Figure 5: Phylogenetic analysis of the whole genome of the PCV2 isolates from this study with other sequences from genbank. The sequences used to build this tree are cited in Table 2. The phylogenetic tree was constructed using the Neighbour-Joining Method and the image was reduced to 45%. Isolates derived from this study are shown with the symbol ♦. The evolutionary distances were computed using the Maximum Composite Likelihood method. Analyses were conducted using Mega 5.