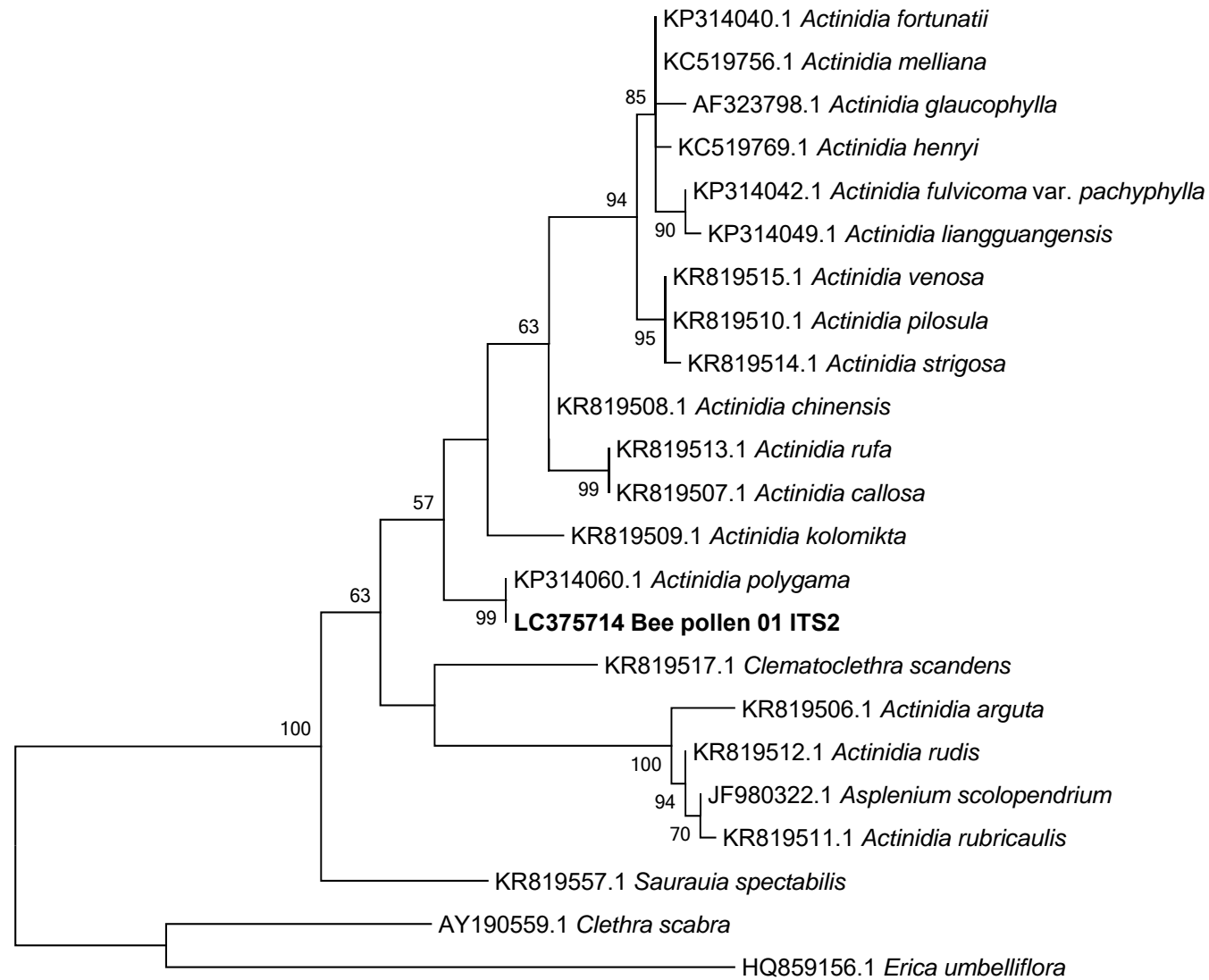


**Fig. S2 Molecular phylogenetic trees of honeybee pollen pellets by maximum likelihood method in ITS2**

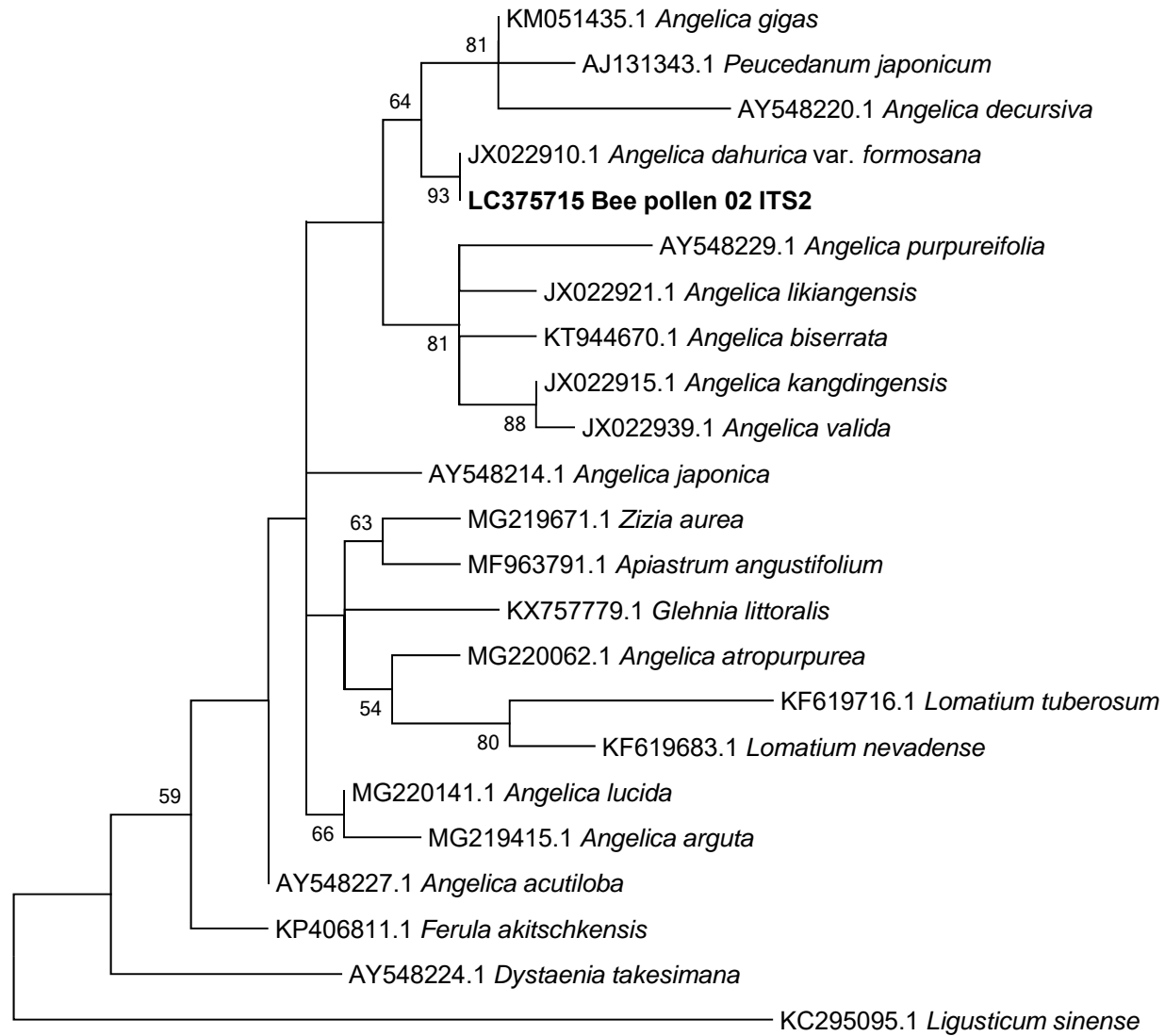
The evolutionary history was inferred by using the maximum likelihood method based on the Tamura–Nei model. The tree with the highest log likelihood is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically by applying the Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the maximum composite likelihood approach, and then selecting the topology with superior log likelihood value. Each tree is drawn to scale, with branch lengths indicating the number of substitutions per site. The analysis involved 10–26 nucleotide sequences. All positions containing gaps and missing data were eliminated. Evolutionary analyses were conducted in MEGA7. The numbering of honeybee pollen pellets is as follows: (a) No. 1; (b) No. 2; (c) No. 3; (d) No. 4; (e) No. 5; (f) No. 6; (g) No. 7; (h) No. 9; (i) No. 12; (j) No. 13; (k) No. 15; (l) No. 16; (m) No. 19; (n) No. 20; (o) No. 21; (p) No. 22; (q) No. 23; (r) No. 24; (s) No. 25; (t) No. 26; (u) No. 27; (v) No. 28; (w) No. 29; (x) No. 30.

