



WEB FIG. 1 Phylogenetic tree of Indian mumps viruses (demarcated in pink) and WHO reference mumps virus genotypes. The tree was drawn based on entire SH gene using the neighbor-joining method of MEGA5 program. The parameter employed was Kimura 2-parameter model and the robustness of the internal branches was determined by 1,000 bootstrap replications. The horizontal length of the bar denotes percentage difference between sequences and the bootstrap numbers (%) are given at each node.