CONCLUSION
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In the present study the non synonymous substitutions in the positions 4476C>G, 4616A>C in the RdRp region, 107T>C, 115G>A, 341A>G in the Methyltransferase region of the non structural ORF 1 protein, 5771T>C and 5921C>T in the ORF 2 region encoding the capsid protein and insertion of one nucleotide C at position 5404 in the ORF 3 region were significantly associated with acute liver failure with HEV genotype 1. Comparison at the amino acid level revealed that H105R, D29N and V27A mutations at the methyltransferase region, C1483W and N1530T mutations in the RdRp region, both in the non structural ORF 1 region, P259S in the ORF 2 region and S108A in the ORF 3 region were significantly obtained in HEV sequences derived from ALF patients and also in pregnant patients. These mutations were also associated with the disease severity including high viral load and the final outcome of the disease in these patients. Besides, the H105R mutation was found to be associated with low viral load of the disease. The siRNA targets identified from the present study may help in designing si RNAs against HEV.

Finally, the findings from the present study exhibit the above interesting findings leading to the detection of novel mutations which might have a strong correlation with viral load during pregnancy and also with the final outcome of the disease but these findings needs to be confirmed by several in vitro mutagenesis studies which would decipher the underlying mechanism behind this disease.