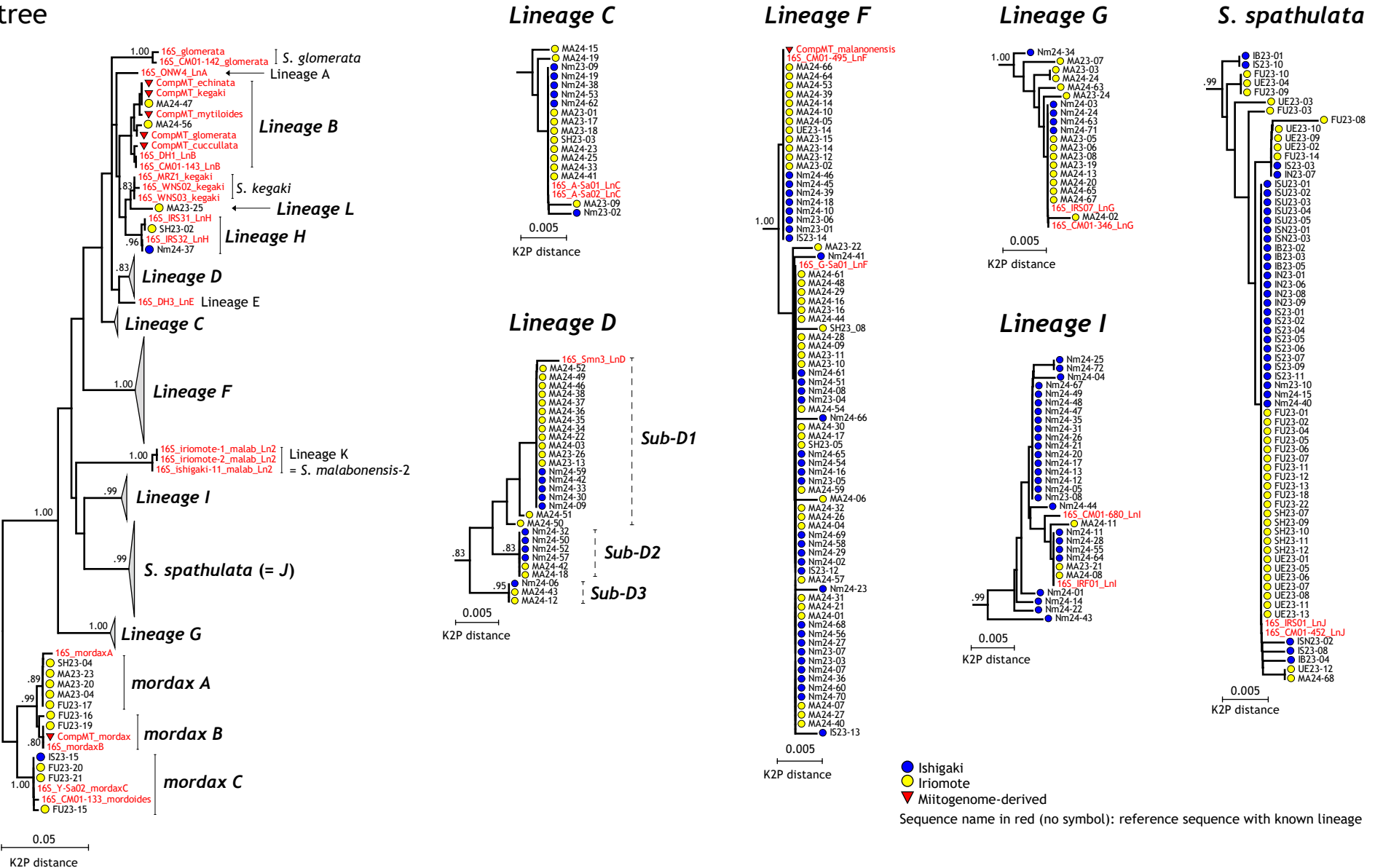
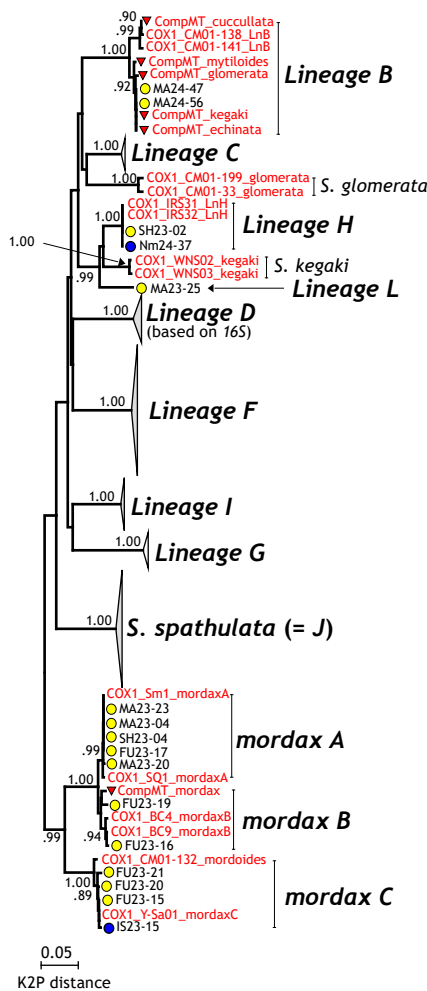