(a)



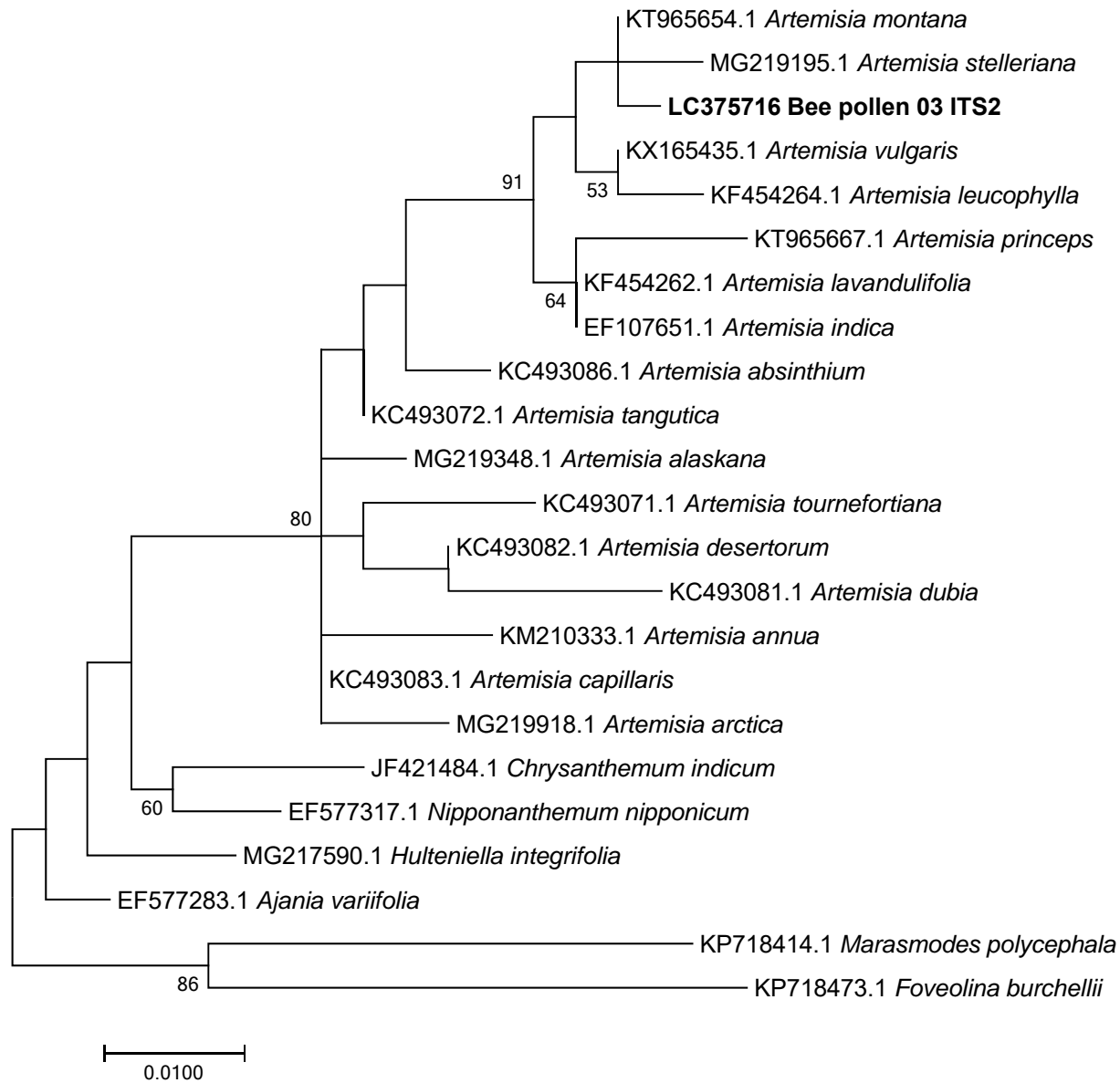
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(b)

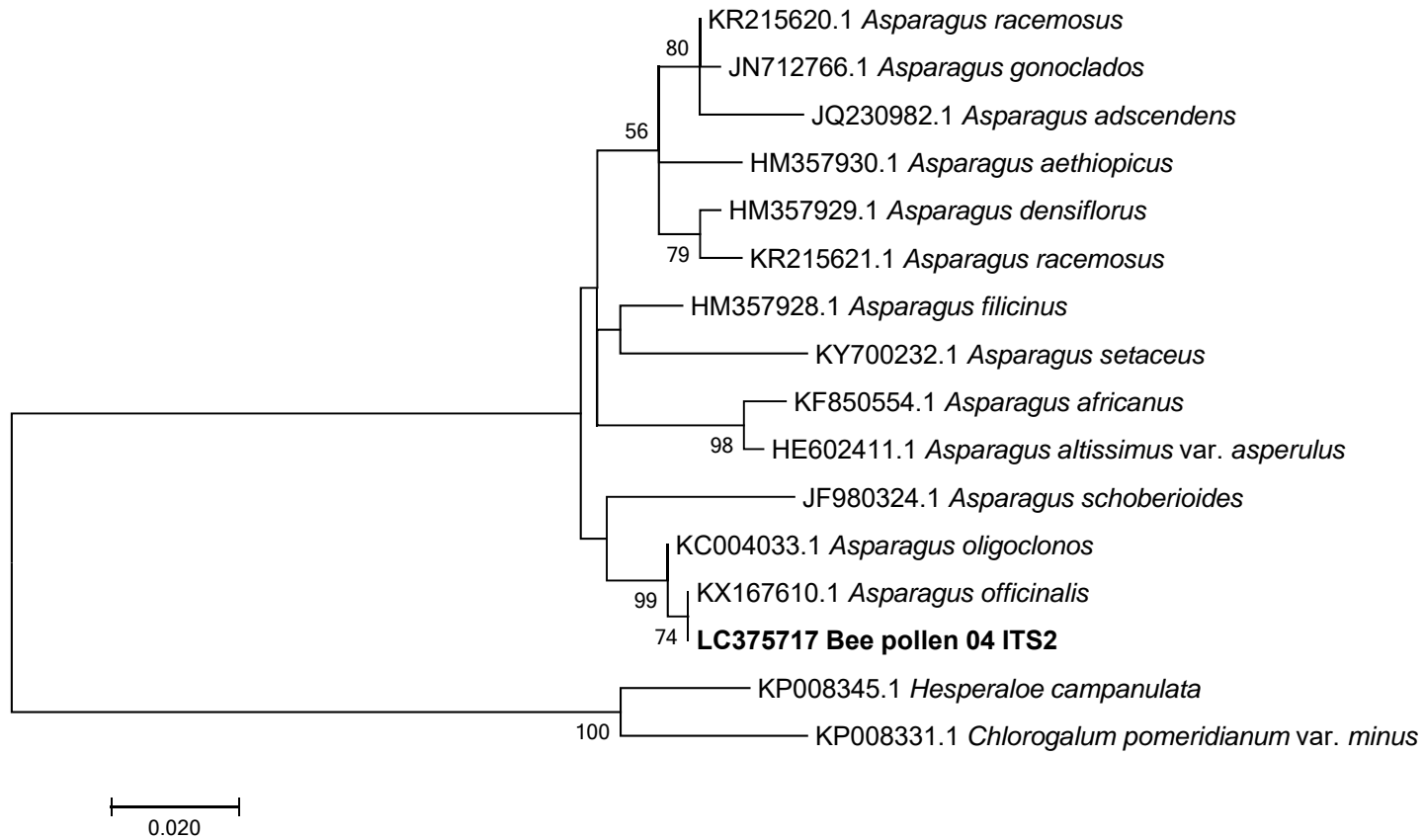


0.0100

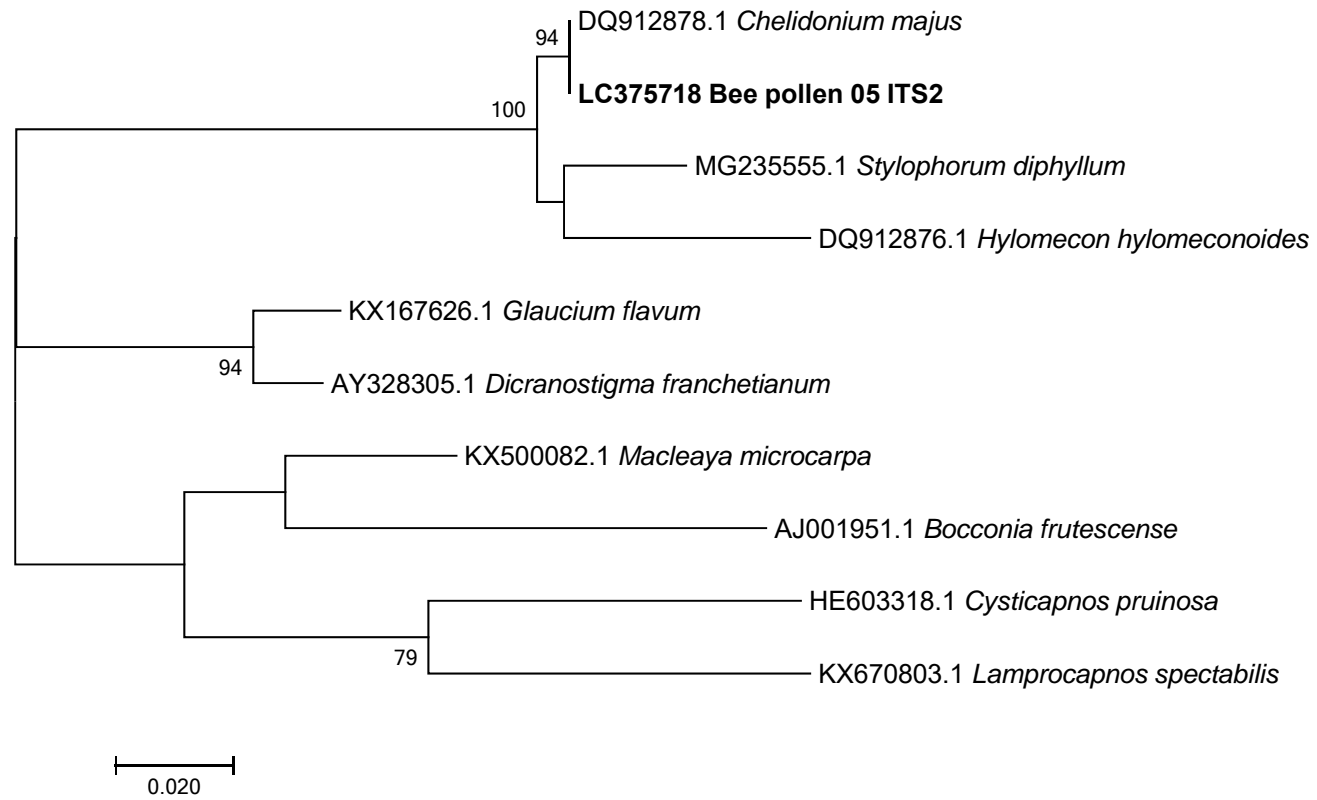
(c)



