

INTISARI

Identifikasi dan Karakterisasi Molekuler Virus *Foot and Mouth Disease* Berbasis Fragmen Gen VP1 pada Sapi Madura dan Sapi Peranakan Ongole di Boyolali, Jawa Tengah

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Foot and Mouth Disease (FMD) adalah penyakit vesikular menular pada hewan berkuku belah yang disebabkan oleh virus FMD. Penyakit ini bersifat akut, sangat menular, dan memiliki banyak keragaman genetik. Penelitian ini bertujuan untuk mengkonfirmasi kasus yang terdiagnosa di Boyolali pada bulan Juli 2022 sebagai infeksi FMD, melalui identifikasi dan karakterisasi molekuler berdasarkan sekuen fragmen gen VP1 virus FMD. Penelitian ini diharapkan dapat memberikan informasi mengenai prediksi serotipe, *clustering* virus, serta menambah *scientific data* molekuler virus FMD di Indonesia. Sampel penelitian berjumlah 26 ekor yang berasal dari sapi potong jenis Madura dan Peranakan Ongole yang memperlihatkan gejala klinis terindikasi FMD. Sampel dikumpulkan dari cairan vesikel sel epitel lepuh (lidah, gusi, dan langit-langit), swab oral, dan swab nasal. Sampel tersebut dilakukan *screening test* melalui metode *realtime Reverse Transcription-Polymerase Chain Reaction* (rRT-PCR) dengan target gen 3D untuk mendeteksi adanya infeksi FMD. Hasil uji rRT-PCR menunjukkan sebesar 46,15% (12/26) sampel yang diperiksa positif virus FMD. Sampel-sampel positif FMD hasil rRT-PCR, dilanjutkan karakterisasi molekuler dengan sekuensing *deoxyribonucleic acid* (DNA) berbasis teknik *Sanger* dengan gen target VP1 virus FMD. Analisis hasil sekuensing DNA meliputi penyusunan basa-basa nukleotida, pensejajaran nukleotida, prediksi asam amino, jarak genetik, dan rekonstruksi pohon filogenetik menggunakan *software* MEGA X. Hasil penelitian ini menunjukkan bahwa sapi Madura dan Peranakan Ongole yang terkonfirmasi terinfeksi virus FMD melalui pengujian molekuler menggunakan teknik rRT-PCR maupun sekuensing DNA, mengalami gejala klinis yang sama antara lain hipersalivasi, disfagia, serta terbentuk lesi atau vesikel pada mulut dan kaki yang khas dan parah. Hasil analisis filogenetik menunjukkan bahwa virus-virus FMD yang terdeteksi pada penelitian ini teridentifikasi FMD serotipe “O”, topotipe “*Middle East South Asia* (ME-SA)”, *lineage* “Ind-2001”, dan *sublineage* “e” atau disingkat O/ME-SA/Ind-2001e, yang memiliki homologi tinggi pada gen VP1 (99-100%) antar virus-virus yang diteliti maupun terhadap virus-virus yang ditemukan pada awal wabah FMD di Indonesia pada tahun 2022.

Kata kunci: *Foot and Mouth Disease*, serotipe O, karakterisasi molekuler, analisis filogenetik, gen VP1

ABSTRACT

Identification and Molecular Characterization of *Foot and Mouth Disease* Virus Based on VP1 Gene Fragments in Madura Cattle and Ongole Crossbreed Cattle in Boyolali, Central Java

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Foot and Mouth Disease (FMD) is an infectious vesicular disease of cloven-hoofed animals caused by the FMD virus. This disease is acute, highly contagious, and has a lot of genetic diversity. This study aims to confirm cases diagnosed in Boyolali in July 2022 as FMD infections through identification and molecular characterization based on the VP1 gene fragment sequence of the FMD virus. This research is expected to provide information about serotype prediction, virus clustering, and add molecular scientific data on the FMD virus in Indonesia. The samples used in this study consisted of 26 heads from Madura and Ongole Crossbreed cattle, which showed clinical signs of FMD. Samples were collected from the vesicular fluid of blister epithelial cells (tongue, gum, and hard palate), oral swabs, and nasal swabs. These samples were subjected to a screening test using the real-time Reverse Transcription-Polymerase Chain Reaction (rRT-PCR) method with a 3D gene target to detect FMD infection. The rRT-PCR results showed that 46.15% (12/26) of the samples were positive for the FMD virus. The FMD positive samples resulting from rRT-PCR, were followed by molecular characterization using *deoxyribonucleic acid* (DNA) sequencing based on the Sanger technique with the VP1 target gene of the FMD virus. Analysis of DNA sequencing results includes the arrangement of nucleotide bases, nucleotide alignment, amino acid prediction, genetic distance, and phylogenetic tree reconstruction using MEGA X software. The results of this study show that Madura and Ongole Crossbreed cattle, which were confirmed to be infected with the FMD virus through molecular testing using the rRT-PCR technique and DNA sequencing, experienced the same clinical signs, including hypersalivation, dysphagia, and distinctive and severe lesions or vesicles on the mouth and feet. The results of phylogenetic analysis show that the FMD viruses detected in this study were identified as FMD serotype "O", topotype "Middle East South Asia (ME-SA)", lineage "Ind-2001", and sublineage "e" or abbreviated as O/ME-SA/Ind-2001e, which has high homology to the VP1 gene (99-100%) between the viruses studied and the viruses found at the beginning of the FMD outbreak in Indonesia in 2022.

Keywords: *Foot and Mouth Disease*, serotype O, molecular characterization, phylogenetic analysis, VP1 gene