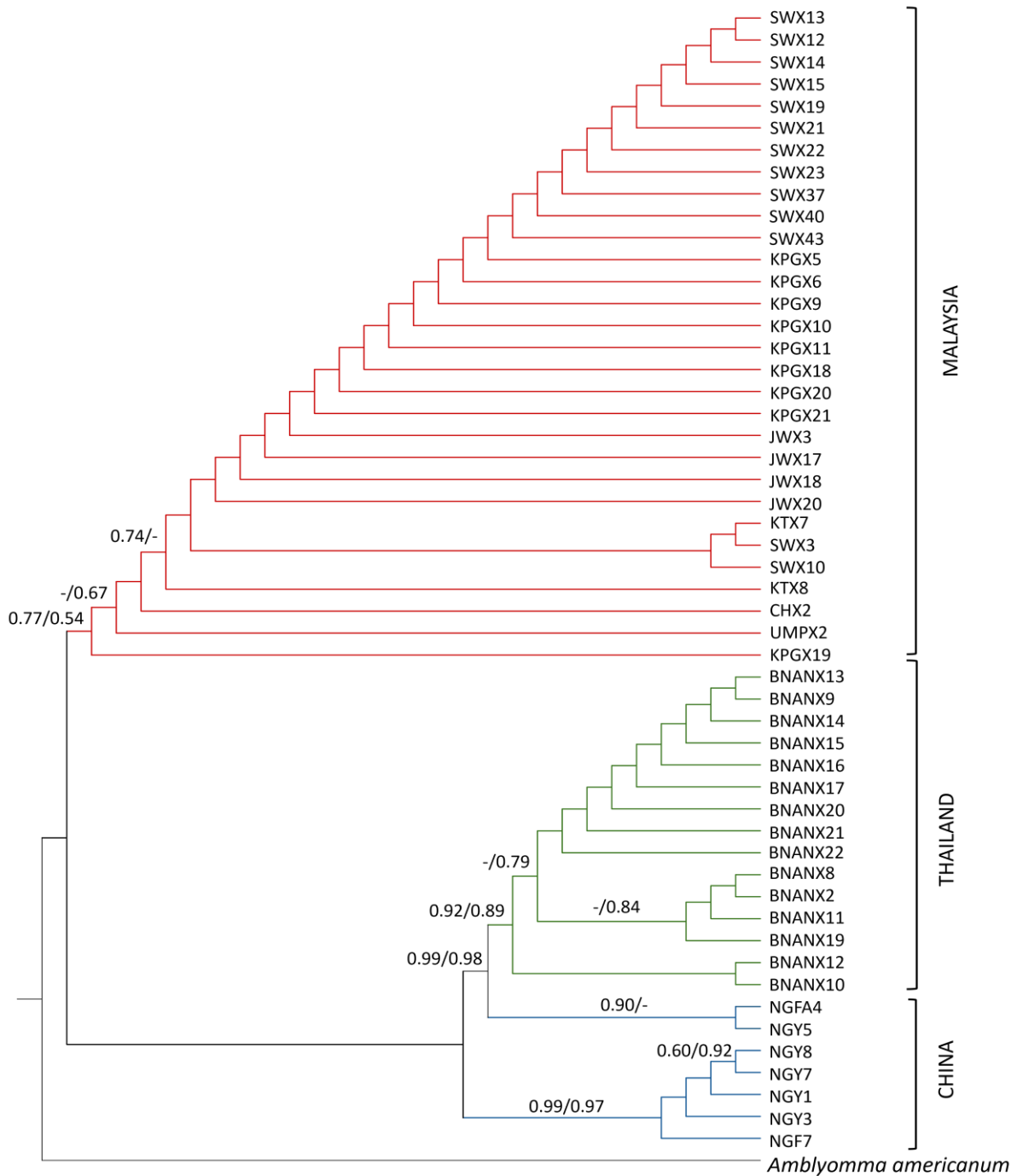


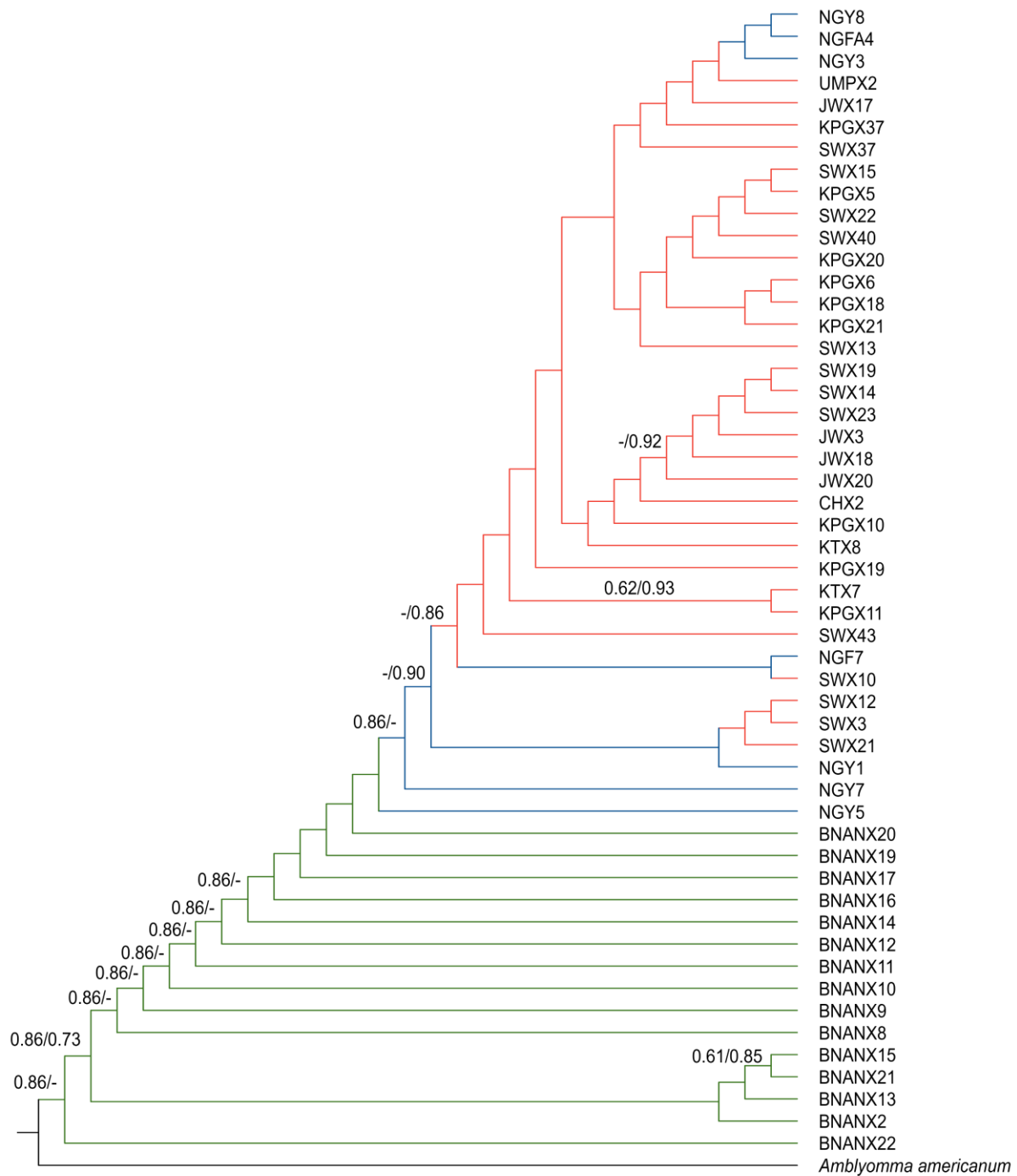
Supplementary information

Additional file 1: Fig S1.



Phylogenetic relationships among *N. gallinarum* populations from Malaysia, Thailand, and China were inferred through Neighbour Joining (NJ) and Maximum Likelihood (ML) analysis based on the sequences of mitochondrial cytochrome c oxidase subunit 1 (COI). Bootstrap values (NJ/ML) are shown on the branches. Vertical bars on the right are the population groups. Coloured branches indicate different countries, red for samples from Malaysia, green for samples from Thailand and blue for samples from China. Bootstrap values less than 0.50 are not shown in the figure.

Additional file 2: Fig S2.



Phylogenetic relationships among *N. gallinarum* populations from Malaysia, Thailand, and China were inferred through Neighbour Joining (NJ) and Maximum Likelihood (ML) analysis based on the sequences of nuclear-encoded internal transcribed spacer 2 (ITS2). Bootstrap values (NJ/ML) are shown on the branches. Coloured branches indicate different countries, red for samples from Malaysia, green for samples from Thailand and blue for samples from China. Bootstrap values less than 0.50 are not shown in the figure.