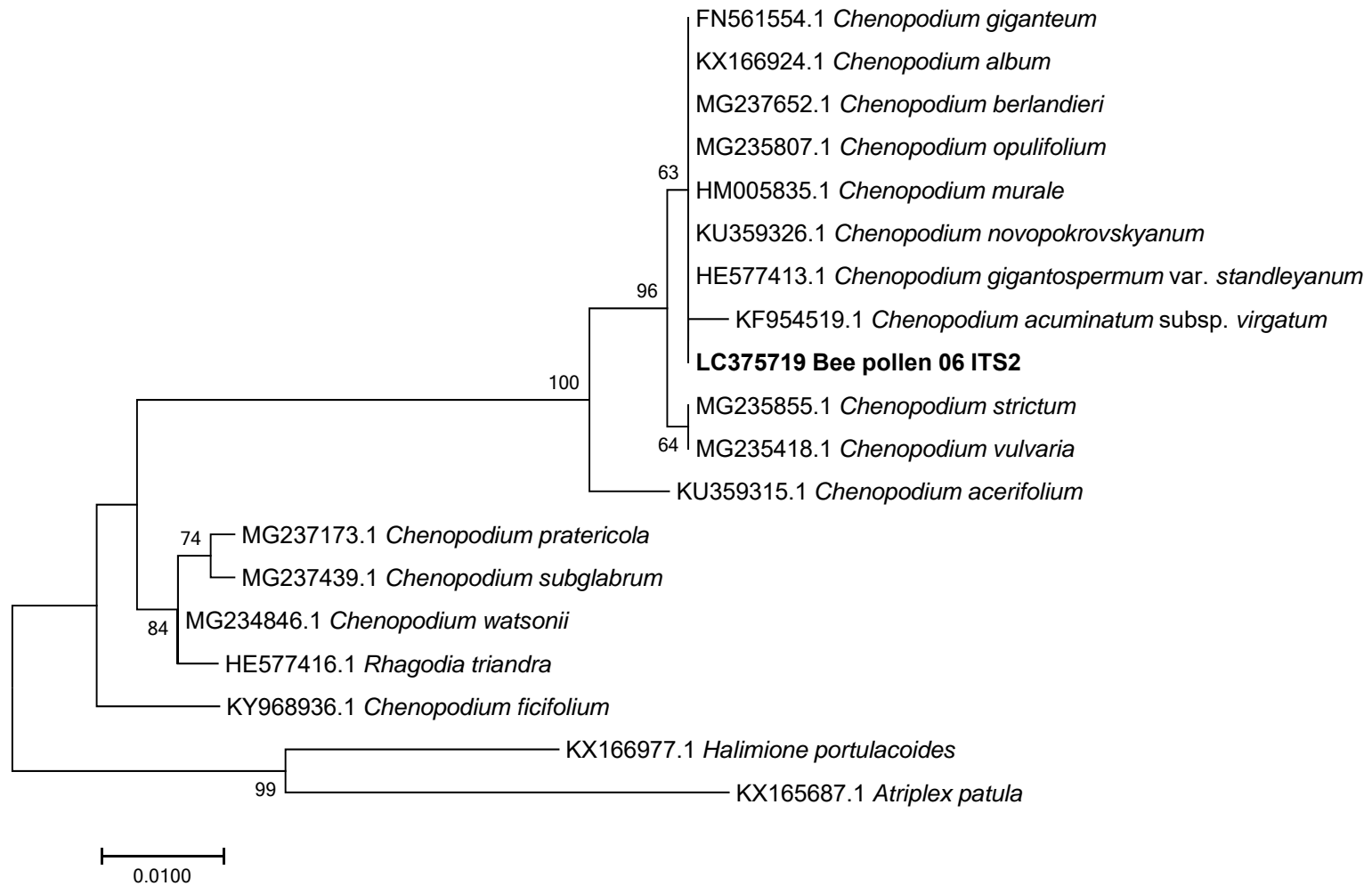
(d)



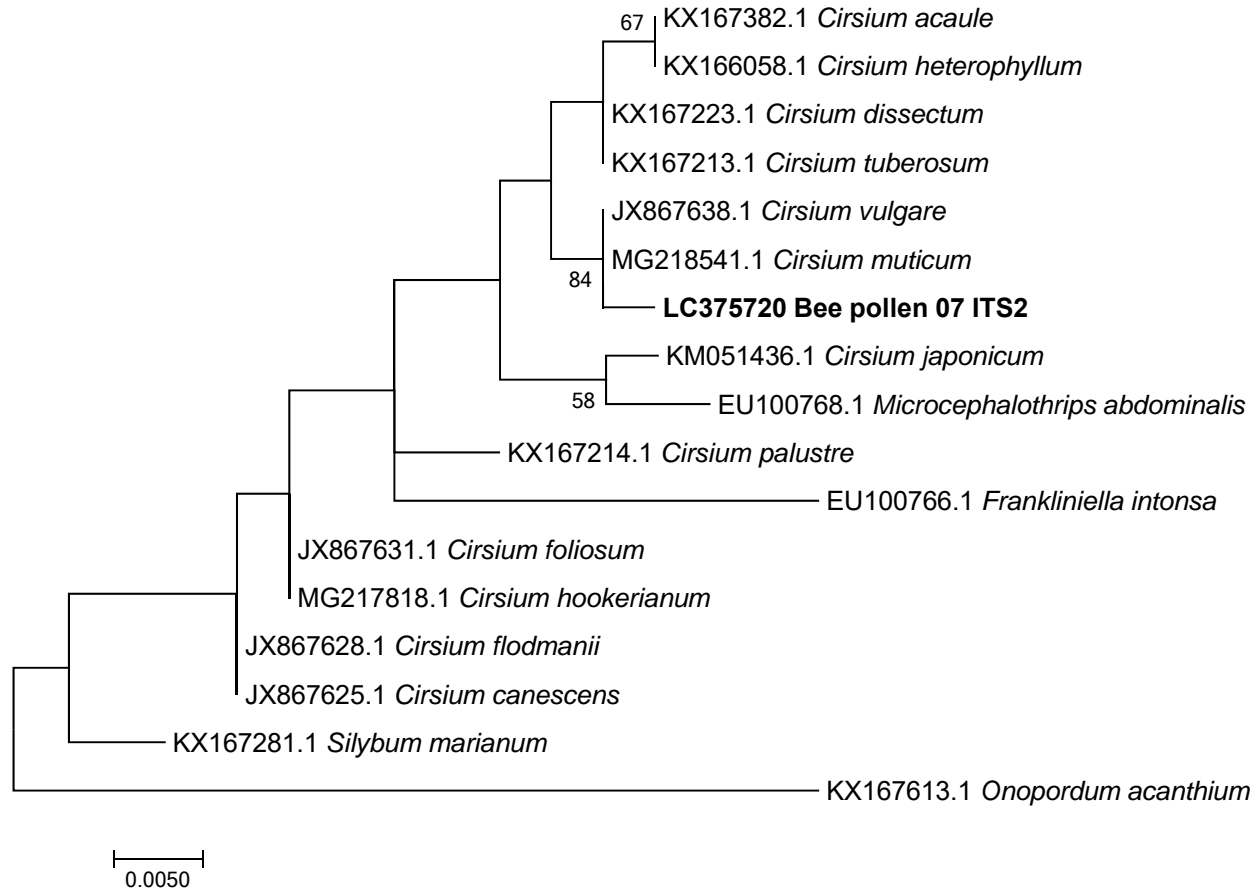
(e)



(f)

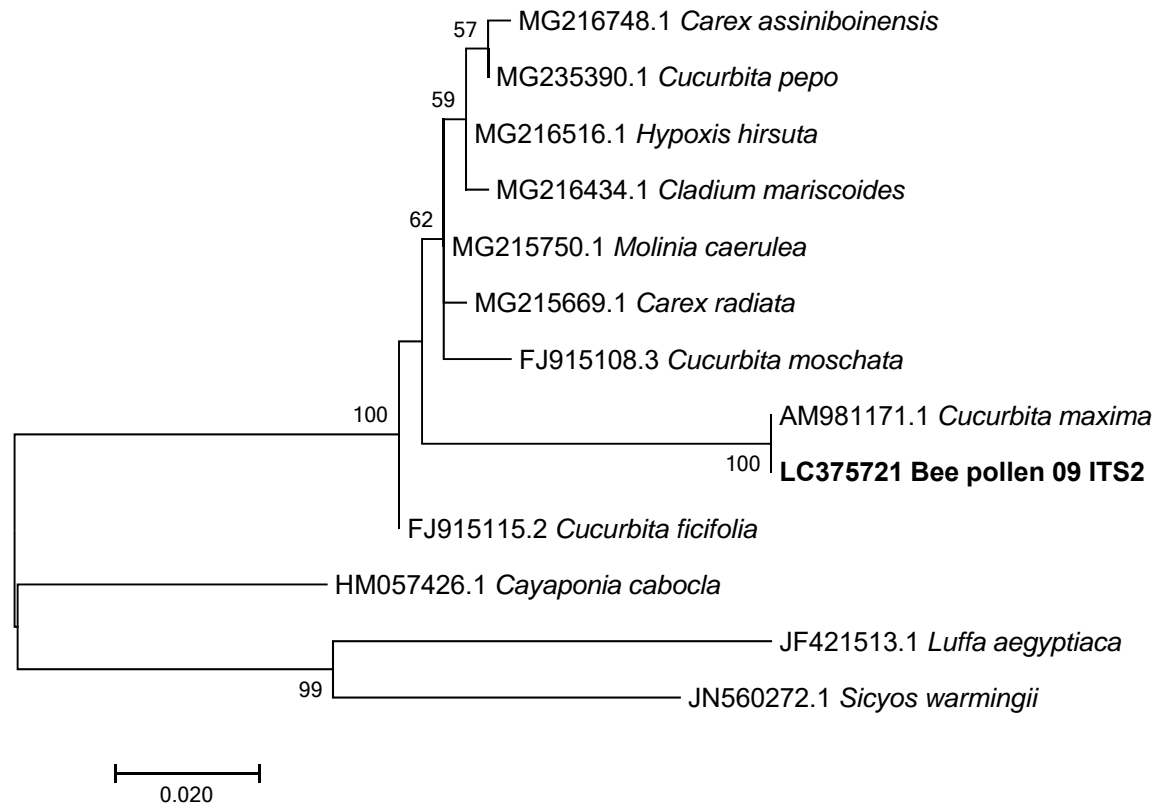


(g)

