



Molecular epidemiology of FMD virus serotype 0 in Thailand during 2017-2019

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Introduction

- * FMD caused by Aphthovirus:- 7 Serotypes: O, A, C, Asia1, SAT1, SAT2, SAT3
- * Only 3 serotypes were found in Thailand: O, A and Asia1
- * Asia1 was last found in Thailand in 1998 but O and A were outbreak normally
- * Previous report on FMDV serotype O in Thailand showed the common lineage-virus: O/Mya-98/SEA, O/PanAsia/ME-SA and O/CATHAY (WRL-fmd report)
- * Recent molecular epidemiological work was concerned about O new lineage (O/Ind2001/ME-SA) that commonly found in the Indian Subcontinent (Qiu et al., 2017)
- * O/Ind2001/ME-SA; (5 sub-lineage: a, b, c, d and e)

Introduction (cont.)

- * But only 2 sub-lineages, O/Ind2001d and O/Ind2001e, were found in South East Asia (Bachanek-Bankowska et al., 2018)
- * The objective of this study was performed a molecular epidemiology of FMDV serotype O for emerging or re-emerging lineage-virus outbreak in Thailand during 2017-2019

Material and Method

- * Tissue samples were collected from the field in 2017, 2018 and 2019 (152, 276 and 51 samples, respectively)
- * All samples were tested by qRT-PCR and ELISA typing to confirm FMDV and serotyping
- * Total 57 samples of FMDV serotype O were used for nucleotide sequencing investigation
- * RNA extraction by Trizol[®]LS Reagent (AMBION, USA)
- * one-step RT-PCR and VP1 region sequencing by one-step reagent (LightCycler[®], Roche) with 1C609 and NK61 primers (Knowles and Samuel, 1988; Knowles et al., 2016)

Material and Method (cont.)

