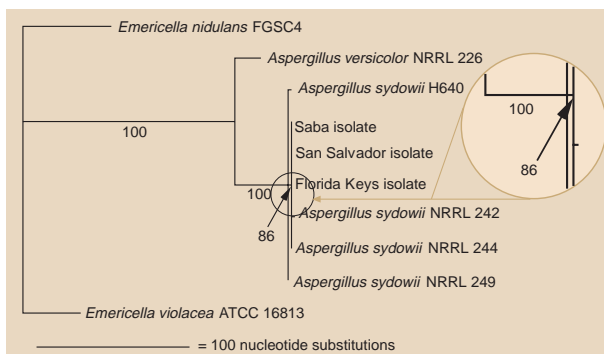


Florida, *A. sydowii* was found in both eu-littoral zones and oceanic zones, and was isolated from waters collected as deep as 4,450 m (ref. 7). Many *Aspergillus* species, including *A. sydowii*, are tolerant of salt concentrations as high as, or higher than, those found in the marine environment.

To further test the virulence of *A. sydowii*, we used isolates from non-marine environments (NRRL 242, 244 and 249) and two isolates from sea fans (those from Saba and San Salvador) to challenge small (~20 cm in height) *G. ventalina* colonies in flow-through seawater aquaria at the Bahamian Field Station in San Salvador. We directly inoculated sea fan colonies with pure *A. sydowii* cultures in separate experimental aquaria and inoculated colonies with sterile media in control aquaria. All replicates inoculated with the Saba and San Salvador isolates showed recession of coenenchyme at the point of inoculation, exposing the axial gorgonin skeleton (central core). These are typical signs of aspergillosis of sea fans<sup>2</sup>. This response did not occur in colonies inoculated with non-marine strains of *A. sydowii* or in controls. We conclude that, under these conditions, isolates of *A. sydowii* taken from diseased sea fans possess pathogenic potential not seen in isolates taken from other sources.

Several *Aspergillus* species have a tendency to be opportunistic animal pathogens, generally striking individuals with compromised immune systems. The infection of West Indian sea fans by *A. sydowii* may also be opportunistic, owing to weak

**Figure 2** Parsimony phylogenetic analysis of sequences from the 58 non-translated region of the *trpC* gene. The DNA region was amplified using the polymerase chain reaction and sequenced with the primers *trpC1* (58-GACGGGAAATAG-GCTTCC) and *trpC3* (58-CGC-CTTGGTGGGATGGTG) as described<sup>5</sup>. The aligned sequences were subjected to par-



simony analysis using the PAUP v3.11 software package (D. Swofford). One of the two equally most parsimonious trees produced (length 308 steps) is shown (consistency index 0.987, retention index 0.981). Numbers below branches represent bootstrap values, taken from 1,000 replicates. FGSC4, NRRL 226, H640, NRRL 242, NRRL 244, NRRL 249 and ATCC 16813 are isolate numbers. GenBank accession numbers: *E. nidulans*, X02390; *A. versicolor*, AF058967; *A. sydowii* H640, AF058968; Saba, AF058969; San Salvador, AF058970; Florida Keys, AF058971; NRRL 242, AF058972; NRRL 244, AF058973; NRRL 249, AF058974; *E. violacea*, AF058975.

from Israel, Canada and the United Kingdom. We found 112 compound haplotypes (see Supplementary information). Despite

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