

Molecular Characterization of *Rat* Hepatitis E in Rats

ABSTRACT

Background: Hepatitis E infection is a global health problem and zoonotic. Mammals that play a role as a HEV reservoir include: pigs, boars, camels, cows, buffalos, goats, sheeps, deers, foxes, minks, rabbits, and rats. RatHEV infection has been reported to infect humans. Data of rat Hepatitis E virus in Banyumas and Demak districts have not been reported. Detection of ratHEV in rat liver using the RdRp gene target in ORF 1 and characterization using the *ORF1-ORF2* junction region gene target.

Objective: The aims of study was to detect and characterize the Hepatitis E virus from rat liver in Banyumas and Demak districts.

Method: The sample of study was rat liver samples in RNA taken from spot survey of the Institute Vector Reservoir Control Research and Development Salatiga. RatHEV genome amplification was performed by nested-PCR. Data analysis used comparative from GenBank database. Phylogenetic trees were constructed using Mega 6 program.

Results: ratHEV were detected in rat from Banyumas (1,34%) and Demak (1,5%). ratHEV were detected in *Rattus norvegicus* and *Rattus tanezumi*. The results showed that ratHEV from Banyumas and Demak had 75,3-93,8% nucleotide similarities and 89%-99,6% amino acid similarities with sequences from GenBank. RatHEV from Banyumas had highest similarity (93,8%) with ratHEV from Solo (ratESOLO-006SF). While ratHEV from Demak had highest similarity (91,4%) with ratHEV from Solo (ratESOLO-014SF and ratSOLO-061). Analysis of phylogenetic showed that the ratHEV strain from Banyumas was closer to the ratHEV from Solo, Germany, France, and Belgium. RatHEV strain from Demak was closer to ratHEV from Solo and Myanmar.

Conclusion: Nested-PCR using the RdRp gene target and the ORF1-ORF2 junction region was able to detect ratHEV in *Rattus norvegicus* and *Rattus tanezumi*. ratHEV from Banyumas had similarity with ratHEV from Solo, Germany, France, Belgium and ratHEV from Demak had similarity with ratHEV from Solo, Myanmar.

Keywords: ratHEV, *RdRp*, *junction region*, nested-PCR, Banyumas, Demak

Deteksi Dan Karakterisasi Molekuler *Rat* Hepatitis E Pada Tikus

INTISARI

Latar belakang: Infeksi Hepatitis E masih menjadi masalah kesehatan global dan bersifat zoonosis. Hewan mamalia yang berperan sebagai reservoir HEV antara lain: babi, babi hutan, onta, sapi, kerbau, kambing, domba, rusa, rubah, mink, kelinci, dan tikus. Infeksi *ratHEV* telah dilaporkan menginfeksi pada manusia. Data mengenai Hepatitis E virus pada tikus belum pernah dilaporkan di Kabupaten Banyumas dan Demak. Deteksi *ratHEV* pada hati tikus menggunakan target gen *RdRp* pada ORF 1 dan dan karakterisasi menggunakan target gen *junction region* ORF1-ORF2.

Tujuan: Penelitian ini bertujuan untuk mendeteksi dan mengkarakterisasi Virus Hepatitis E dari hati tikus di kabupaten Banyumas dan kabupaten Demak

Metode: Sampel penelitian yang digunakan adalah hati tikus dalam RNA *later* yang diambil dari spot survei tikus Balai Besar Penelitian dan Pengembangan Vektor dan Reservoir Penyakit Salatiga. Amplifikasi *ratHEV* dilakukan dengan *nested-PCR*. Analisis menggunakan data pembandingan dari GenBank. Pohon filogenetik dikonstruksi menggunakan program Mega 6.

Hasil: *ratHEV* terdeteksi pada tikus asal Banyumas (1,34%) dan Demak (1,5%). Tikus terkonfirmasi positif *ratHEV* yaitu *Rattus norvegicus* dan *Rattus tanezumi*. Hasil penelitian menunjukkan *ratHEV* asal Banyumas dan Demak memiliki kesamaan nukleotida dengan beberapa sekuen asal GenBank sebesar 75,3-93,8 % dan kesamaan asam amino sebesar 89%-99,6%. Isolat asal Banyumas memiliki kesamaan nukleotida tertinggi dengan sekuen *ratHEV* asal Solo (*ratESOLO-006SF*) sebesar 93,8%. Sedangkan isolat asal Demak memiliki kesamaan nukleotida tertinggi dengan sekuen *ratHEV* asal Solo (*ratESOLO-014SF* dan *ratSOLO-061*) sebesar 91,4%. Hasil analisis filogenetik menunjukkan strain *ratHEV* asal Banyumas lebih dekat dengan *ratHEV* asal Solo, Jerman, Perancis, dan Belgia. Strain *ratHEV* asal Demak memiliki kedekatan dengan *ratHEV* asal Solo dan Myanmar.

Kesimpulan: Pemeriksaan *nested-PCR* menggunakan target gen *RdRp* dan *junction region ORF1-ORF2* mampu mendeteksi *ratHEV* pada *Rattus norvegicus* dan *Rattus tanezumi*. Karakteristik sekuen *ratHEV* asal Banyumas mempunyai kesamaan dengan *ratHEV* asal Solo, Jerman, Perancis, Belgia dan sekuen *ratHEV* asal Demak mempunyai kesamaan dengan *ratHEV* asal Solo, Myanmar.

Kata kunci: *ratHEV*, *RdRp*, *junction region*, nested-PCR, Banyumas, Demak