Supplementary Material 7. Single-gene NJ trees

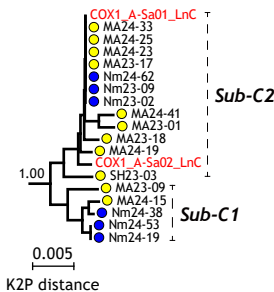
The *mordax* group was set as the outgroup. Lineages detected in the present study are indicated by bold, enlarged, and italicized names. Node credibility values are given for nodes with bootstrap probability ≥ 0.80 . Because no reference sequence was available for Lineage D in the *COX1* gene, and for Lineages B, D as well as the three *mordax* lineages in the *COX3* and *NAD3* genes, clustering patterns in *16S* and/or *COX1* trees were cross-referenced to identify these lineages in each gene tree. Sublineages (within Lineages C, D, and *S. spathulata*) were defined based on concatenated sequences (see main text). When clusters corresponding to these sublineage were detected in gene-specific trees, the respective sublineage names were assigned to those clusters.



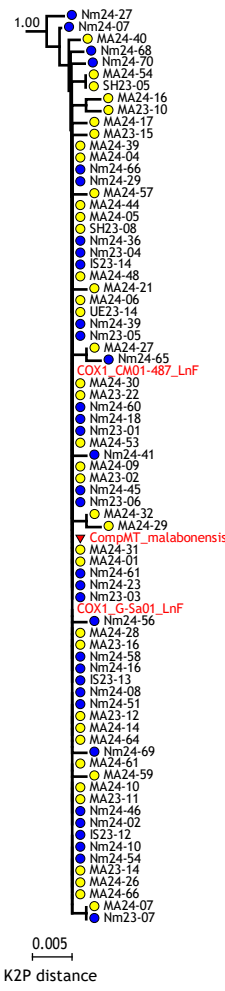
NJ-COX1 tree



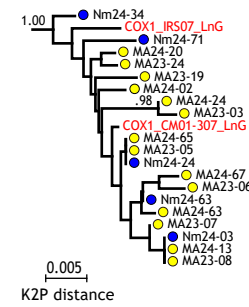
Lineage C



