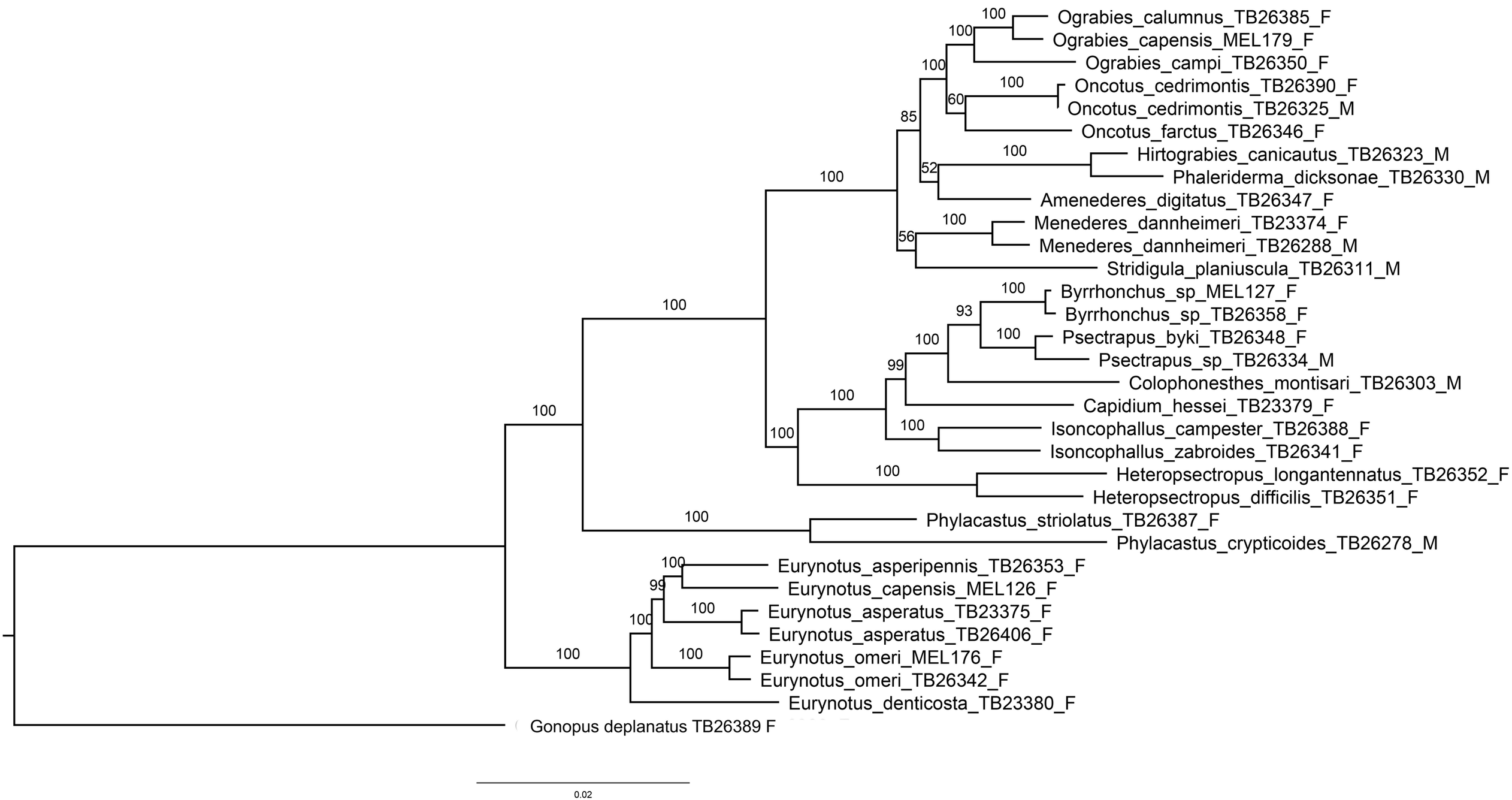

Phylogeny of the subtribe Eurynotina inferred from targeted enrichment and mitochondrial datasets. The tree shown is the Majority Rule consensus from IQ-TREE2 analysis of the concatenated matrix comprising 510 loci resulting in 157,567 aligned amino acid positions. Branch support is indicated as Ultrafast bootstrap values. Specimens labeled "M" indicate data derived from pinned museum material; "F" denotes fresh specimens.