

Acanthamoeba

T2 - T6

T4 - T16

T4

T2 - T4 - T11

T4

T2 - T6

T4 - T6

T4

T3 - T11

OUTGROUP

T7 - T8 - T9 - T17

New helix 10

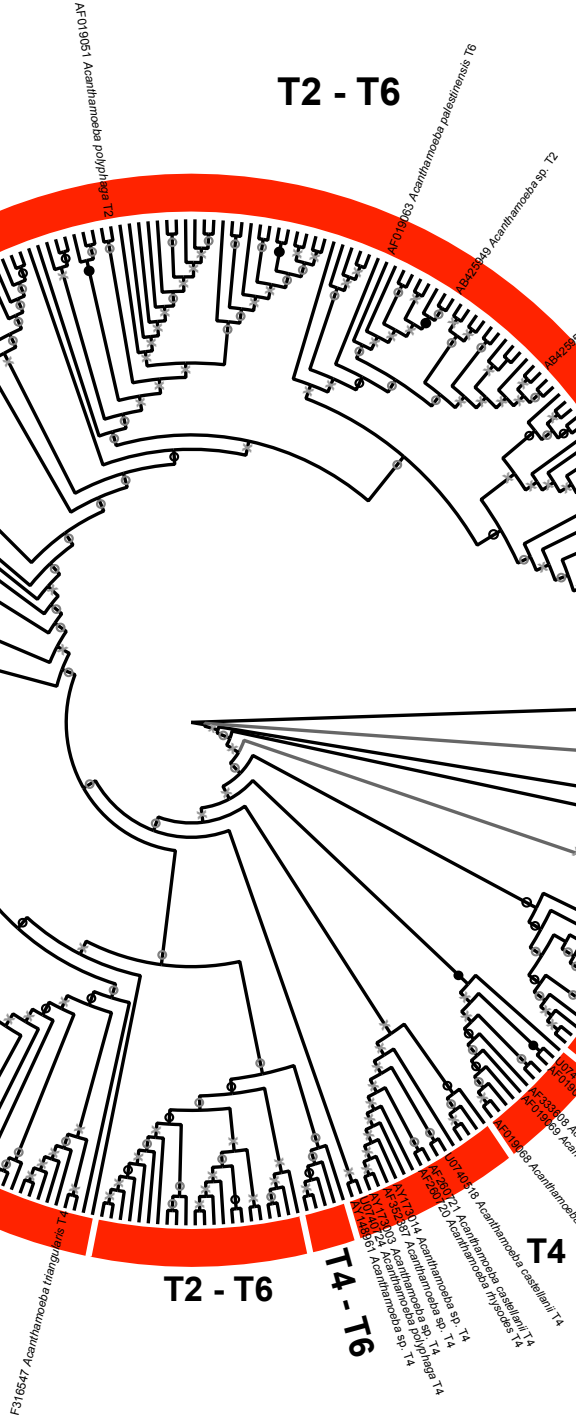
New helix 10

T5

T1 - T10 - T12 - T14 - T15

T13 - T16

Figure S1.
Acanthamoeba ML phylogenetic tree, log likelihood = - 6209.18922, rooted with *Balamuthia*, *Protacanthamoeba* and "Protosteliales sp. LH105", alignment = 239 positions, 321 taxa. Approximate likelihood support shown on branches. Environmental OTUs shaded in red, named according to BLAST best hit, except "new helix 10". 48 reference sequences are named.



10.0
fraction of substitutions per site

Support symbols:

