MORPHOMETRIC SPECIES RECOGNITION AND PHYLOGENY RECONSTRUCTION IN
SCLERACTINIAN REEF CORALS

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Scleractinian reef corals have a number of properties that are
somewhat unique in morphometrics and therefore require methodologies
different from those used in more structurally complex, non-colonial
organisms with determinate growth. Most importantly, characters
used in species recognition occur at two levels: (1) within modules
and (2) among modules within colonies. Due to structural
constraints imposed by radial symmetry and to the fact that growth
is accomplished primarily by continuous accretion along the upper
skeletal surface, most characters at the first level are continuous
and consist either of architectural features related to corallite
size or to the upward growth of vertical structures forming the
septa and columella. Because of high environmental variability,
these features are best described using landmark based methods.
Patterns of distribution of modules across colonies are best
estimated using spatial statistics that can be related to underlying
rules of budding and overall colony shape.
    Here we demonstrate how traditional multivariate statistical
procedures can be applied to these two different levels of data to
recognize species in the common branching and massive coral Porites,
and to derive characters useful in phylogeny reconstruction.
Discrete morphologic units are first identified by subdividing
modules from the same colony into two groups of so-called "colony
halves", running cluster analysis on distances among halves, and
using the relative positions of halves from the same colony and a
modified jackknife procedure to establish cutoffs on the dendrogram
for group recognition. The resulting clusters are tested using
crossvalidation procedures in discriminant analysis which compare
classification results for corallite level and colony level data
sets, and similar results for different portions of the same
colonies. Iterative procedures are then used to maximize the
probability of correct group assignment for each colony. Using
multiple comparisons among the resulting species, a set of
independent characters that maximize group separation are selected
for use in phylogeny reconstruction. Comparison with
electrophoretic analyses on the same material shows high
correspondence in both species assignments and phylogenetic trees
based on the morphometric and allozyme approaches.