APPENDIX D

Phylogenetic tree reconstruction of the parrot and cockatoo families using MrBayes and various methods and models in MEGA5
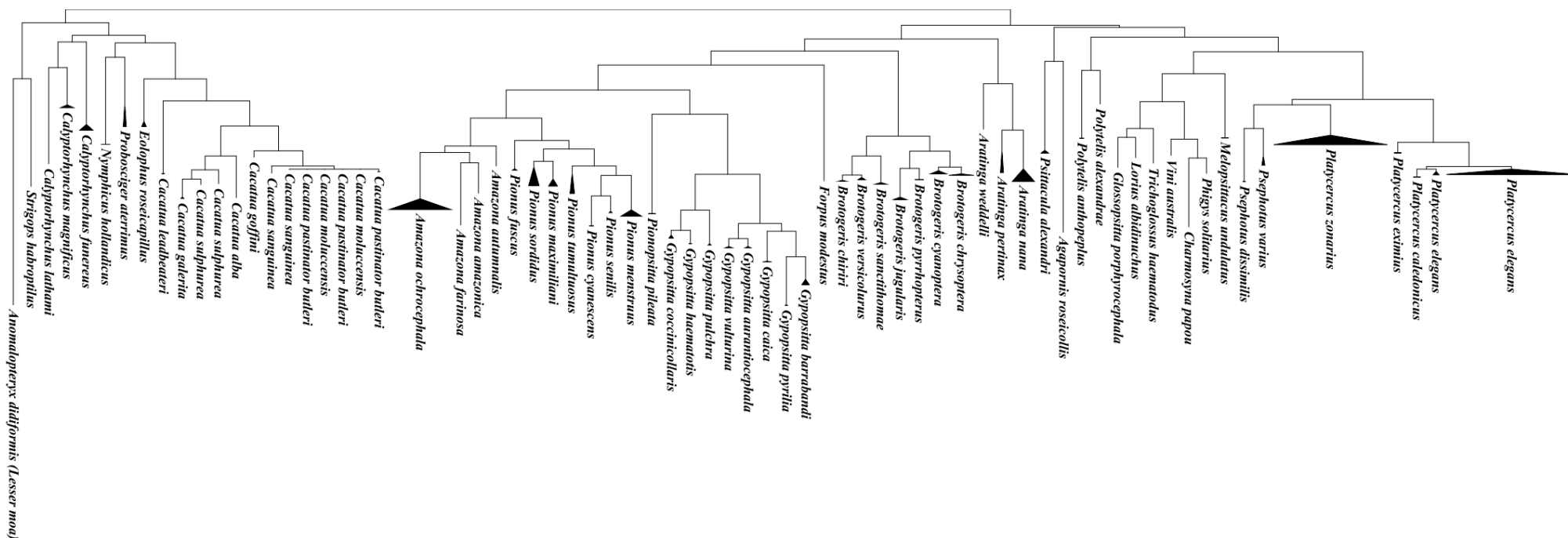

Figure D.1: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND2 gene of parrot and cockatoo species using Maximum Likelihood method, Jukes-Cantor model in MEGA 5 program.
