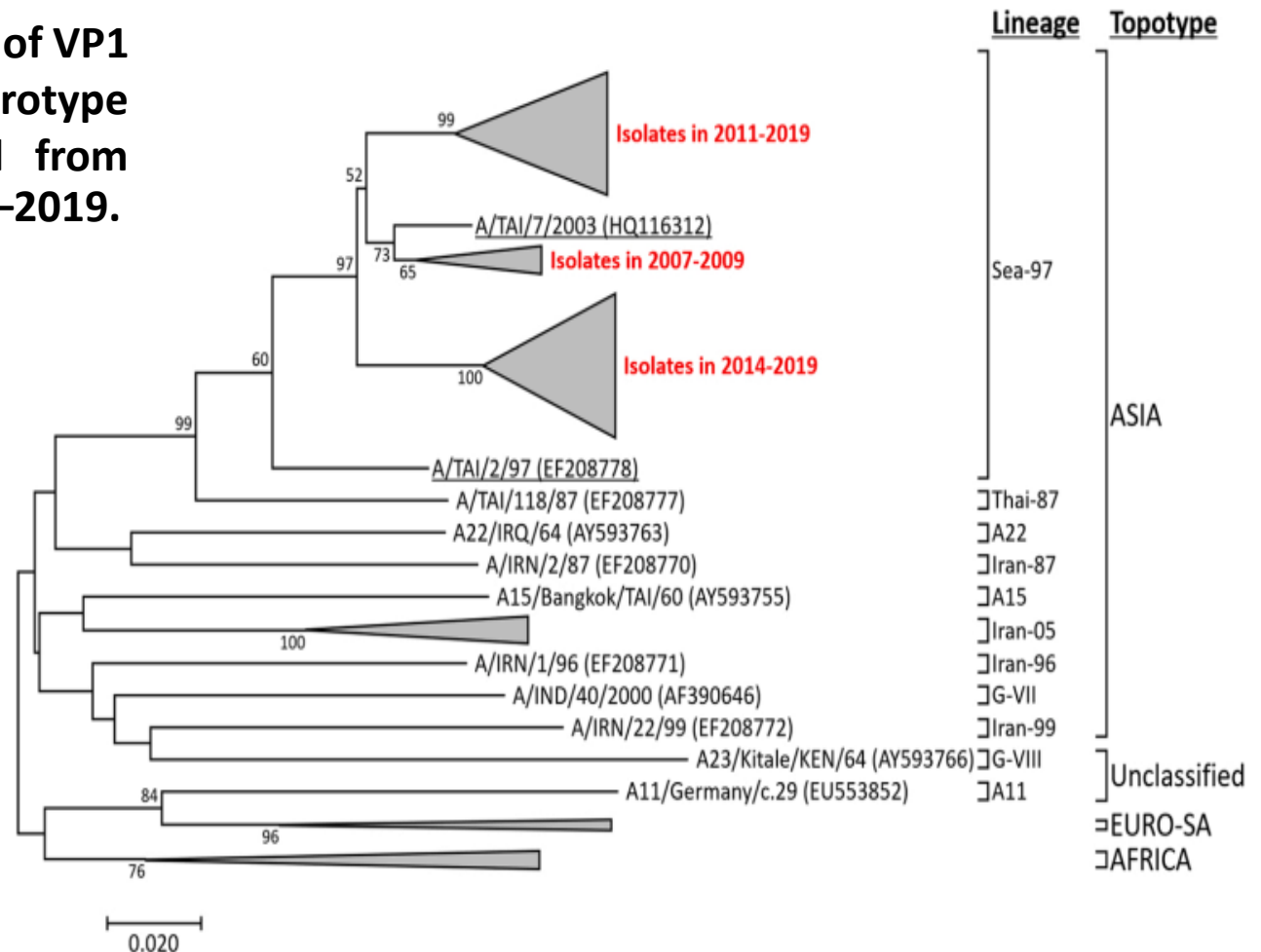
Serological relationships between FMDV field isolates and vaccine strains.

Year	Vaccine strain		
	A/118/87	A/Sakolnakorn/97	A/Lopburi/2012
2007	87.50	25.00	25.00
2008	100	69.23	30.77
2009	0	0 ^a	0 ^a
2010	0	100	100
2011	0	81.25	93.75
2012	0	0	75.00
2013	0	62.50	100
2014	0	100	100
2015	0	80.00	90.00
2016	0	100	44.44
2017	0	69.23	30.77
2018	0	75.00	100
2019	0	30.30	93.93

Frequencies (%) of isolates with r-value ≥ 0.4 (Good matching) compared with three vaccine strains. a Moderate matching. Shaded boxes indicate frequencies $\geq 65\%$.

