



SUPPL. FIG. 1. Maximum likelihood (ML) simultaneous analysis phylogram inferred from the three gene matrix (*ITS*, *LUMINIDEPENDENS* and *psbJ-petA*). Terminal names are generalized to reflect generic membership only. The mean, standard deviation, and range of branch lengths leading to *Leavenworthia* and *Selenia* clades

scored from 100 individual ML bootstrap trees are provided above the branches leading to each clade and are also summarized in Table 2. The branch lengths leading to the two clades were found to be of significantly different lengths with no overlap in range and confidence intervals ( $p < 0.0001$ ,  $t = 40.2362$ , degrees of freedom = 198).