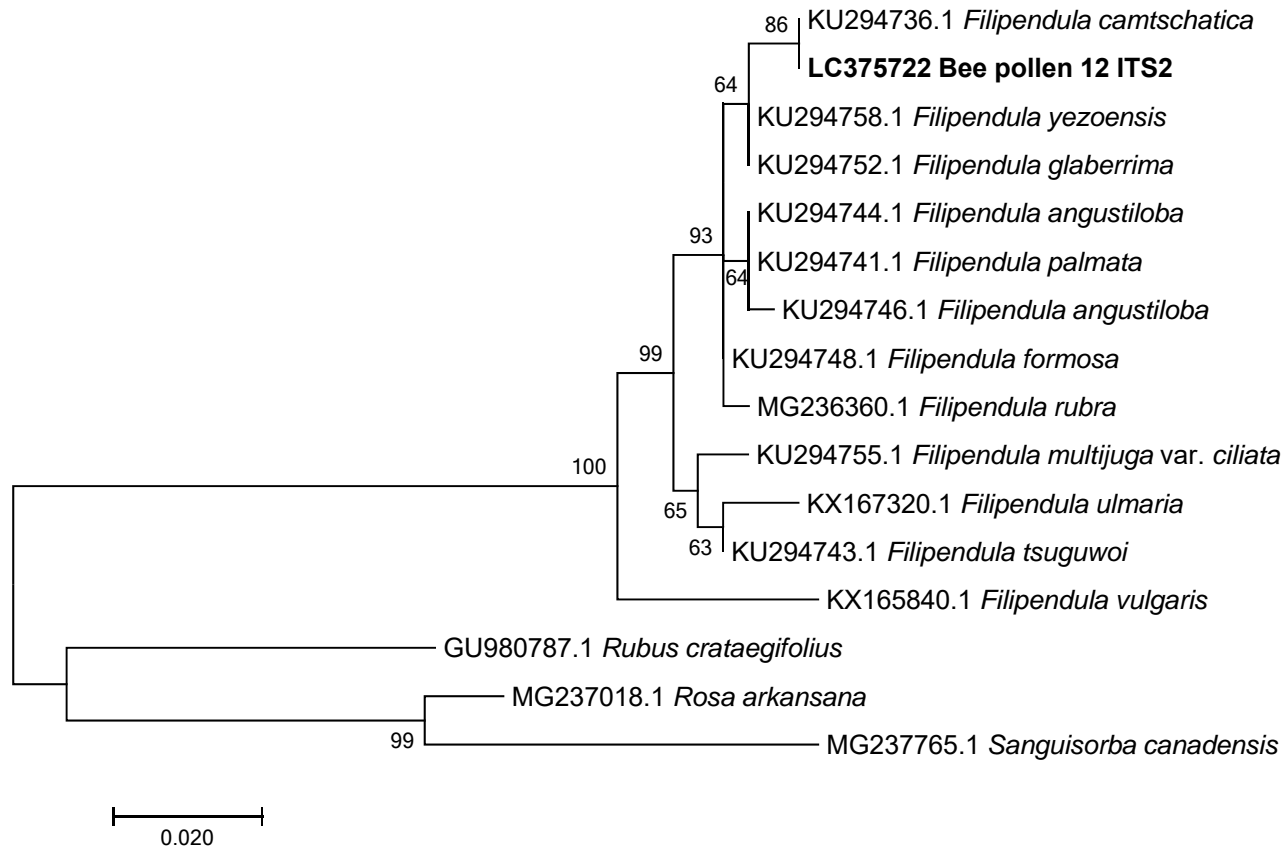




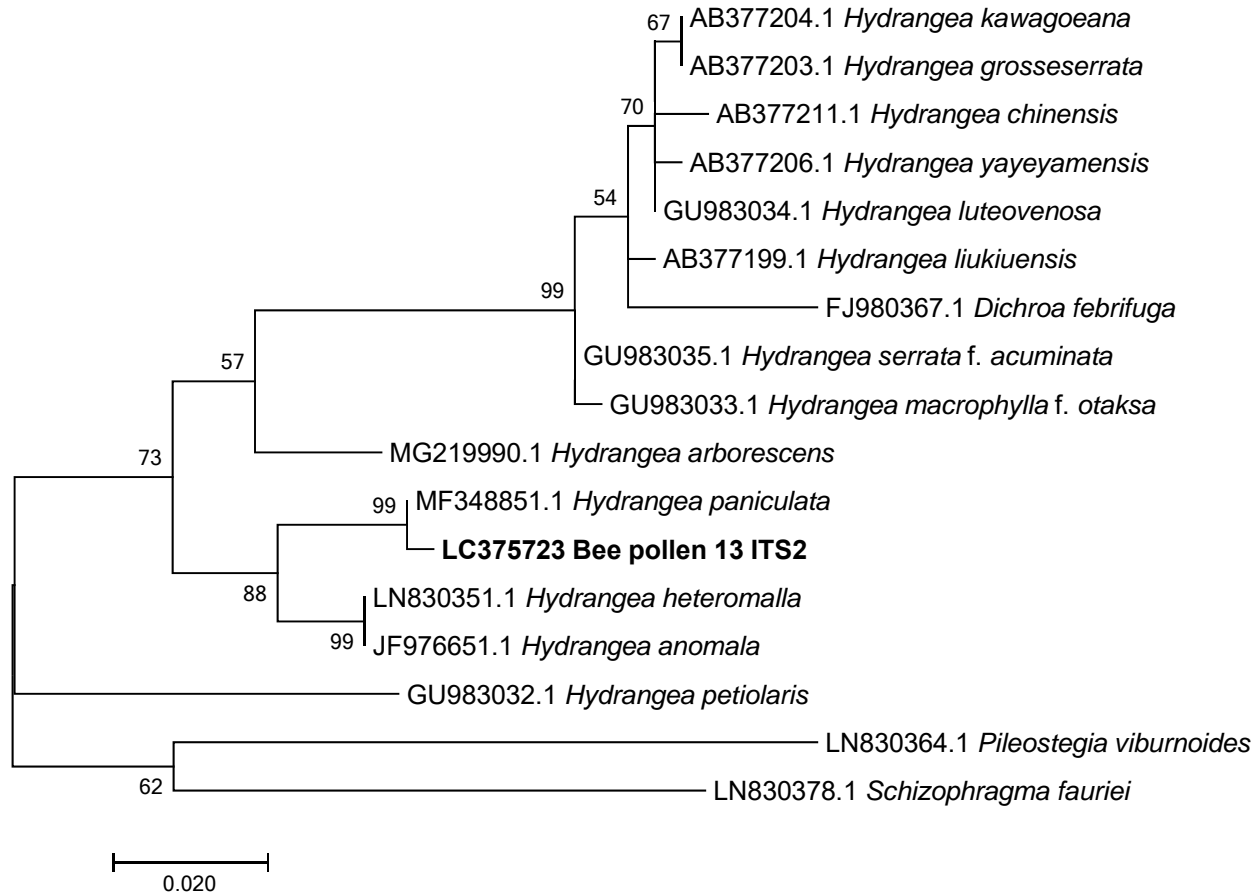
(h)



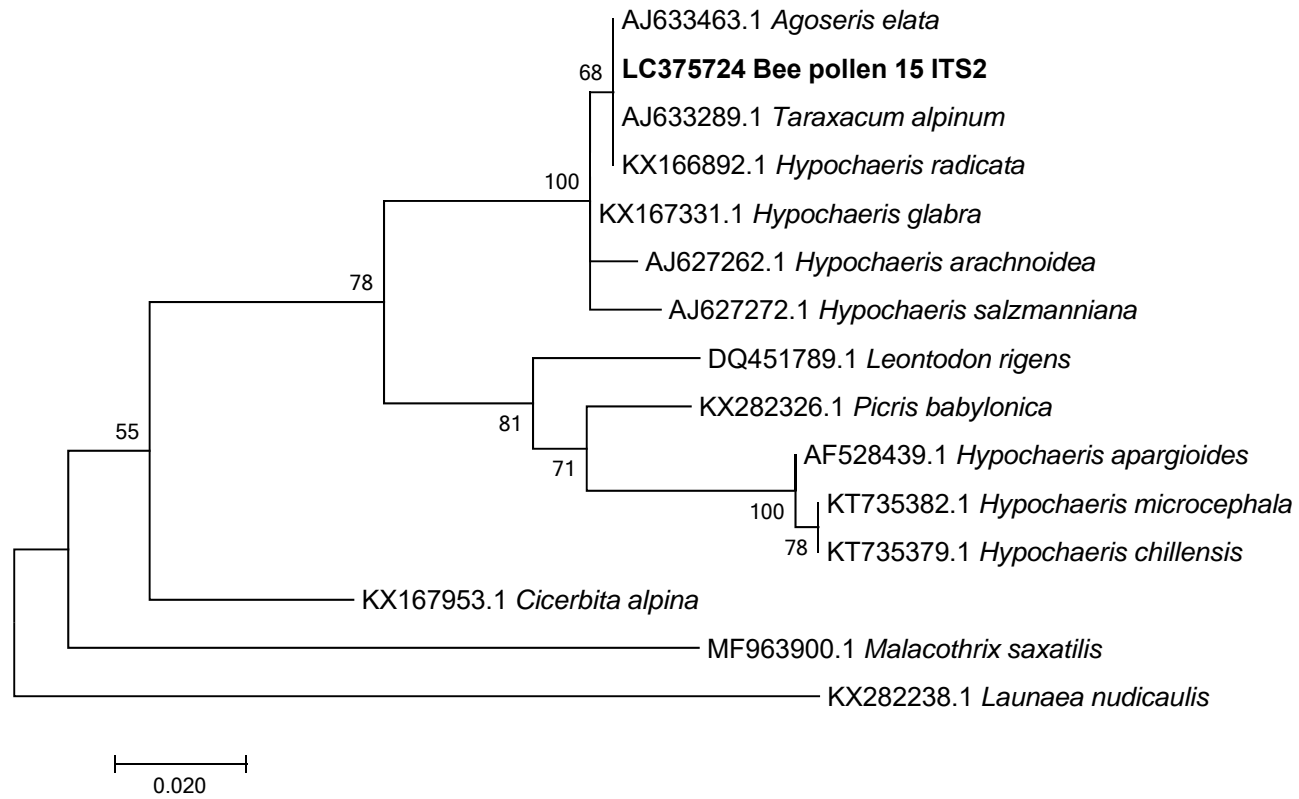
(i)



