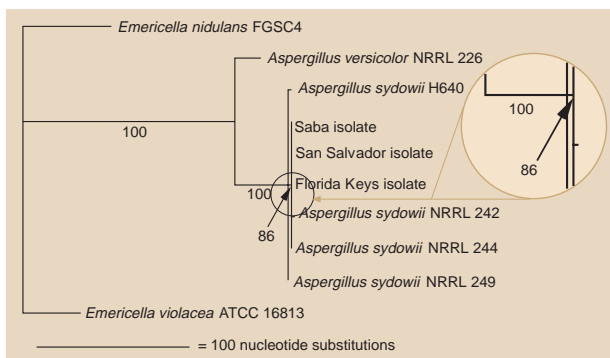


Florida, *A. sydowii* was found in both eu-littoral zones and oceanic zones, and was isolated from waters collected as deep as 4,450 m (ref. 7). Many *Aspergillus* species, including *A. sydowii*, are tolerant of salt concentrations as high as, or higher than, those found in the marine environment.

To further test the virulence of *A. sydowii*, we used isolates from non-marine environ-

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**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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