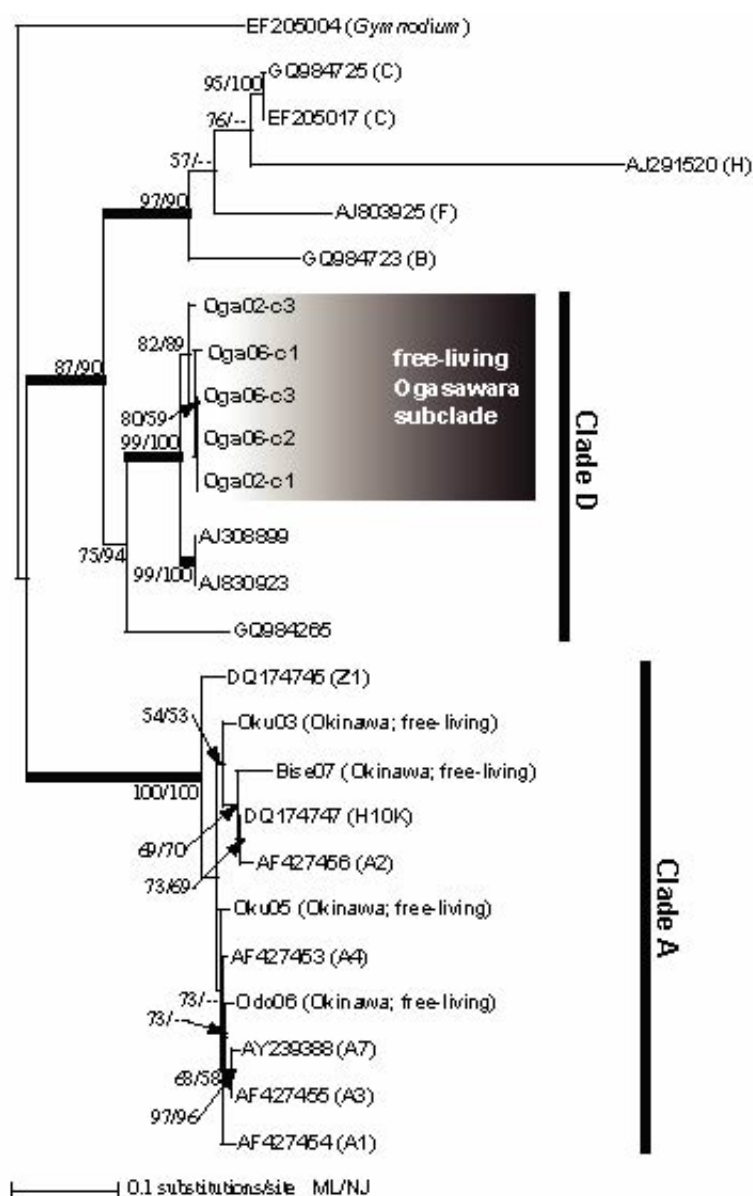# Electronic supplementary material

Figure 3 - Maximum likelihood tree of 28S ribosomal DNA (28S rDNA) sequences for Symbiodinium including specimens from this study. Values at branches represent ML and NJ bootstrap probabilities, respectively. Monophylies with more than 95% Bayesian posterior probabilities are shown by thick branches. New isolates and sequences from this study in bold. Sequences used in the alignment for this tree are in Table 1.