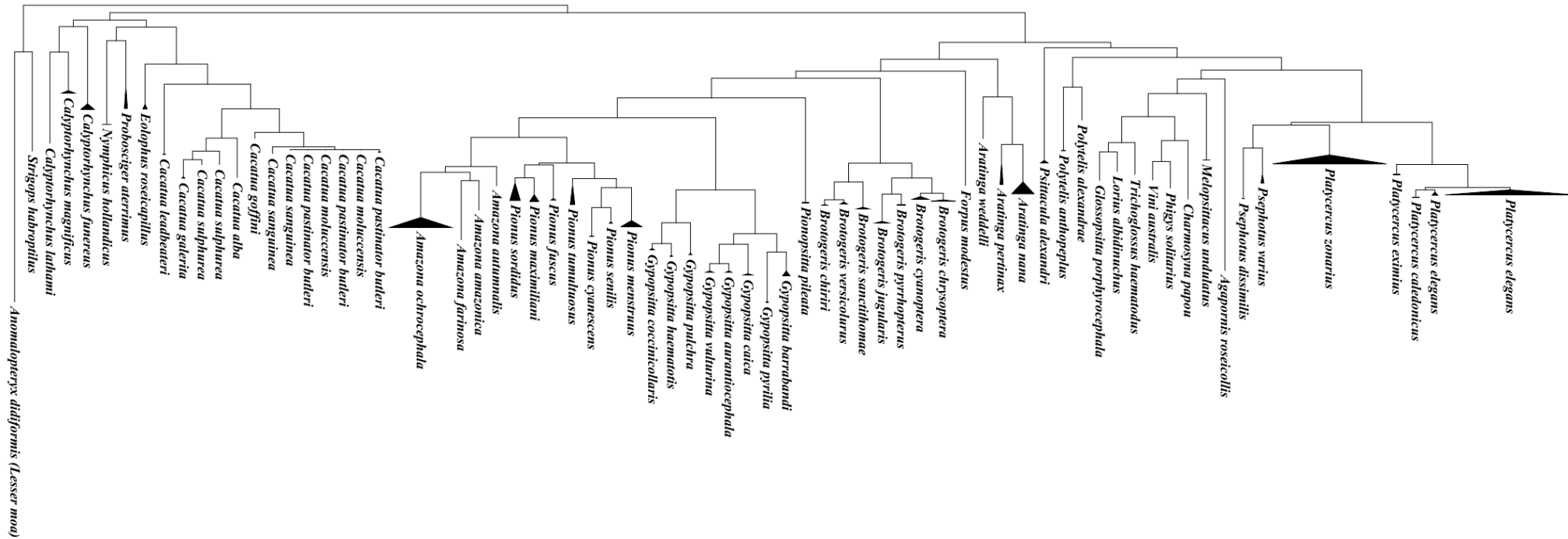
Figure D.2: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND2 gene of parrot and cockatoo species using Maximum Likelihood method, Kimura 2-parameter model in MEGA 5 program.

Figure D.3: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND2 gene of parrot and cockatoo species using