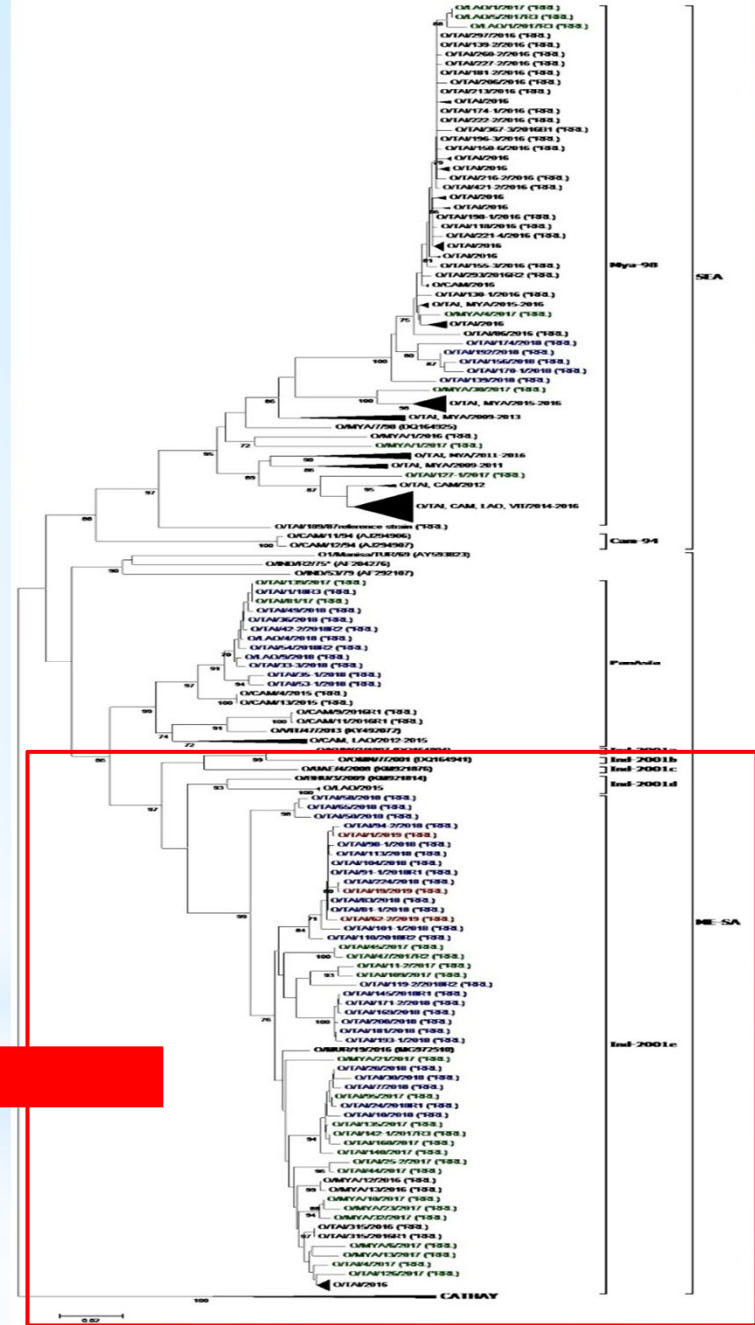
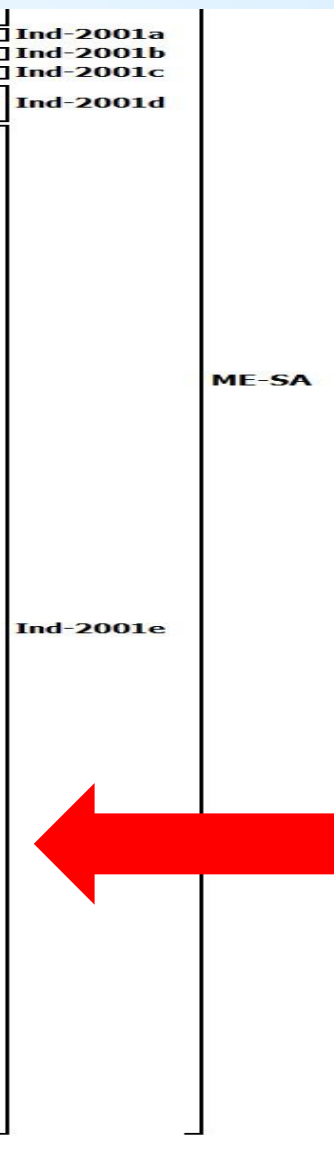
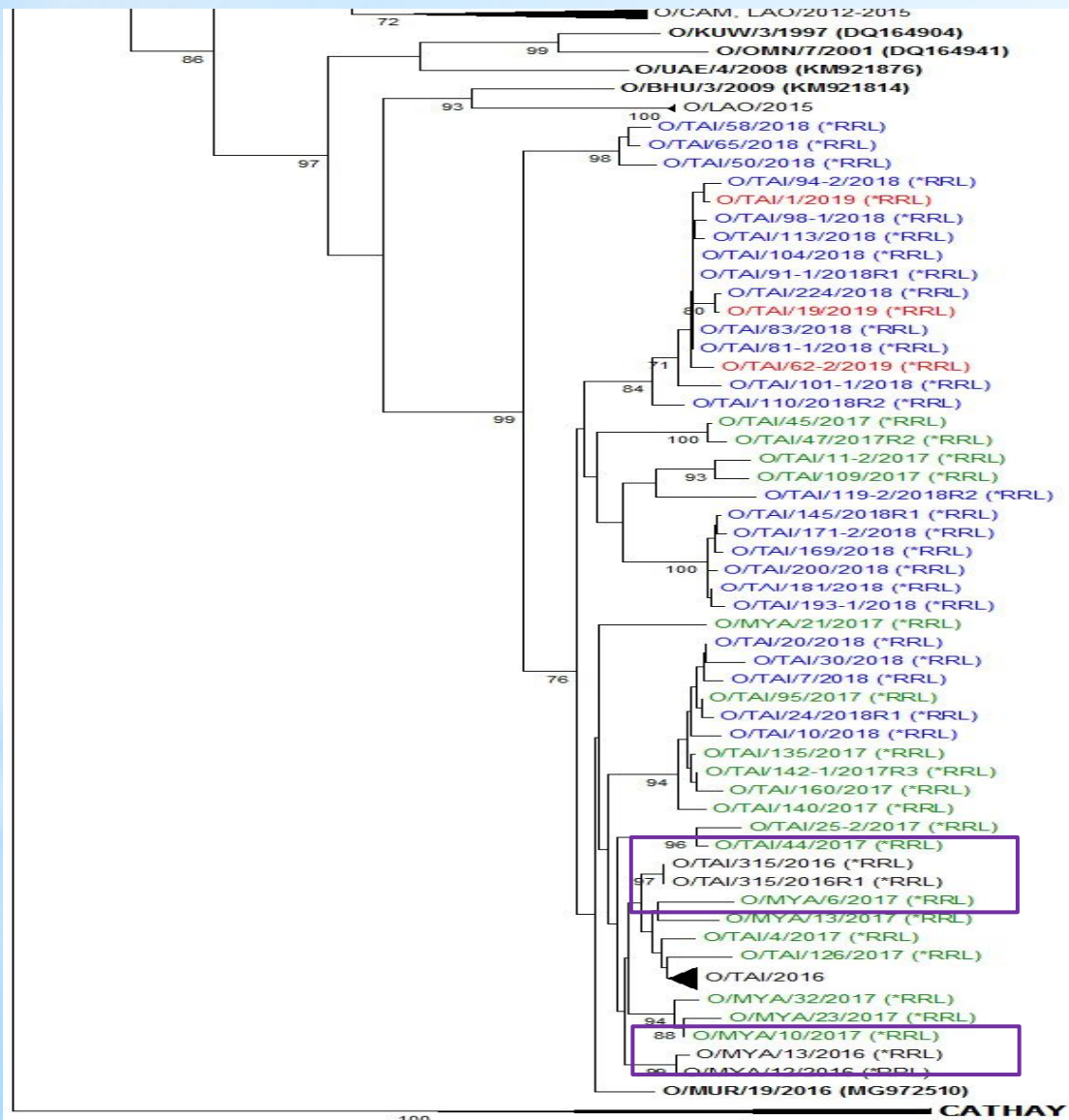
- * PCR product was purified with QIAquick PCR purification kit, and labeled with BigDye[®] terminator v3.1 cycle sequencing kit and NK72 primer.
- * Excess BigDye[®] terminator was removed by Centri-Sep[™] columns. The labeled sample was dried, resuspended with HiDi formamide and then subjected to nucleotide sequencing by using ABI3500 Genetic Analyzer.
- * Phylogenetic analysis: using BioEdit software version 7.2.5.
 - Phylogenetic analysis based on the multiple alignment using MEGA software version 6.0 by the neighbor-joining method with 1,000 replications of bootstrap values