Fig. S1 ML tree of 28S-rDNA sequences for *Symbiodinium*, including specimens from this study. *Values at branches* represent ML and NJ bootstrap probabilities, respectively. Monophylies with more than 95% Bayesian posterior probabilities are shown by thick branches. New isolates and sequences from this study in *bold*. Sequences used in the alignment for this tree are in Table 1 (JPEG 54 kb)
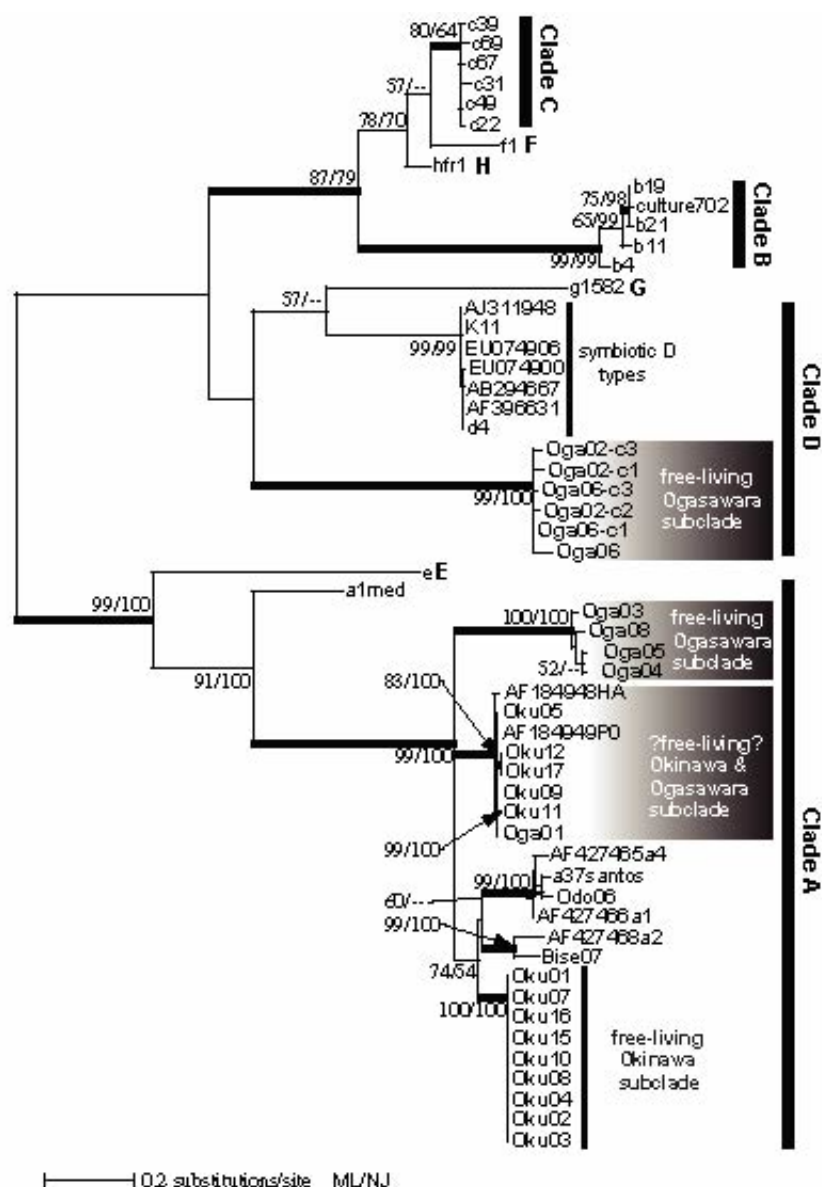
High resolution image. (EPS 338 kb)

Figure 4 - Maximum likelihood tree of the internal transcribed spacer of ribosomal DNA (ITS-rDNA) sequences for Symbiodinium including specimens from this study. Values at branches represent ML and NJ bootstrap probabilities, respectively. Monophylies with more than 95% Bayesian posterior probabilities are shown by thick branches. New isolates and sequences from this study in bold. Sequences used in the alignment for this tree are in Table 1.

Fig. S2 ML tree of the ITS-rDNA sequences for *Symbiodinium*, including specimens from this study. *Values at branches* represent ML and NJ bootstrap probabilities, respectively. Monophylies with more than 95% Bayesian posterior probabilities are shown by *thick branches*. New isolates and sequences from this study in *bold*. Sequences used in the alignment for this tree are in Table 1 (JPEG 58 kb)

High resolution image (EPS 374 kb)