



Fig. 1. Sampling sites for *Codium* species during the Atimo Vatae expedition along the South coast of Madagascar and included in this study.

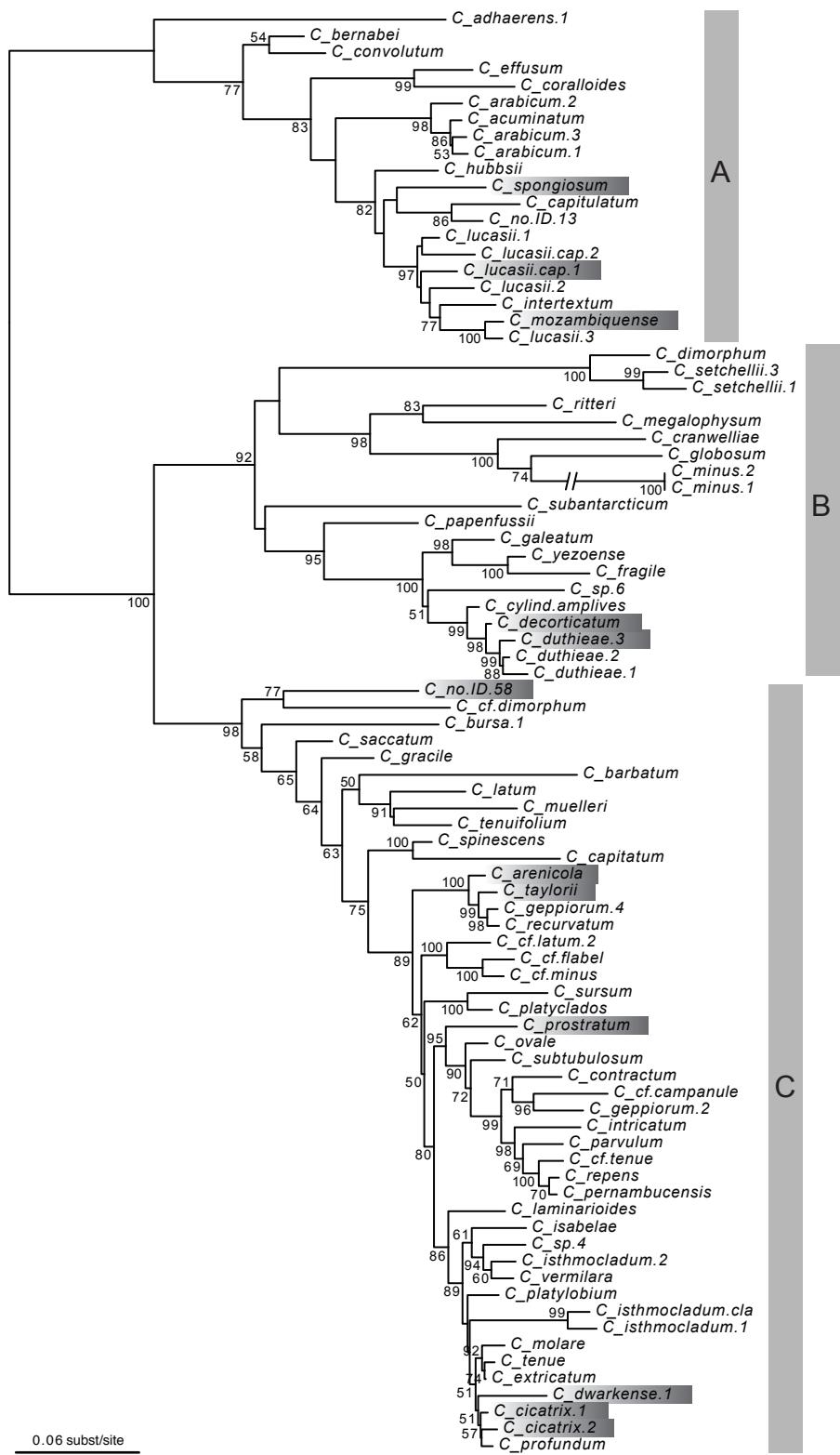
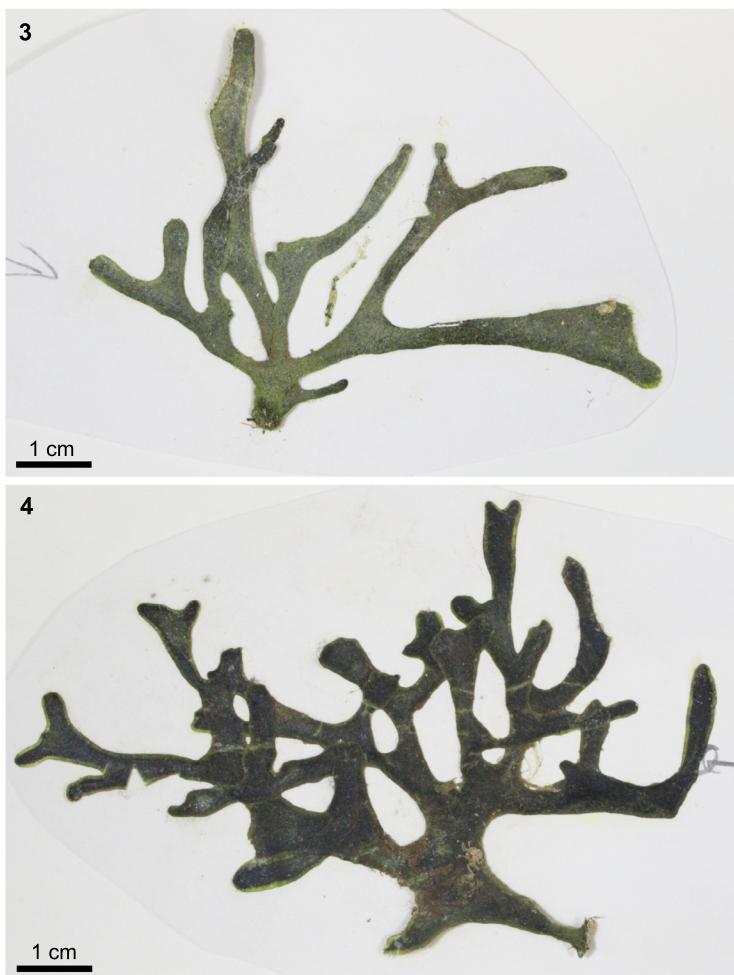
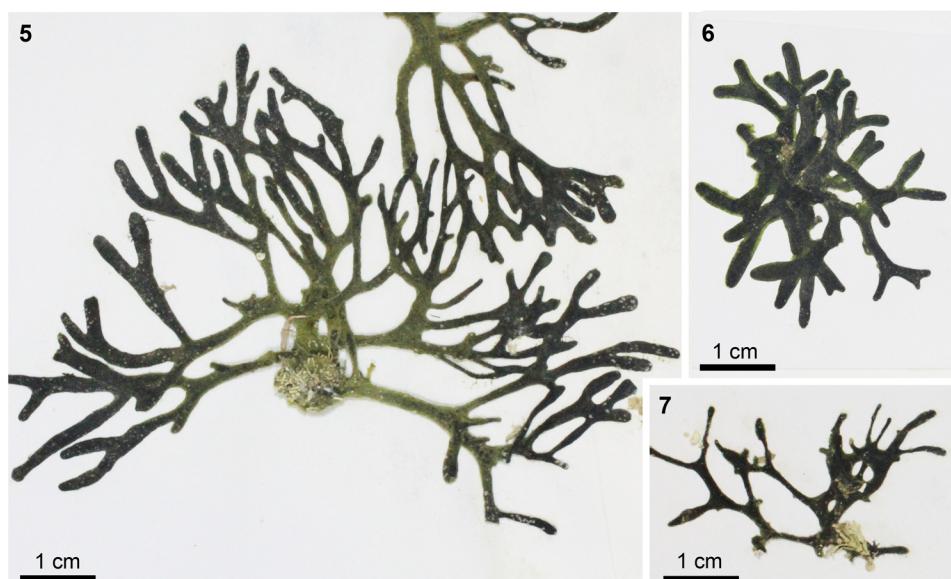