Result

- * The phylogenetic tree showed three lineages of FMDV serotype O (Ind2001e/ME-SA= 41 samples, PanAsia/ME-SA= 10 samples and Mya-98/SEA= 6 samples)
- * O/Ind2001e/ME-SA was predominant and these virus isolates were closely related to O/ME-SA/Ind2001e samples from Thailand and Myanmar in 2016
- * O/PanAsia/ME-SA virus isolates were closely related to sample from Cambodia in 2015
- * O/Mya-98/SEA virus isolates looked like the previous virus isolates in Thailand in 2016

Phylogenetic tree

O/Ind2001e/ME-SA in Thailand 2017-2019

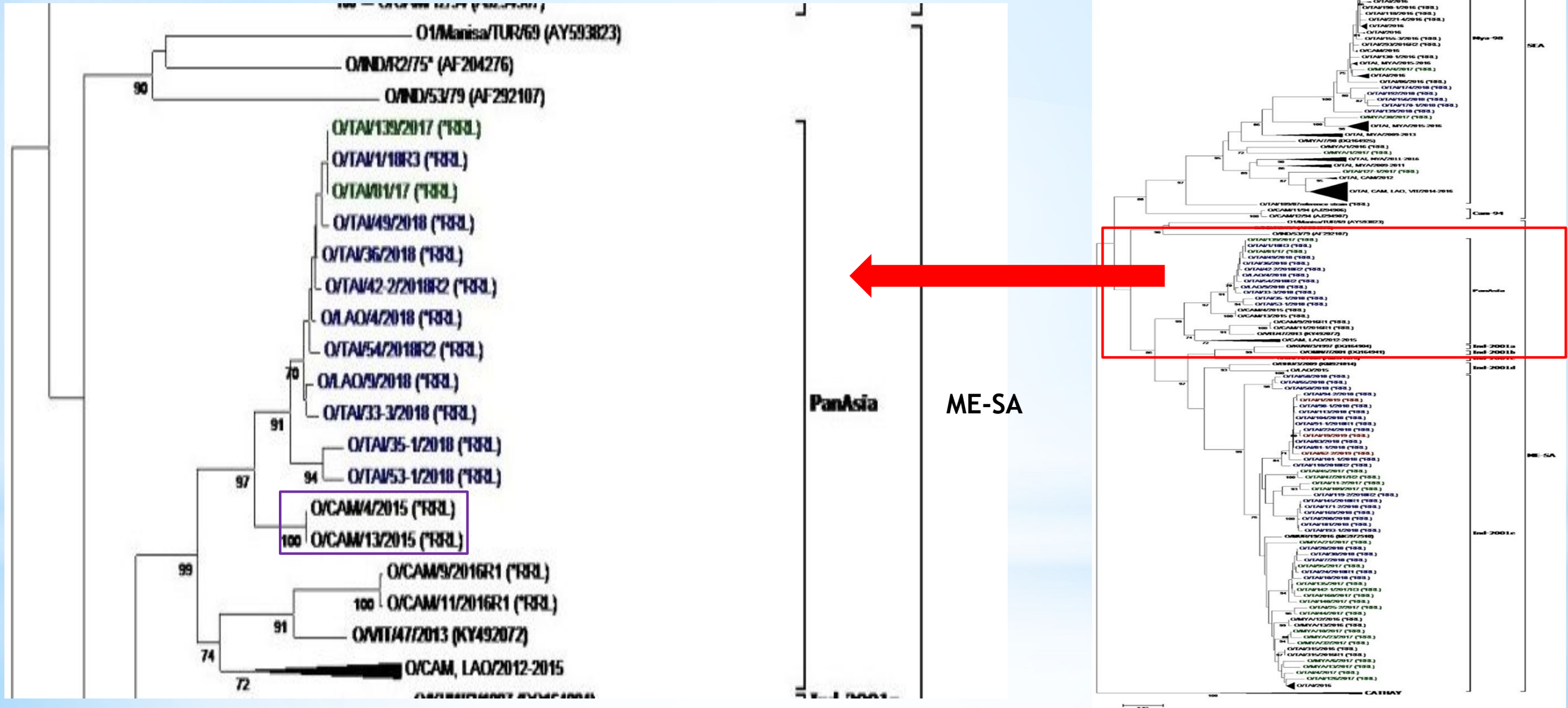


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Phylogenetic tree

O/PanAsia/ME-SA in Thailand 2017-2018

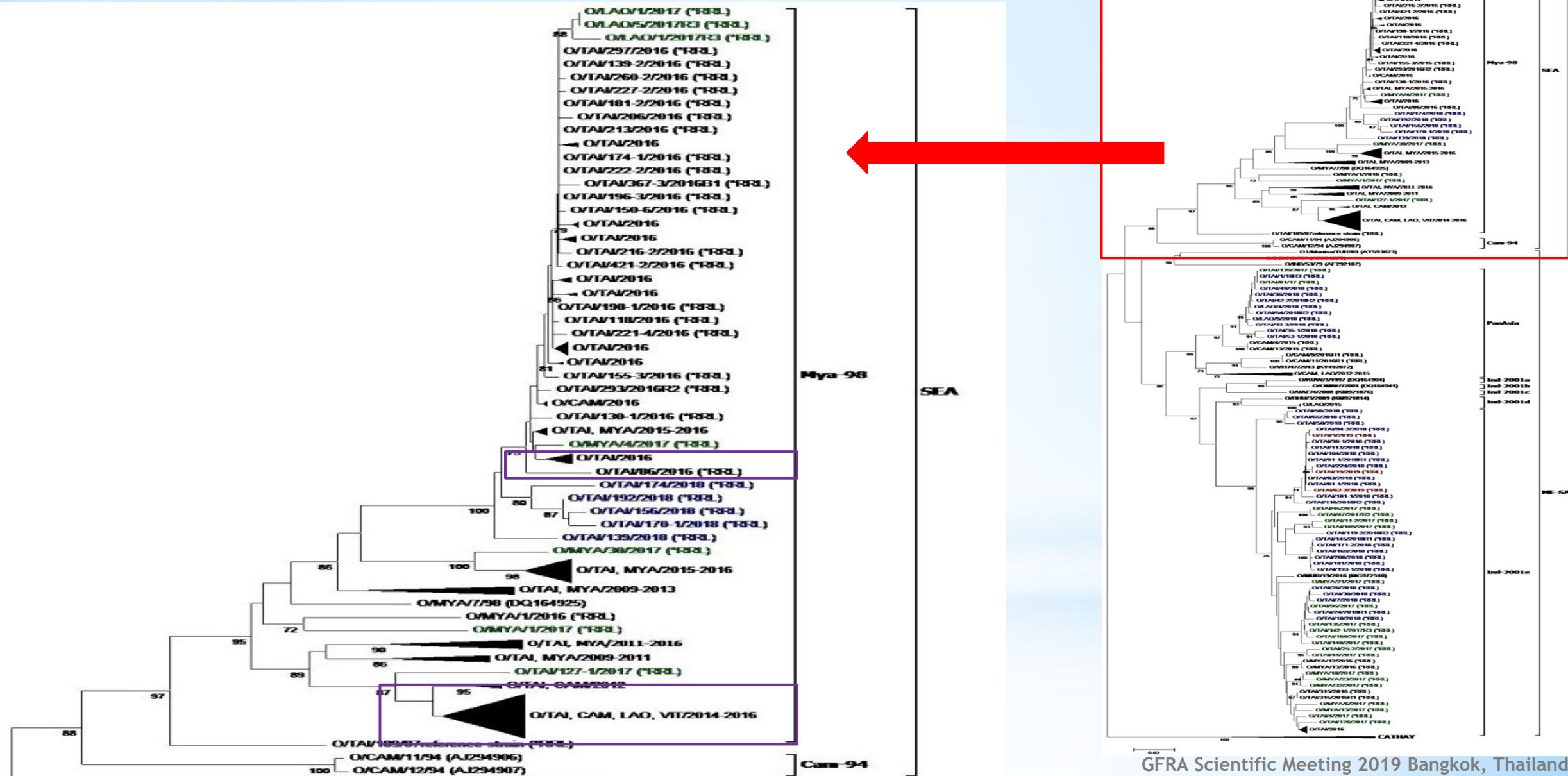


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Phylogenetic tree

O/Mya-98/SEA in Thailand 2017-2018



Conclusion

- * The molecular epidemiological investigation of FMDV type O, which caused the outbreaks in Thailand during 2017-2019, was found that three lineages: O/Ind2001e/ME-SA, O/PanAsia/ME-SA and O/Mya-98/SEA
- * FMDV serotype O in Thailand had genetic characterization (VP1 gene) like the previous virus isolates in SEA
- * Moreover it had to determine antigenic variation, some virus isolates with each lineage of those were tested a vaccine matching with the current Thai vaccine seed strains. The result of vaccine matching showed a good match with Thai vaccine strain (O/Udornthani/87)

Acknowledgement

- * Thank all of my staff in RRL-Pakchong, Thailand for their help to implementation of this study
- * Many thanks Dr. Wilna Vosloo to support for attending this meeting

Thank you for your attention