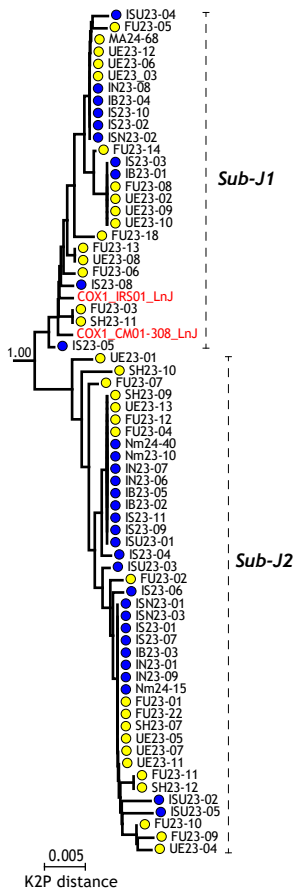
Lineage F



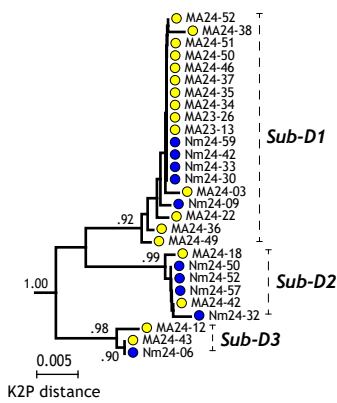
Lineage G



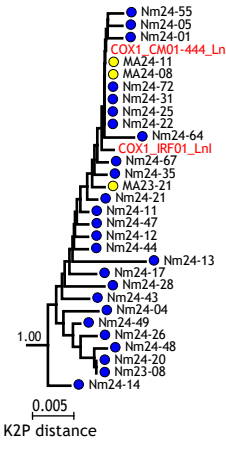
S. spathulata



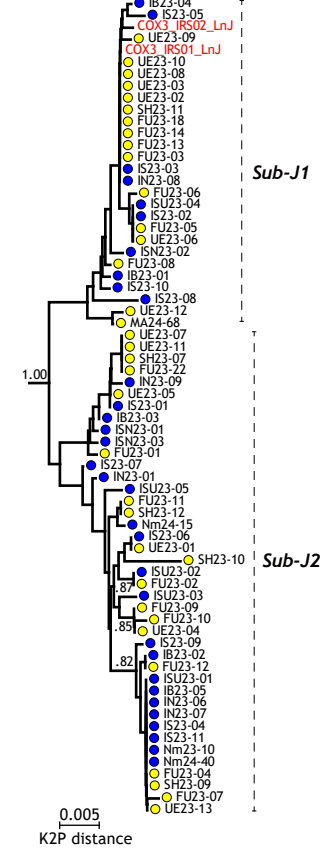
Lineage D



Lineage I

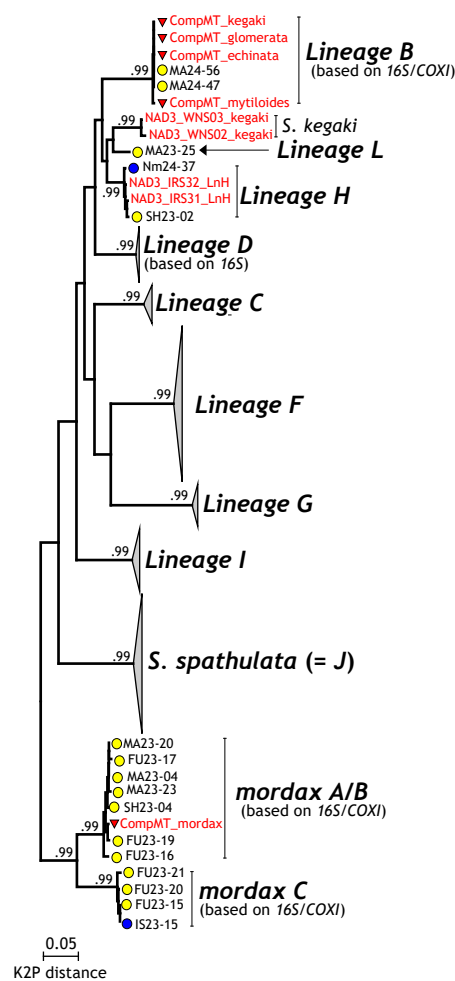


● Ishigaki
● Iriomote
▼ Mitogenome-derived
Sequence name in red (no symbol): reference sequence with known lineage

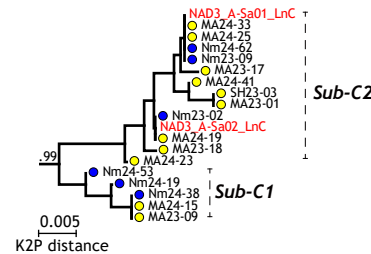


● Ishigaki
 ● Iriomote
 ▼ Mitogenome-derived
 Sequence name in red (no symbol): reference sequence with known lineage

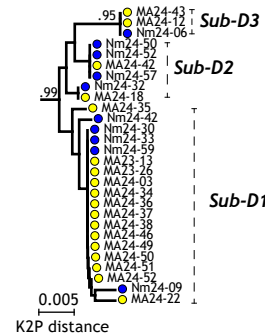
NJ-NAD3 tree



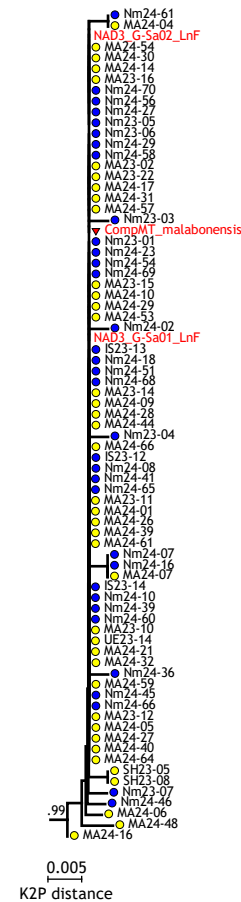
Lineage C



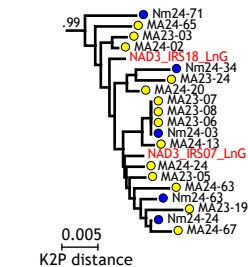
Lineage D



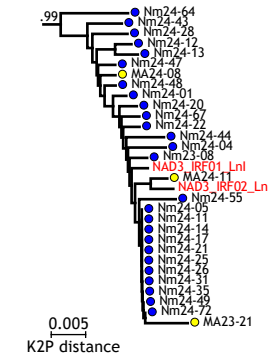
Lineage F



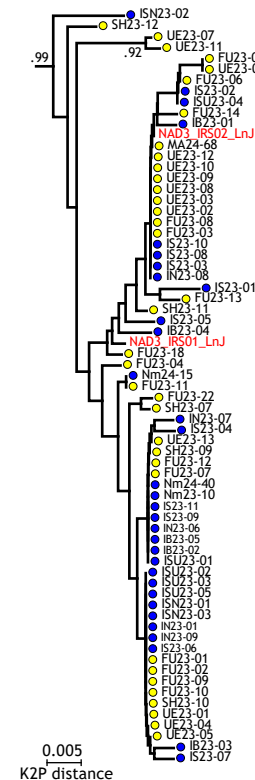
Lineage G



Lineage I



S. spathulata



● Ishigaki
● Iriomote
▼ Mitogenome-derived
Sequence name in red (no symbol): reference sequence with known lineage