Maximum Likelihood method, Tamura 3-parameter model in MEGA 5 program.
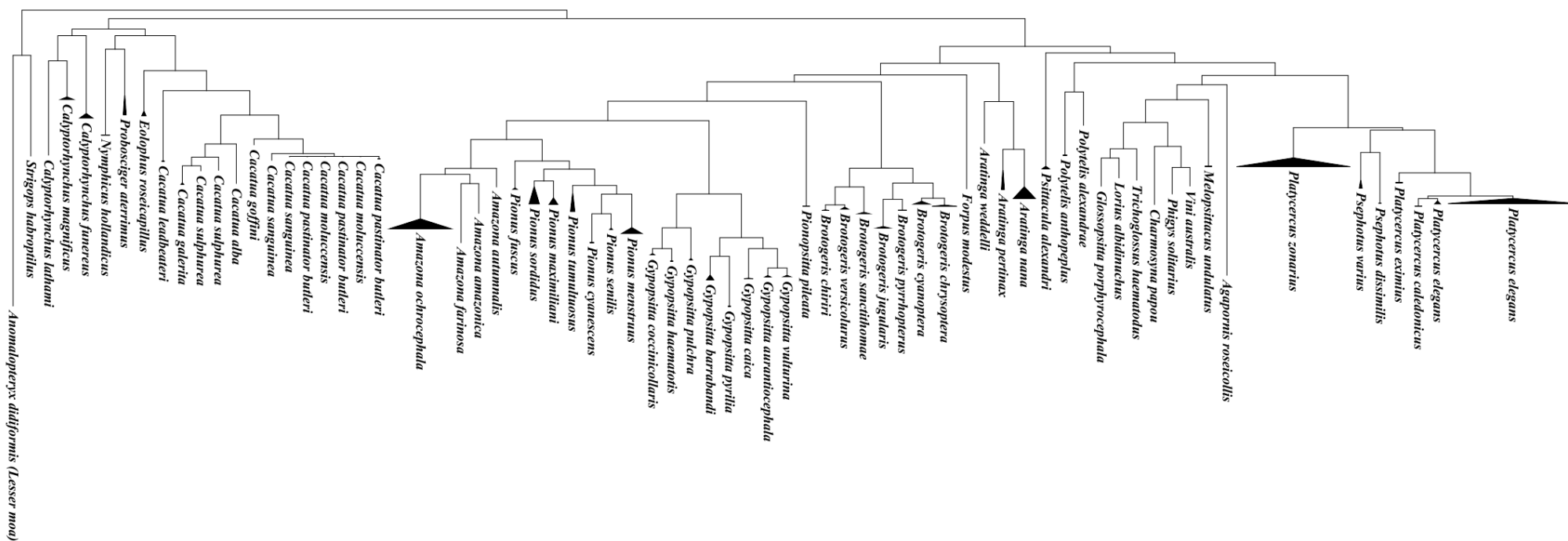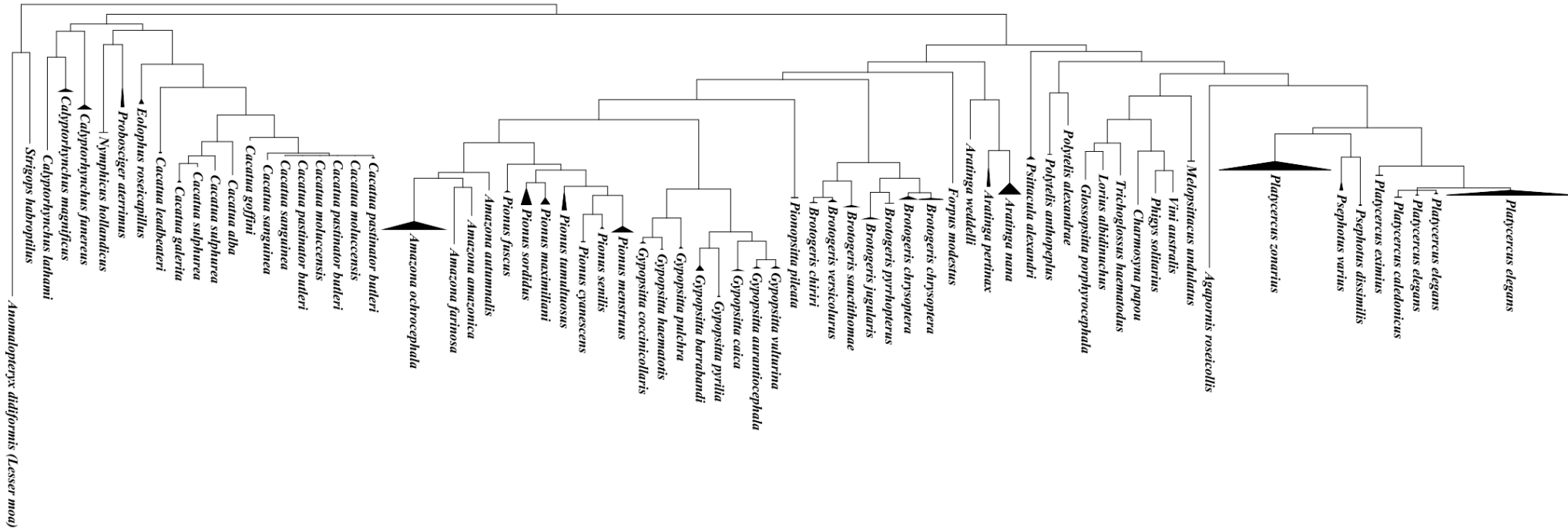
Figure D.4: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND2 gene of parrot and cockatoo species using Maximum Likelihood method, Hasegawa-Kishino-Yano model in MEGA 5 program.