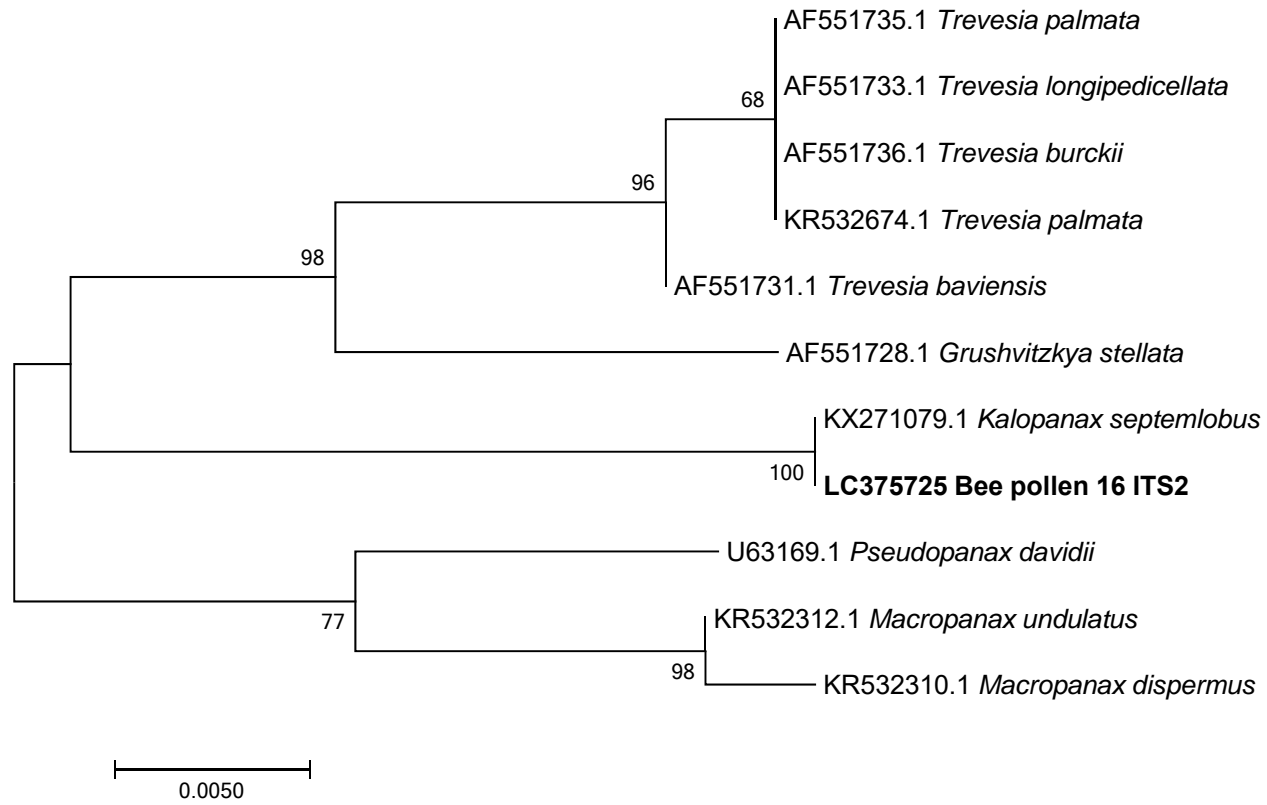
(j)



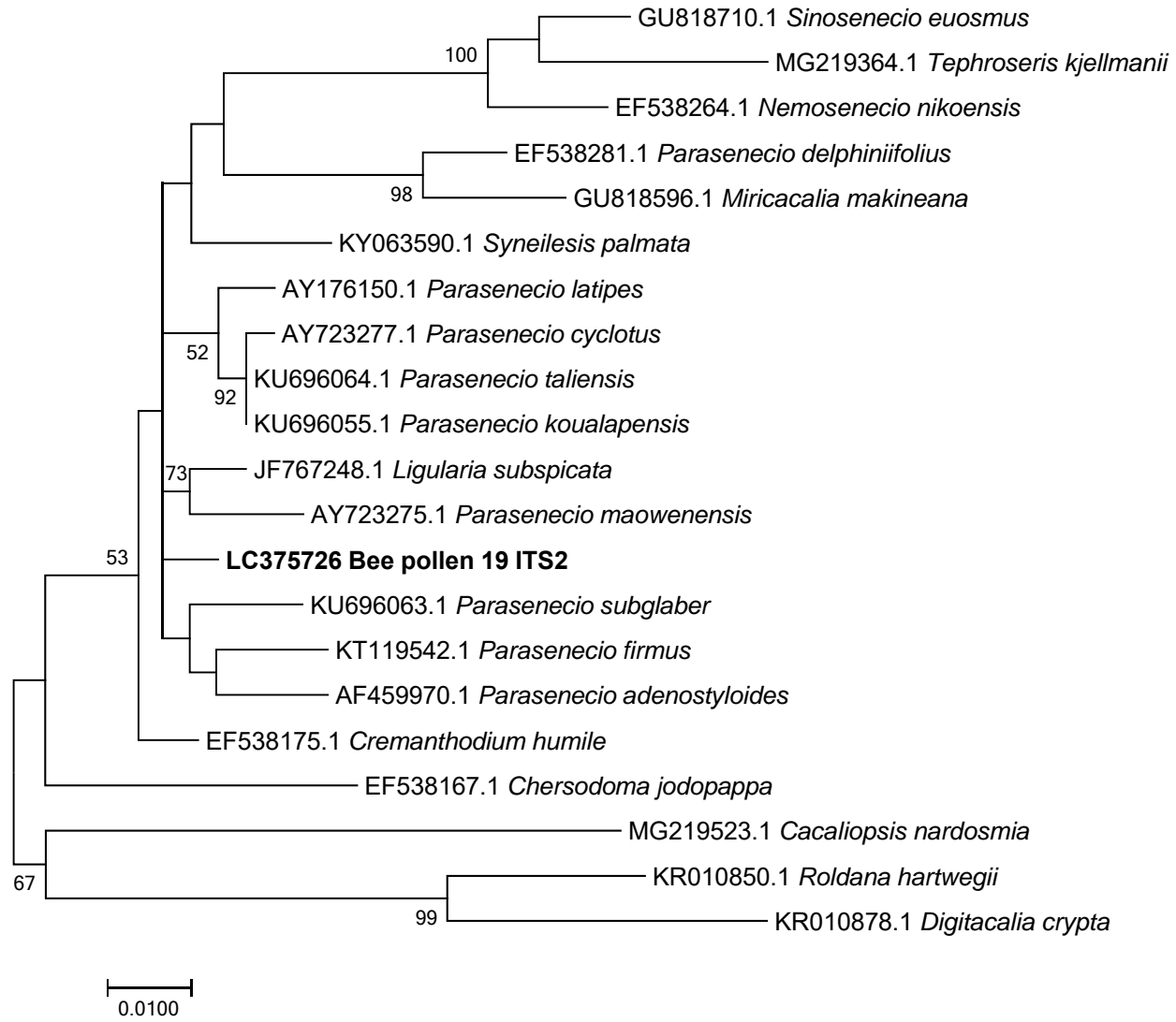
(k)



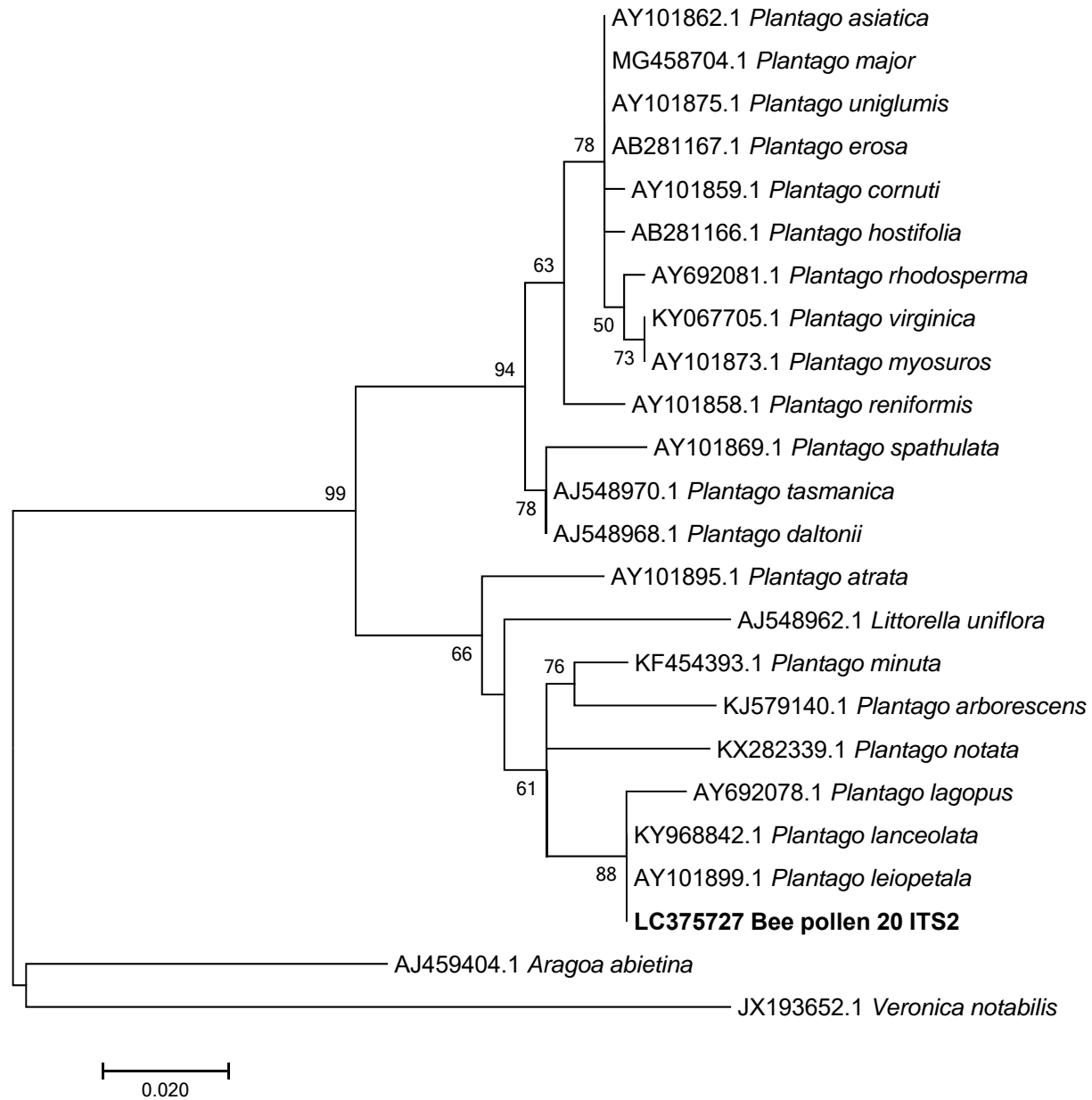
(I)



