Molecular phylogeny of Porites (Poritidae, Scleractinia, Anthozoa) from Japan

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Clade VIII







Background

Porites = too small morphological characters, highly variable within colony = taxonomic studies at the species level have been extremely challenging...

20 out of about 70 nominal species of Porites had been analyzed molecularly, which revealed that they were divided into 12 clades (Forsman et al. 2009).

However, many Porites species still remain unanalyzed molecularly, and none of the Japanese Porites specimens were sequenced.

P. australiensis (MIP009)

P. horizontalata (IRP27)

P. cvlindrica (IRP42)



Sampling sites

Summary

Samples were collected from tropical to temperate regions of Japan.

Four species (P. australiensis, P. heronensis, P. horizontalata, and P. nigrescens) were analyzed here for the first time.

291 sequences of ribosormal ITS, 67 sequences of Histone, and 85 sequences of mitcondrial COI from 172 samples were used for reconstructing ML trees.

A total of 13 clades were recovered, including 12 clades that had been previously reported.

P. okinawensis formed a new monospecific clade.

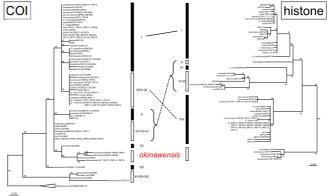
Clade I

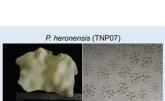
P. australiensis and P. horizontalata belong to clade I.

Clade I is the most complex clade and total 8 species were included and scattered within this clade.



ITS



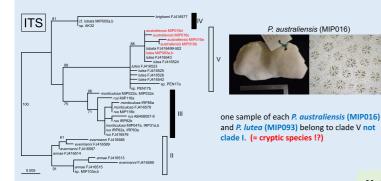




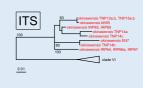
ITS clade I

P. heronensis and P. nigrescens belong to clade VIII. Many branching samples also belong to clade VIII.

Clade II - V



P. okinawensis





P. okinawensis formed a monospecific lineage in all reconstructed trees using

The sequence of "P. okinawensis" from Taiwan deposited in GenBank (FJ825142) was likely to be misidentified since this sequence belonged to clade I according to COL

Size and depth of calices of P. okinawensis were highly variable, and the number of septa was also reduced as little as 8 (most of calice had 10 septa) in P. okinawensis, while other Porites species had 12 septa.

Acknowledgements

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Methods

DNA sequences were aligned with MAFFT 7.

MEGA 7 was used to assume a model, reconstruct a ML tree, and bootstrap analyses (500 replicates).

Future studies

RAD-seq: to resolve species within a clade.

Cross-experiment: check the reproductive isolation between species within same clade.

Micromorphoogy: to detect the cryptic species and find clade-specific morphological characteristics.