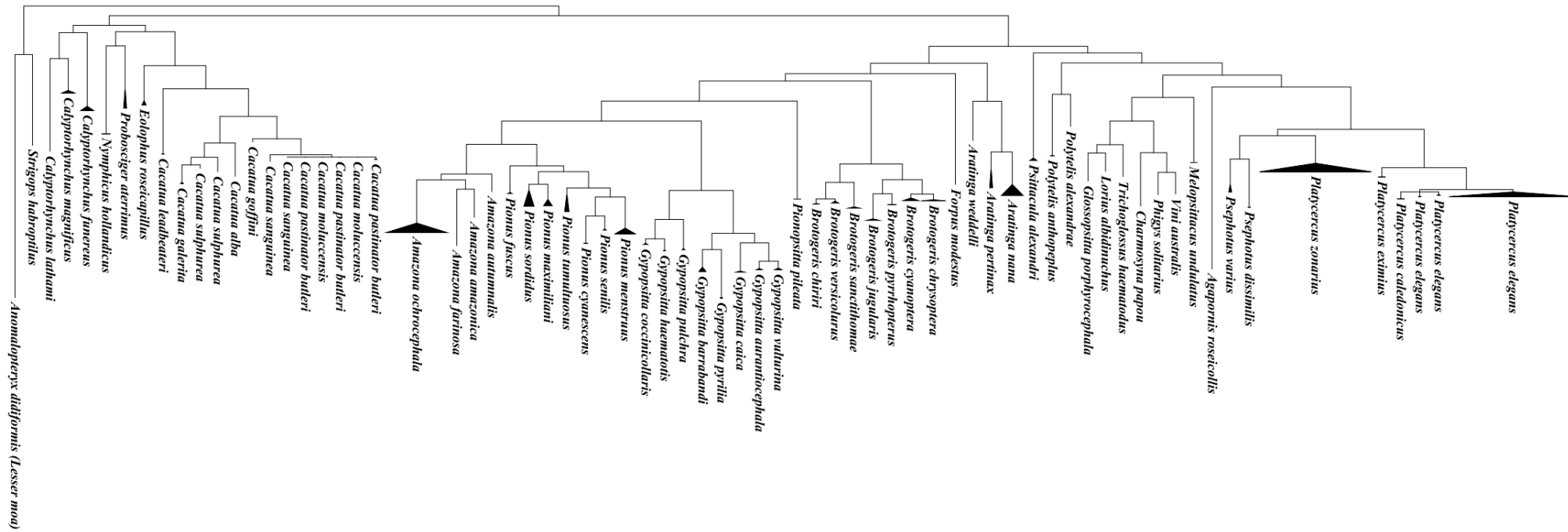
Figure D.5: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND2 gene of parrot and cockatoo species using Maximum Likelihood method, Tamura-Nei model in MEGA 5 program.

Figure D.6: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND2 gene of parrot and cockatoo species using Maximum Likelihood method, General Time Reversible model in MEGA 5 program.
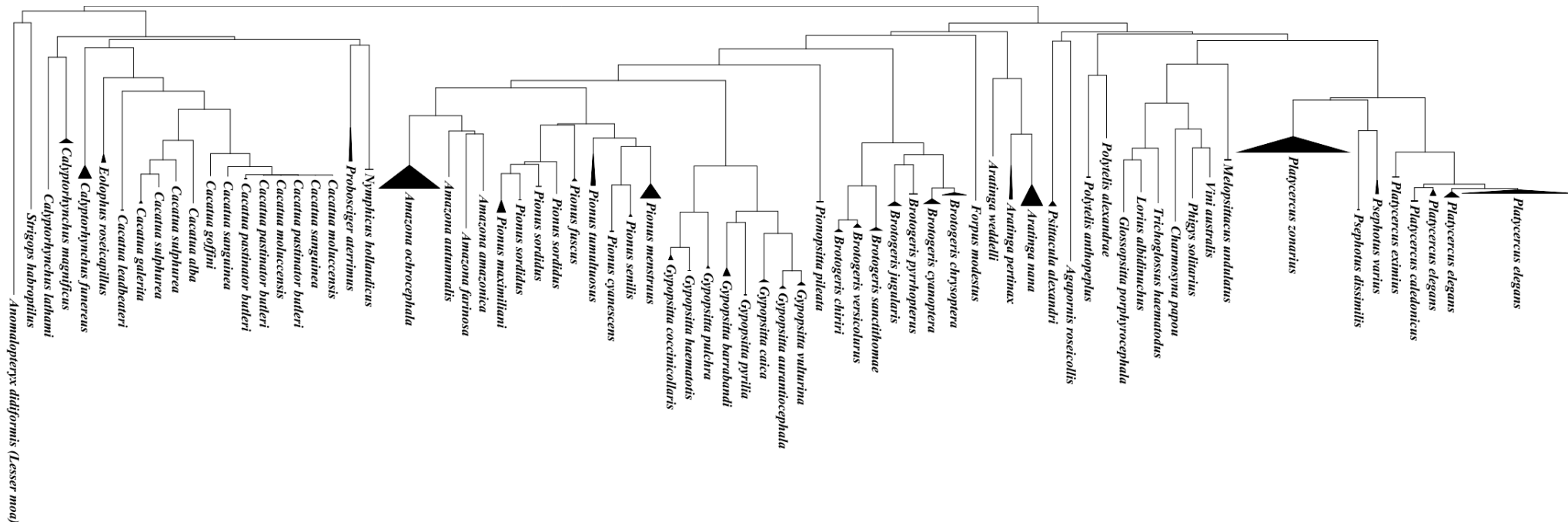
Figure D.7: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND2 gene of parrot and cockatoo species using Neighbor-Joining method, No. of differences model in MEGA 5 program.