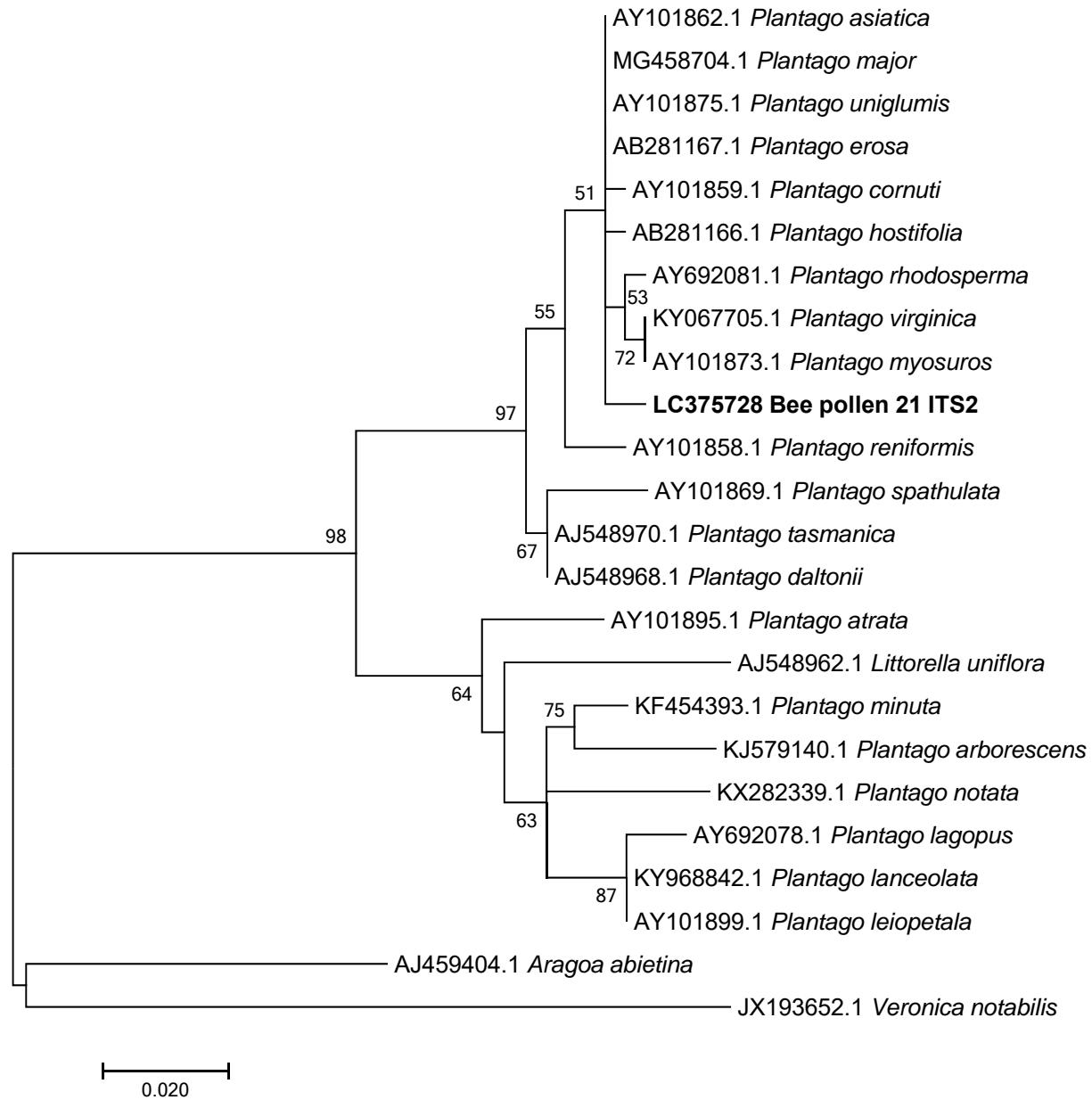
(m)



(n)

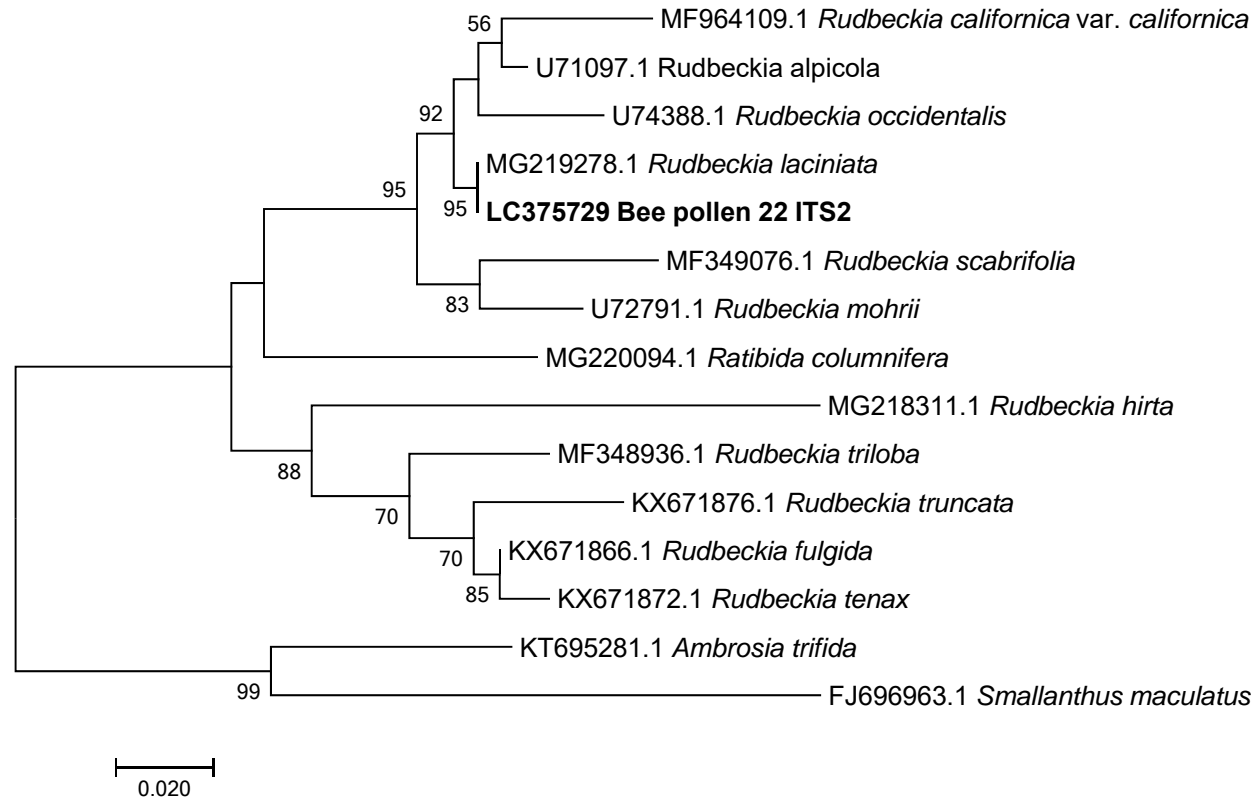


(o)

