



**Figure .** Molecular Phylogenetic analysis of 139 partial RdRp.280nt HEV-3 genomes sequences spanning the region Burma.M73218 : 4284-4563 nt by Maximum Likelihood method based on the Kimura 2-parameter model. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the Maximum Composite Likelihood (MCL) approach, and then selecting the topology with superior log likelihood value. A discrete Gamma distribution was used to model evolutionary rate differences among sites. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. All positions with less than 95% site coverage were eliminated. There were a total of 280 positions in the final dataset. Evolutionary analyses were conducted in MEGA6. Some subtrees are collapsed and shown as  $\blacktriangleleft$ . (\*) - reference sequence cited by Lu. Include the sequences obtained in this study (●).