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**Figure 1.** *Nowakowskiella elegans* **A-I.** Eucarpic, polycentric, and epibiotic thallus of *Nowakowskiella elegans*; apical exit tube or a papilla indicated by an arrow. Bar = 20  $\mu\text{m}$ .

**Figure 2.** *Nowakowskiella hemisphaerospora* **A-D.** Polycentric thallus of *Nowakowskiella hemisphaerospora* **E-F.** Resting spores. Bar = 50  $\mu\text{m}$ .

**Figure 3A.** Zoosporangia of *Nowakowskiella profusa*, arrow indicate discharged sporangia and released zoospores. **B.** Resting spore of *Nowakowskiella ramosa*. Bar = 50  $\mu\text{m}$ .

**Figure 4.** *Nowakowskiella multispora* **A-B.** Sporangia of *Nowakowskiella multispora* with delicate rhizomycelium **C.** Resting spores. **D.** Relatively smaller zoospore with a single lipid globule. Bar = 50  $\mu\text{m}$ .

**Figure 5.** *Nowakowskiella multispora* var. *longa* **A-F.** Sporangia with delicate rhizomycelium and long, branched exit tubes. Bar = 50  $\mu\text{m}$ .

**Figure 6.** *Nowakowskiella macrospora* **A-D.** Sporangia of *Nowakowskiella macrospora* with exit tube of varying length; arrow indicates relatively large zoospore with a single large lipid globule. Bars = 50  $\mu\text{m}$ .

**Figure 7.** Phylogenetic relationship of few representative *Nowakowskiella* isolates along with members of Cladochytriales based on LSU sequence data. The evolutionary history was originated by using the neighbour-joining method. The lengths of the horizontal lines are proportional to the number of nucleotide differences per site. Scale bar indicates number of nucleotide substitutions per site. All the evolutionary analysis was performed using MEGA X.