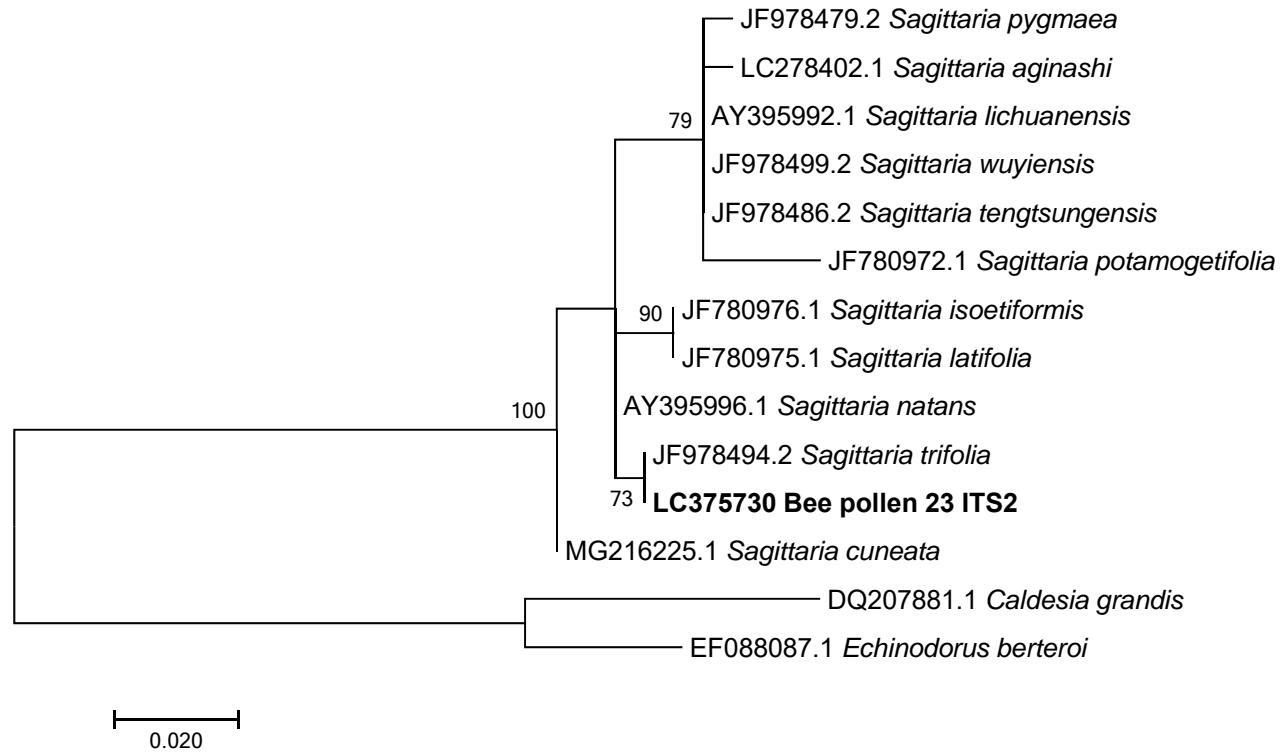




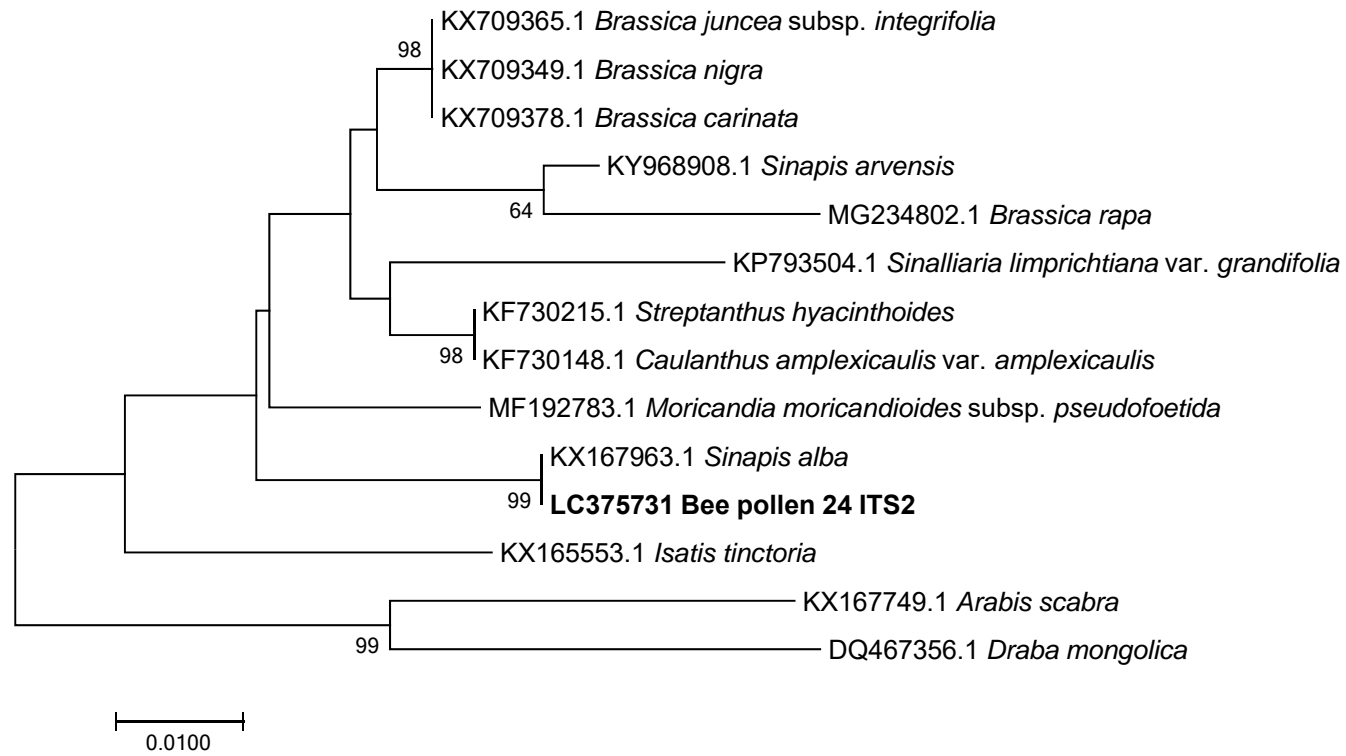
(p)



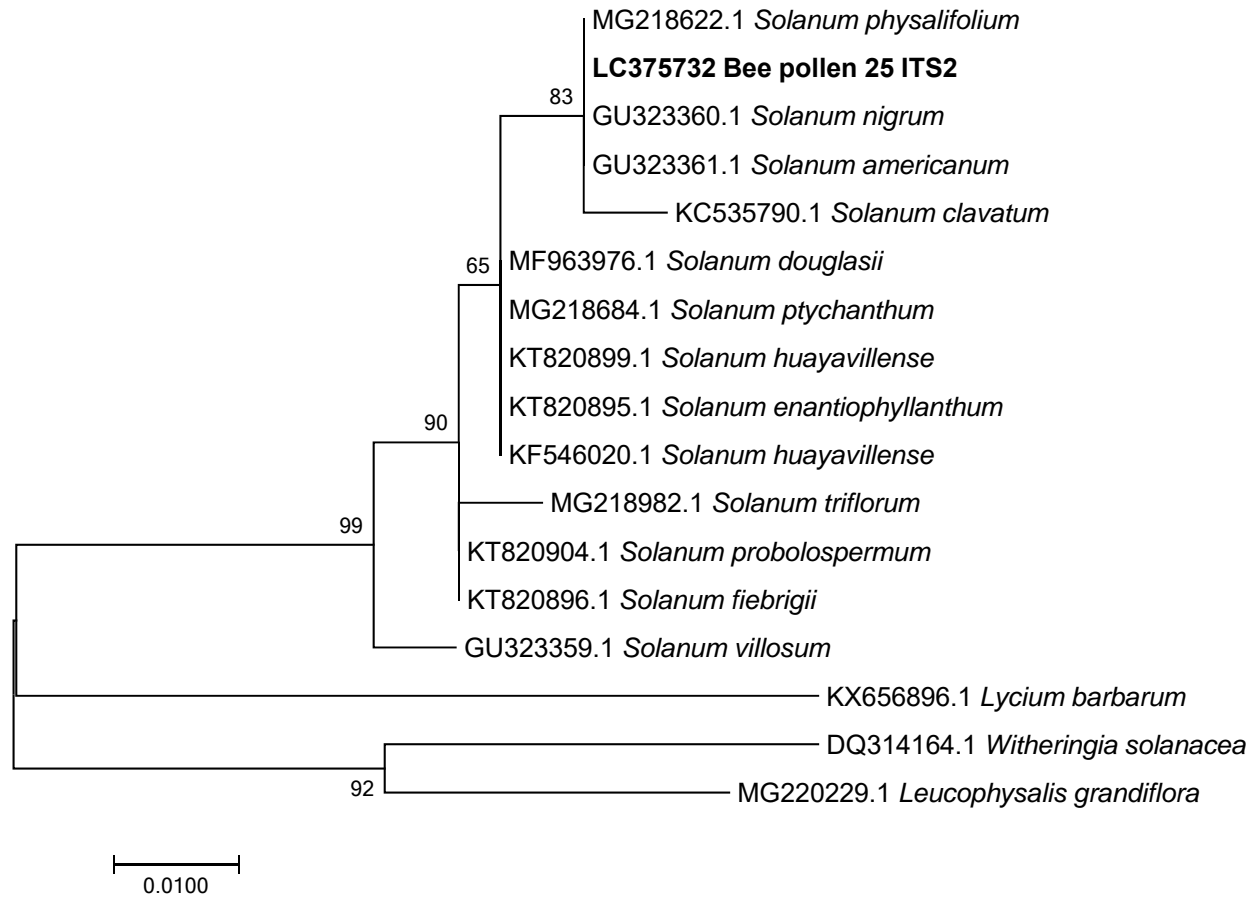
(q)