- x ≤ 65 %
- o ≥ 66 % ≤ 85 %
- ≥ 86 % ≤ 95 %
- ≥ 96 % ≤ 100 %

MYXOMYCETES

PHYSARIDA

Physaridae & Didymiidae



Didymiidae only

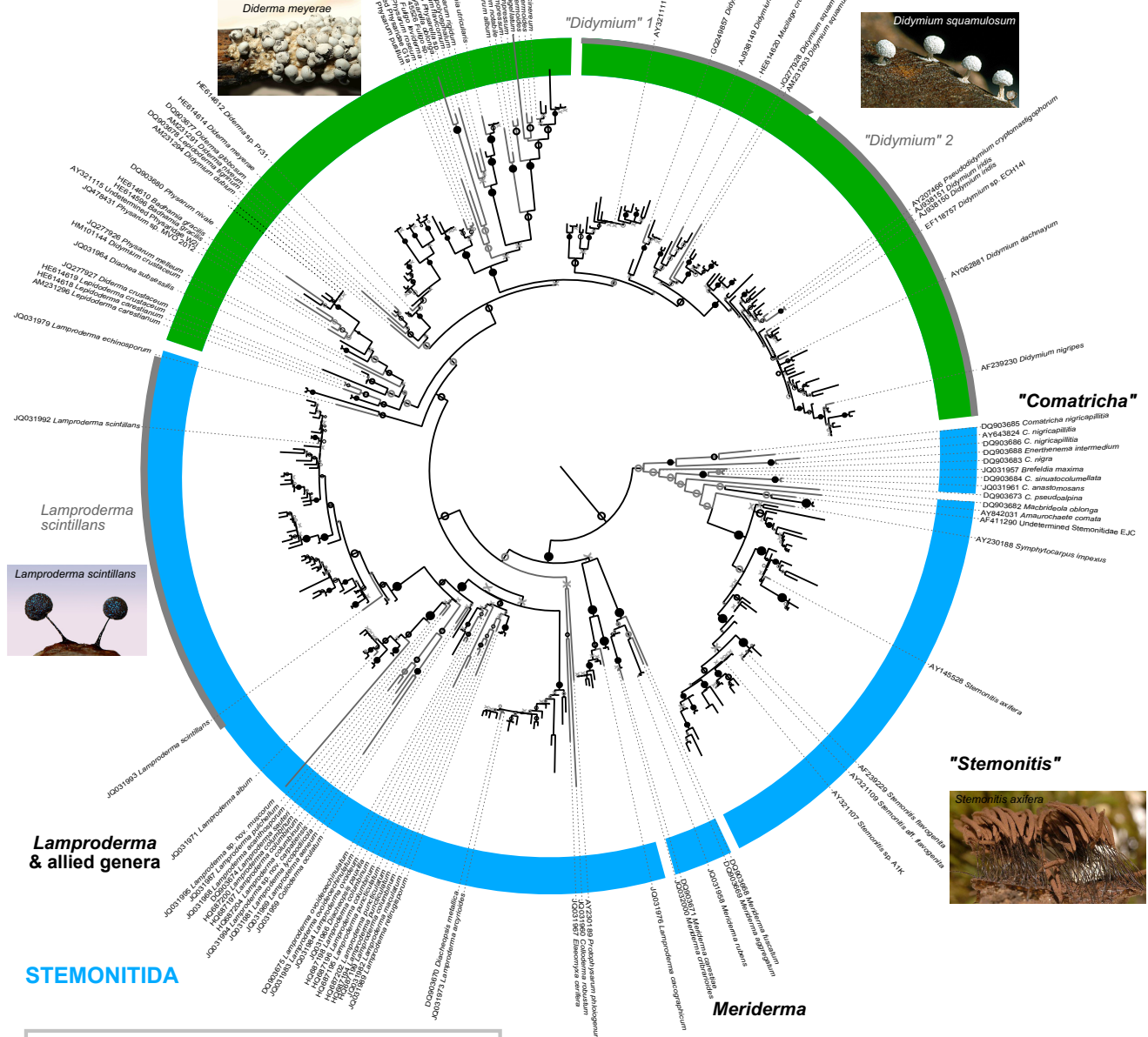


Figure S2. Myxomycetes ML phylogenetic tree (alignment = 384 positions, 442 taxa) (log likelihood = -26237.19632) arbitrarily rooted between Comatricha and Stemonitis and the remaining taxa. Approximate likelihood support shown for each branch. Genotype names according to BLAST best hit. The 104 reference sequences (grey branches) are named. Credit photos: Alain Michaud.

Support symbols:

- ≤ 65 %
- ≥ 66 % ≤ 85 %
- ≥ 86 % ≤ 95 %
- ≥ 96 % ≤ 100 %

