

**AAPG Annual Convention
Salt Lake City, Utah
May 11-14, 2003**

Jorge Frias-Lopez, George Bonheyo, Qusheng Jin, and Bruce W. Fouke, University of Illinois, Urbana, IL

Coral Black Band Disease: A Single Symptom Associated with Different Cyanobacteria in Widely-Spaced Ocean Basins

Black band disease (BBD) is a deadly infection that affects large framework building scleractinian corals in reefs around the world. BBD itself is a 0.5 to 1.5 cm black bacterial mat that migrates across and kills healthy coral tissue at rates that exceed 1 cm/day. Contrary to other coral diseases, BBD leaves behind dead coral tissue that is colonized by algae. This dead encrusted surface of the coral colony never recovers. As a result, BBD is a potent factor in destroying framework corals and re-structuring the benthic ecology of modern and potentially ancient coral reefs.

Although the BBD mat contains a high diversity of bacteria, it has been assumed that a single species of cyanobacteria, *Phormidium corallyticum*, is the dominant microbe in all cases of BBD in coral. *P. corallyticum* is a non-heterocystous, filamentous cyanobacterium that has not been yet been successfully cultured. In the present work we test the hypothesis that one single species of cyanobacteria is the only species associated with BBD in all ocean basins. In order to determine whether similar BBD symptoms can be associated with different bacteria in different ocean basins, BBD mats were collected from infected corals in the Caribbean and Indo-Pacific seas. Surprisingly, our analyses of bacterial 16S rRNA genes using cyanobacteria-specific primers and T-RFLP analyses show that the cyanobacteria collected in these different oceanic settings belong to at least three different groups of cyanobacteria, despite producing similar patterns and symptoms of disease outbreak. Furthermore, each of these different groups of cyanobacteria were able to infect more than one species of coral. Ongoing studies are being conducted to determine whether the the observed diversity among BBD-associated cyanobacteria is representative of coral reef ecosystems in other parts of the world. Assessing the diversity of cyanobacteria present in BBD will permit the pathogenic development and etiology of BBD infections to eventually be determined.