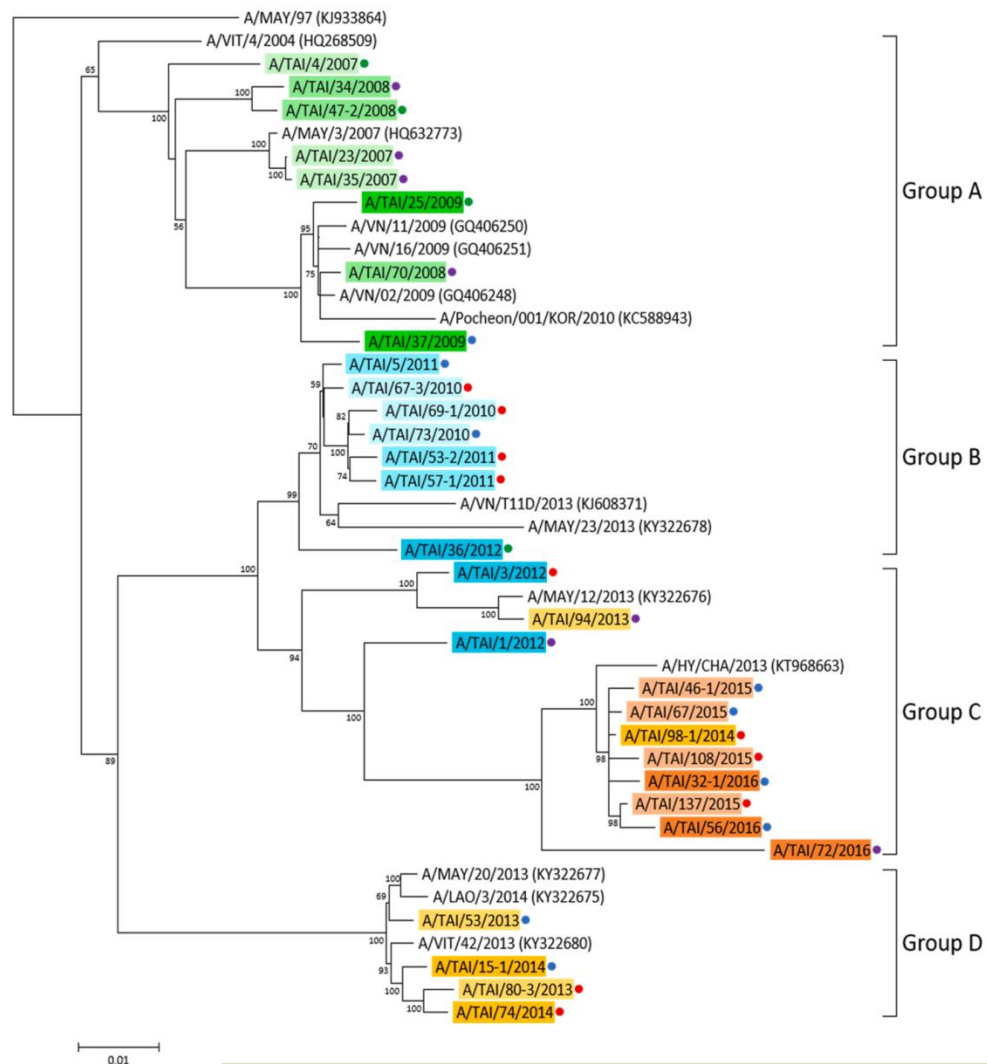
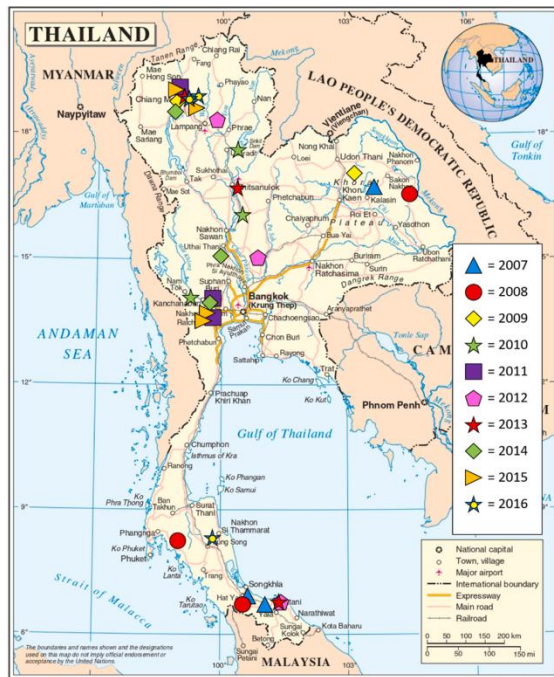
RESULTS

- Phylogenetic analysis of VP1 sequences of FMDV serotype A that were isolated from outbreaks during 2007–2019.



RESULTS

- Phylogenetic analysis of the complete L-fragment genome sequences of 30 FMDV serotype A isolates from outbreaks during 2007–2016.



Year	Color
2007	Light Green
2008	Light Green
2009	Green
2010	Light Blue
2011	Light Blue
2012	Blue
2013	Yellow
2014	Yellow
2015	Orange
2016	Orange

Region	Color
North East	Green
North West	Blue
Central	Red
South	Purple

- The highly variable regions with the lowest average identity 94.56 % which is VP1; and 78.43 %, which is 3A, respectively.

CONCLUSIONS

- FMDV serotype A isolates were collected mainly for antigenic and genetic characterization from most regions of Thailand with the goal of comprehensively protecting against and controlling FMD that from this study showed FMDV serotype A isolates from 2007 to 2019 are highly antigenically diverse, indicate that it will be difficult to control the disease.



- Therefore, continuous and routine surveillance could be conducting combined studies of antigenic and genetic characterization to improve country control strategies.

Thank for you attention

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