Figure 2. Maximum likelihood phylogenetic tree of *Codium* species based on a concatenated alignment of *rbcL*, *tufA* and *rps3-rpl16*. Species present in Madagascar are indicated in grey. Values at nodes indicate bootstrap support (only shown if >50).

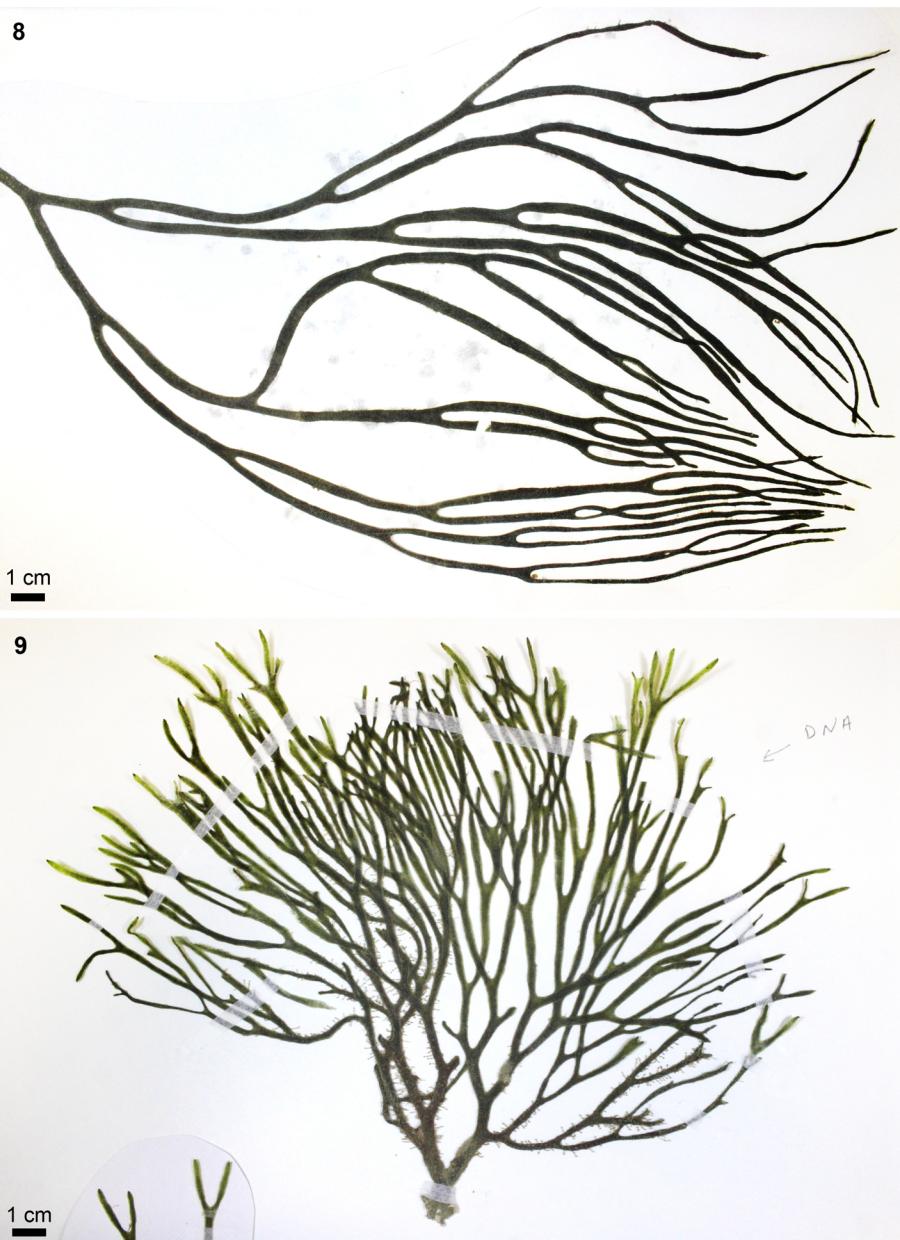


Figs 3-4. Flattened branched *Codium* species.
3. *Codium decorticatum*, specimen MAD0450.
4. *Codium arenicola*, specimen MAD0695.



Figs 5-7. Morphological variability in *Codium dwarkense*.

5. Upright plant, specimen MAD0638.
6. Small non-sprawling plant, specimen MAD0164.
7. Sprawling plant, specimen MAD0311.



Figs 8-9. The morpho-species *Codium cicatrix*.

8. A member of species-level cluster C_cicatrix.2, specimen MAD0853.
9. A member of species-level cluster C_cicatrix.1, specimen MAD1797.

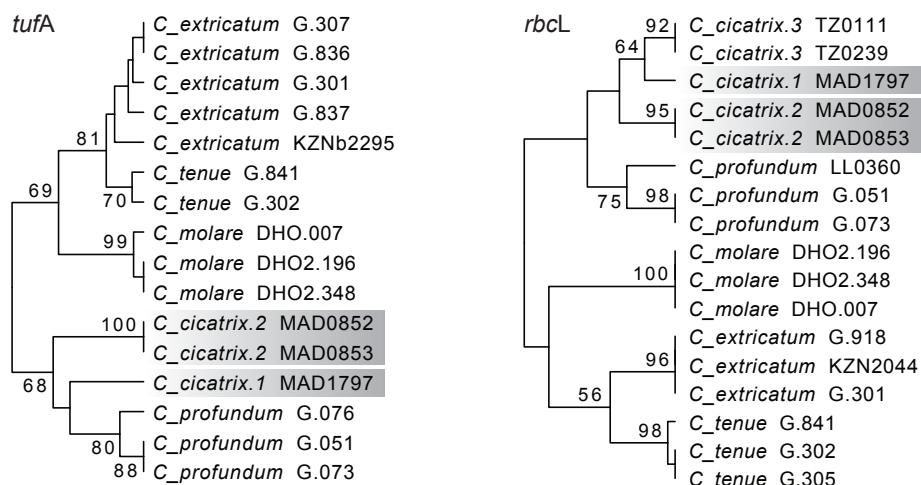


Fig. 10. UPGMA clustering trees of *tufA* and *rbcL* sequences illustrating sequence divergence between species-level clusters *C_cicatrix.1*, *C_cicatrix.2* and related entities. These trees are not to be interpreted as phylogenies; they simply depict sequence similarity. Values at nodes are bootstrap values and are only shown if >50.

Supplement S1. UPGMA trees for sequences of the *tufA* and *rbcL* genes. Note that these trees were built with a simple clustering method and should only be interpreted to investigate inter- vs. intraspecific distances to aid with species delimitation. Relationships between species should not be derived from these trees but from the tree presented in the main text. Values at nodes are bootstrap values (only shown when > 50). As noted in the text, we are now using *tufA* as the primary DNA barcode. We continue to use *rbcL* exon 1 for historical comparison but not all species from Madagascar have been sequenced for *rbcL* (i.e. *prostratum*, *arenicola*, *mozambiquense*).

