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学位の種類	博士 (医学)
報告番号	甲第1501号
学位記番号	第1073号
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授与年月日	平成 27 年 7 月 24 日
	Characterization of Novel Entecavir Resistance Mutations (新規エンテカビル耐性株 (rtI163V/A186T) の同定とその特徴)
学位論文の題名	Journal of Hepatology, 2015 Mar 24, Epub ahead of print

BACKGROUND & AIMS:

Entecavir (ETV) is approved for the first-line treatment of chronic hepatitis B virus (HBV) infections due to a high genetic barrier, but the virus can acquire resistance to the drug. This requires lamivudine resistance mutations (LAMr) and at least one additional mutation. Here, we characterized two novel mutations, rtl163V and rtA186T, associated with viral breakthrough (VBT) in an ETV-refractory patient.

METHODS:

HBV from an ETV-refractory patient was sequenced before ETV treatment and after VBT. Newly-identified mutations (rtl163T and rtA186T) were inserted into a replication-competent clone by mutagenesis. Clones were analyzed for replication efficacy and susceptibility to ETV in vitro. Chimeric mice with human hepatocytes were inoculated with the patient's serum at VBT, and monitored for viral mutation pattern using a next-generation sequencing approach.

RESULTS:

The novel mutations, rtl163V and rtA186T were detected together with LAMr (rtL180M and rtM204V) at VBT. RtA186T plus LAMr reduced susceptibility to ETV as strongly as previously reported ETVr mutations rtS202G plus LAMr, resulting in more than 111.1-fold resistance compared with the wild-type clone. While rtl163V plus LAMr resulted in a 20.4-fold reduction. The novel ETVr mutations did not confer cross-resistance to ADV. RtA186T significantly reduced viral replication efficacy, while the rtl163V mutation rescued it. Interestingly, the viral mutation pattern in the chimeric mice indicated dominant (or selective) proliferation of a clone containing rtl163V and rtA186T mutations plus LAMr under ETV treatment. Three-dimensional docking simulation indicated that rtA186T reduced the binding affinity of the HBV polymerase to ETV. **CONCLUSIONS:**

VBT in this ETV-refractory patient is attributable to the novel ETV resistance mutations rtl163V and rtA186T. RtA186T was apparently responsible for ETV resistance but the selection of a clone with the double mutation plus LAMr suggests that rtl163V is required to sustain viral fitness. RtA186T and rtl163V should be closely monitored when chronic hepatitis B patients exhibit VBT during prolonged ETV treatment.