

GENETIC DIVERSITY OF BOVINE VIRAL DIARRHEA VIRUS 5'-UTR REGION FIELD ISOLATES IN DAIRY CATTLE

ABSTRACT

Bovine viral diarrhoea virus (BVDV) is genus pestivirus in the family flaviviridae. The BVDV genome is a single strand positive sense RNA molecule of approximately 12.3 kilobases in length. This genome flanked by 5' and 3' untranslated regions (UTR). BVDV caused by either BVDV-1 or BVDV-2 is responsible for significant economic losses in cattle. BVDV is endemic in many countries especially in Indonesia. Recent study reported that BVDV infection in Indonesia caused by natural infection. That result showed that P80 in severe cattle. Genetic typing of BVDV has been usually performed using sequences from the 5'-UTR. BVDV is an RNA virus with high genomic and antigenic having consequences on epidemiology, diagnosis and disease control. Genetic monitoring of circulating BVDV in Indonesia was suggested as the first step in BVDV control with the reason to update genetic typing of BVDV. The 5'-UTR nucleotide sequence analysis has been widely used for pestivirus genotype identification. The purpose of this study was identification and evaluation genetic diversity BVDV through nucleotide and phylogenetic analysis genotypes of BVDV were circulating in Indonesia. For the future will contribute to development of vaccine. Using four BVDV isolates. Singer BVDV isolate and 890 isolate is positive control of BVDV-1 and BVDV-2. Two local Indonesian isolates (CP and Ngawi). The viral RNA was extracted using RNA extraction kit and amplification of cDNA was using RT-PCR to targeted 288bp. Visualisation of product cDNA using agarose gel. To determine genetic typing by in silico using bioedit, multAlin and Mega6 software. The results showed that 2 local isolates were positive BVDV by 288 bp. The CP isolate was positive BVDV-1 and Ngawi isolate was positive BVDV-2. In general, these results indicate that BVDV-1 and BVDV-2 were circulating in Indonesia. Moreover, there is genetic diversity in Ngawi local isolate on 5'-UTR region in some position due to mutation. And then, Thus a future might be done through the development potential vaccines.

Key word: BVDV, insilico, phylogenetic, RT-PCR, 5'-UTR

RAGAM GENETIK *BOVINE VIRAL DIARRHEA VIRUS* REGIO 5'-UTR ISOLAT LAPANGAN PADA SAPI PERAH

ABSTRAK

Bovine viral diarrhea virus (BVDV) merupakan genus Pestivirus, famili Flaviviridae. Genom BVDV berupa positif untai tunggal RNA dengan panjang genom ~12,5 kb. Genom BVDV diapit oleh 5' dan 3' *untranslated region* (UTR). BVDV-1 dan BVDV-2 dapat menyebabkan kerugian ekonomi secara signifikan. BVDV endemik di berbagai negara, khususnya di Indonesia. Penelitian terbaru dilaporkan bahwa, infeksi BVDV di Indonesia disebabkan oleh infeksi alami. Hal ini dibuktikan dengan adanya P80 pada sapi yang terinfeksi BVDV. Pemetaan genom BVDV dapat menggunakan sekuen 5'-UTR. BVDV merupakan virus RNA yang memiliki keragaman genetik dan antigenik tinggi, hal ini berperan dalam kajian epidemiologi molekuler, diagnosis dan kontrol penyakit. Monitoring BVDV yang bersirkulasi di Indonesia merupakan tahap awal untuk kontrol BVDV, karena memberikan informasi terbaru terkait genotipe BVDV. 5'-UTR digunakan secara luas untuk identifikasi genotipe BVDV. Tujuan dari penelitian ini adalah mengidentifikasi dan mengevaluasi ragam genetik BVDV melalui analisis nukleotida dan filogenetik genotipe BVDV yang bersirkulasi di Indonesia. Kedepannya dapat berkontribusi sebagai upaya pengembangan vaksin. Digunakan 4 isolat BVDV, yaitu BVDV Singer dan BVDV 890 sebagai kontrol positif untuk BVDV-1 dan BVDV-2. Dua BVDV lokal (CP dan Ngawi). RNA virus diekstraksi menggunakan *RNA extraction kit* dan amplifikasi cDNA menggunakan RT-PCR. Visualisasi produk RT-PCR menggunakan gel agarose 1,5%. Penentuan genotipe BVDV secara *in silico* menggunakan Bioedit, MultAlin, dan Mega6 *software*. Hasil penelitian menunjukkan bahwa, isolat CP BVDV positif BVDV-1 dan isolat Ngawi merupakan BVDV-2. Secara garis besar mengindikasikan bahwa, BVDV-1 dan BVDV-2 bersirkulasi di Indonesia. Selain itu, terdapat keragaman genetik pada isolat lokal Ngawi pada regio 5'-UTR di posisi tertentu akibat mutasi. Kedepannya, dapat dilakukan pengembangan vaksin yang potensial untuk semua infeksi BVDV di Indonesia.

Kata kunci: BVDV, *in silico*, filogenetik, RT-PCR, 5'-UTR