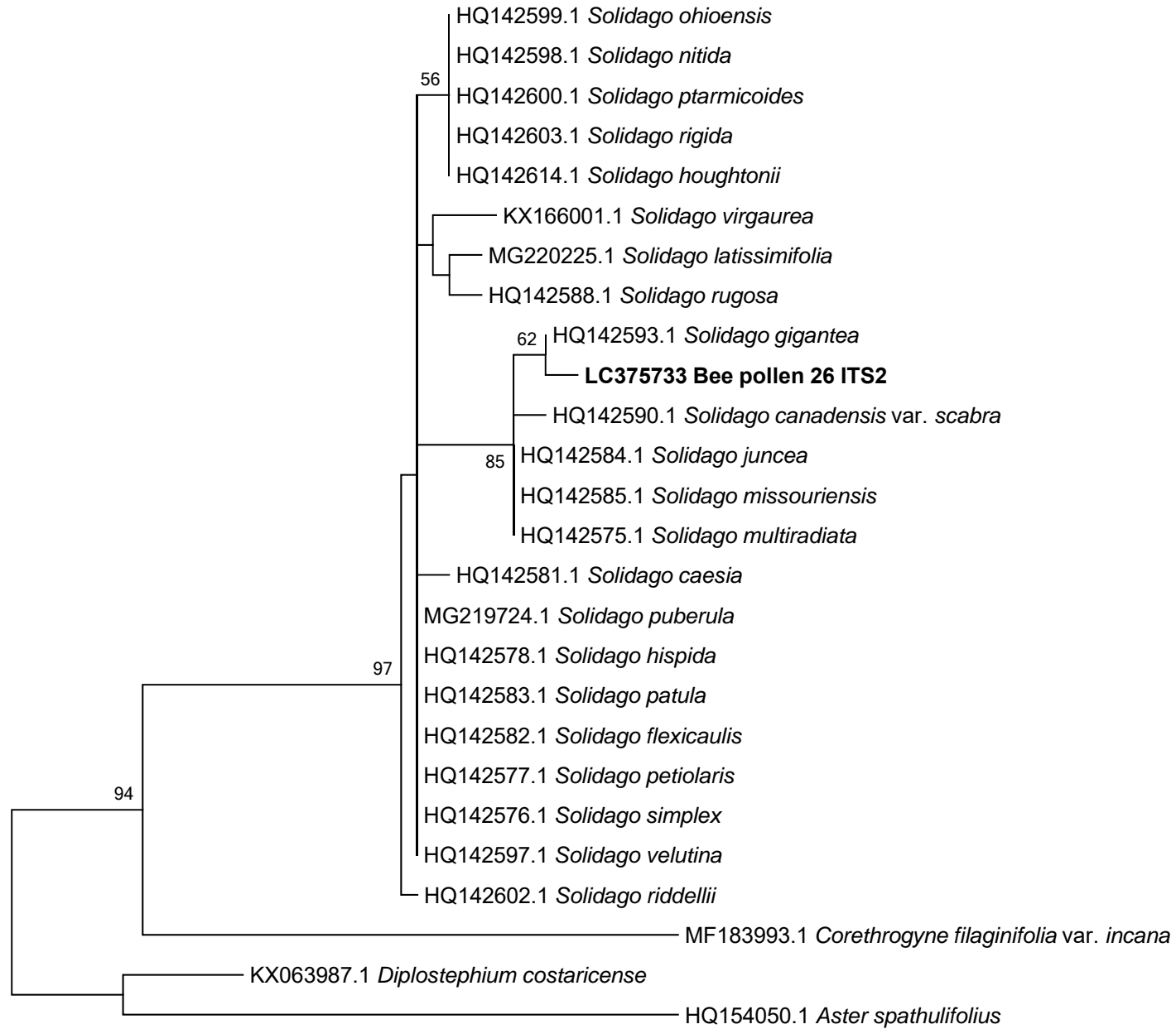
(r)



(s)



(t)



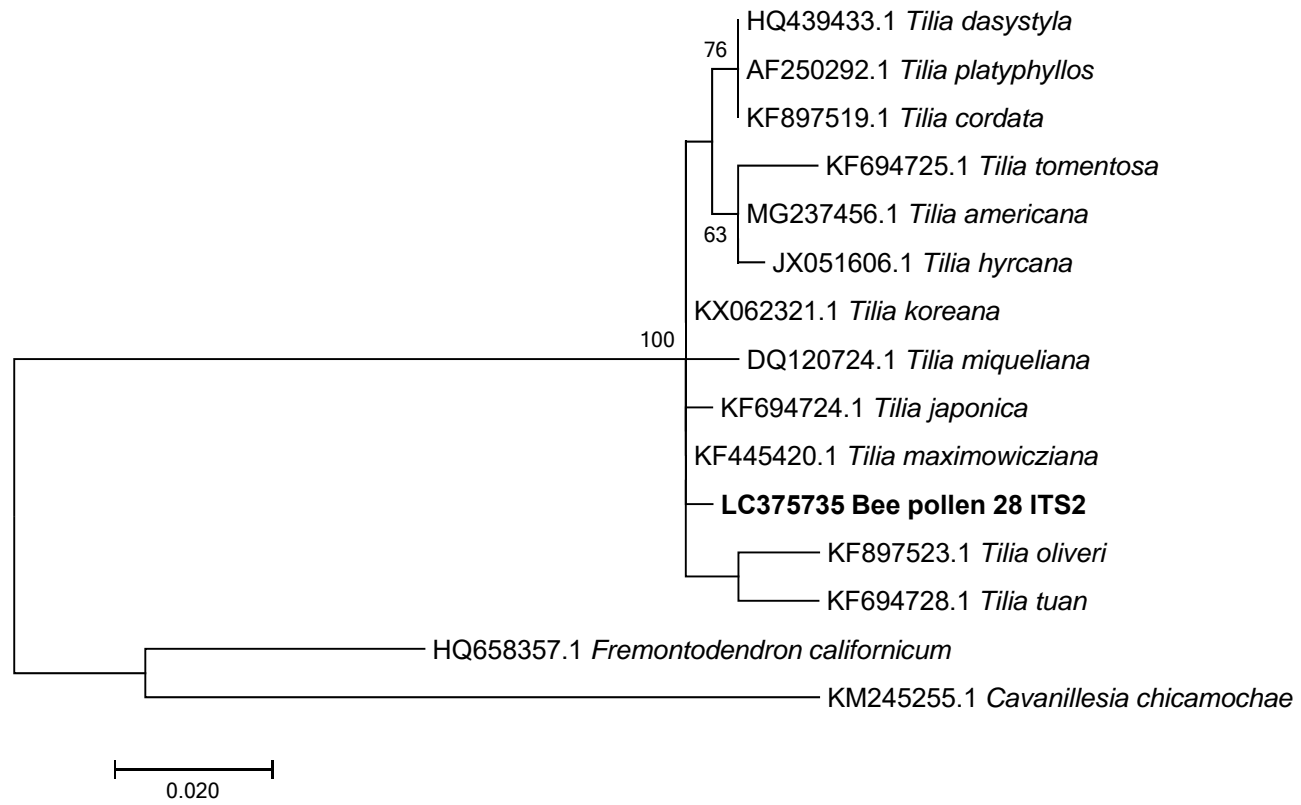
0.0100

(u)

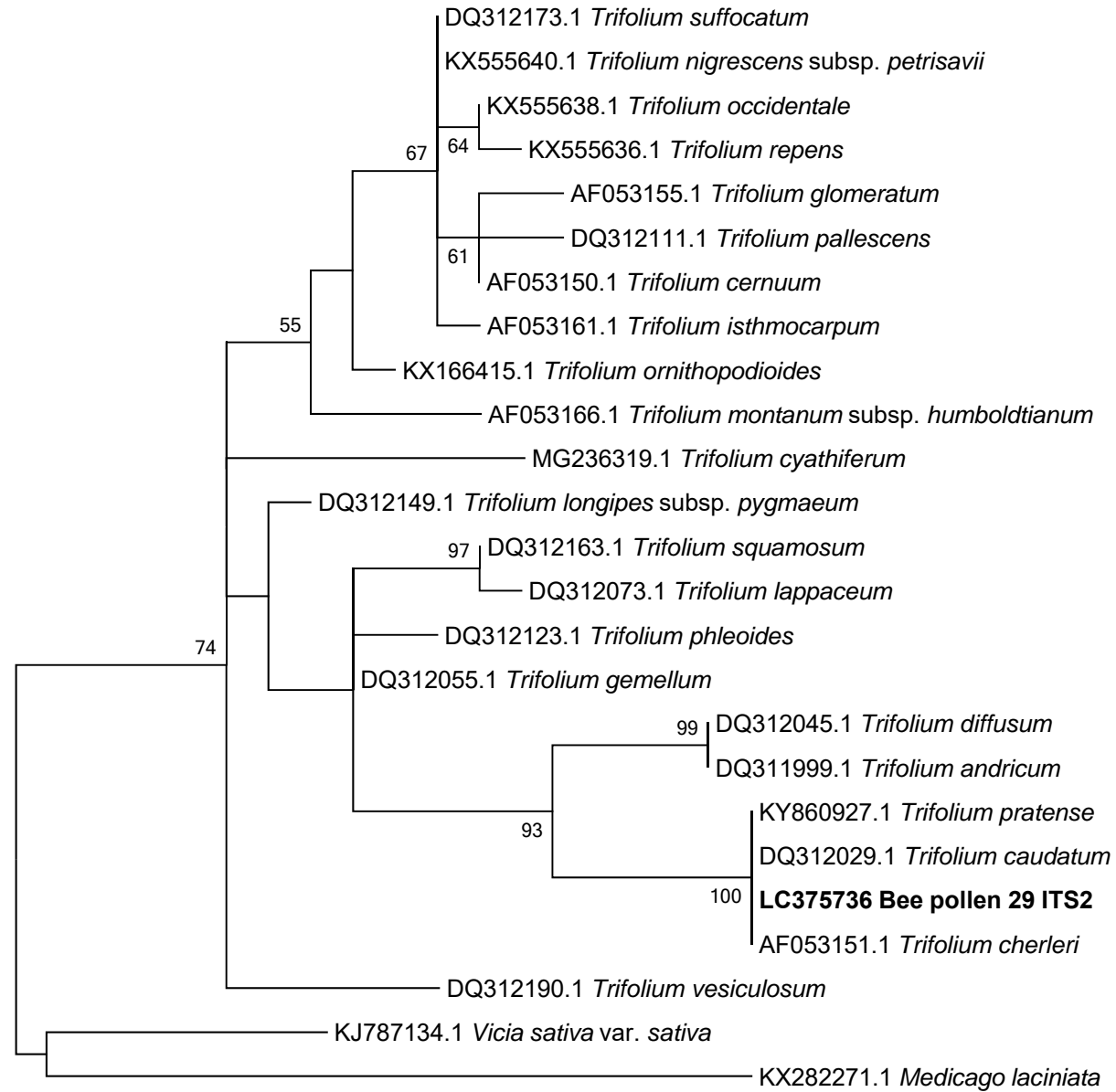


0.0100

(v)



(w)





(X)

