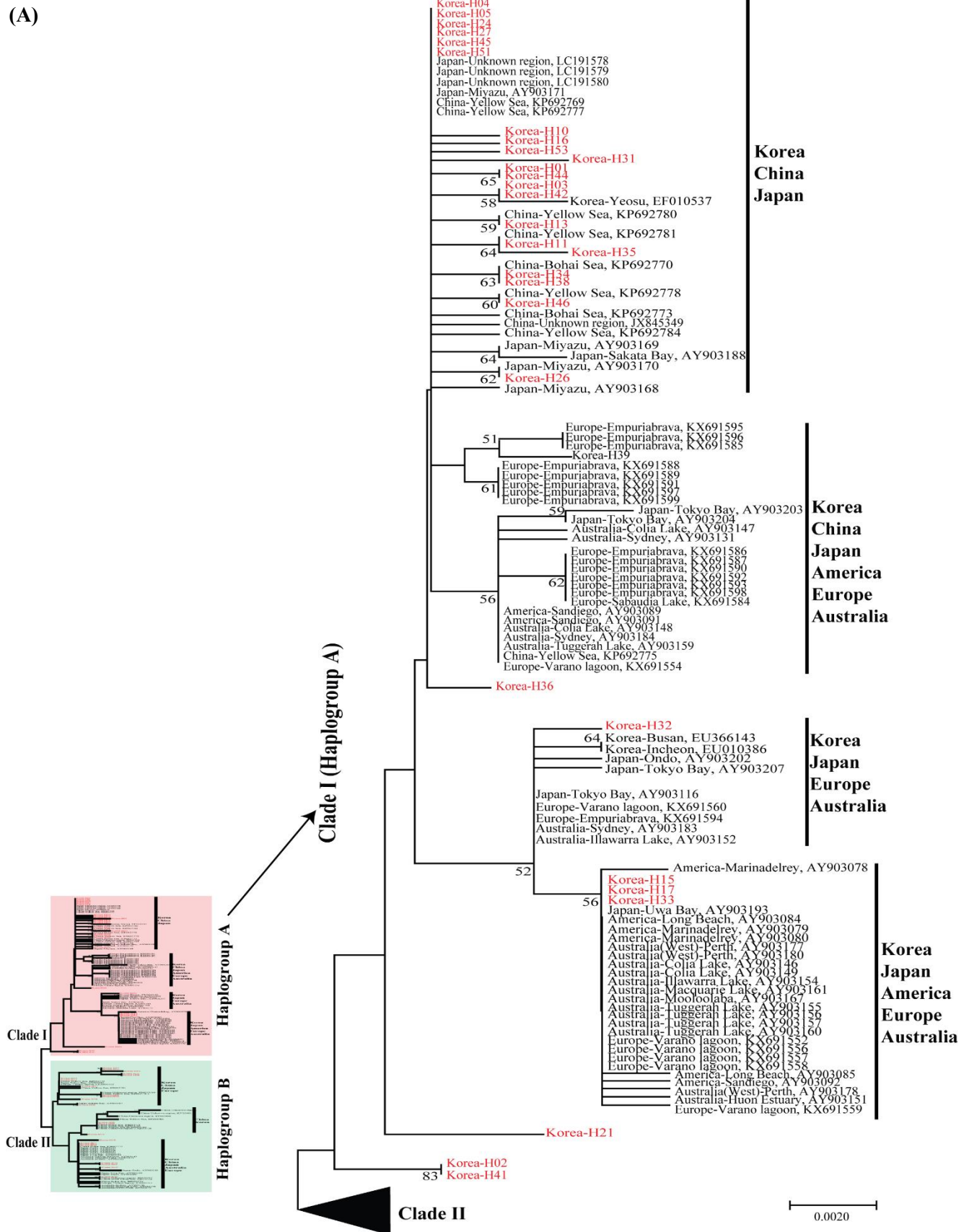


Fig. S1. Phylogenetic analysis showing the global distribution of *Aurelia coerulea* collected from Korean coasts. The tree was constructed based on the *A. coerulea* COI sequences determine in this study (marked in red) and the global *A. coerulea* (*Aurelia* sp.1) retrieved from the GenBank database. All the *A. coerulea* populations were divided into two main clades; clade I (a) and clade II (b). The tree was inferred using Neighbor-joining (NJ) computed with Kimura 2-parameter model (Kimura 1980), the taxa were clustered together on the 1000 bootstrap value and the numbers at the nodes (> 50 are shown) are bootstrap values (percentage)



(B)