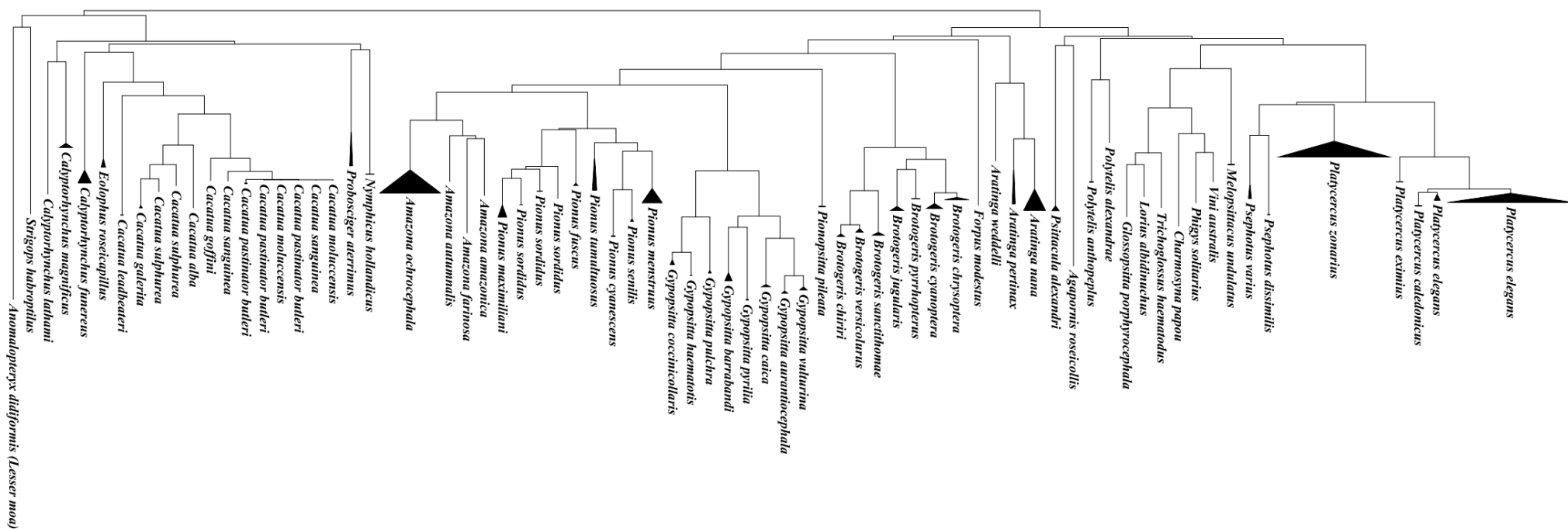
Figure D.8: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND2 gene of parrot and cockatoo species using Neighbor-Joining method, p-distance model in MEGA 5 program.

Figure D.9: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND2 gene of parrot and cockatoo species using Neighbor-Joining method, Jukes-Cantor model in MEGA 5 program.
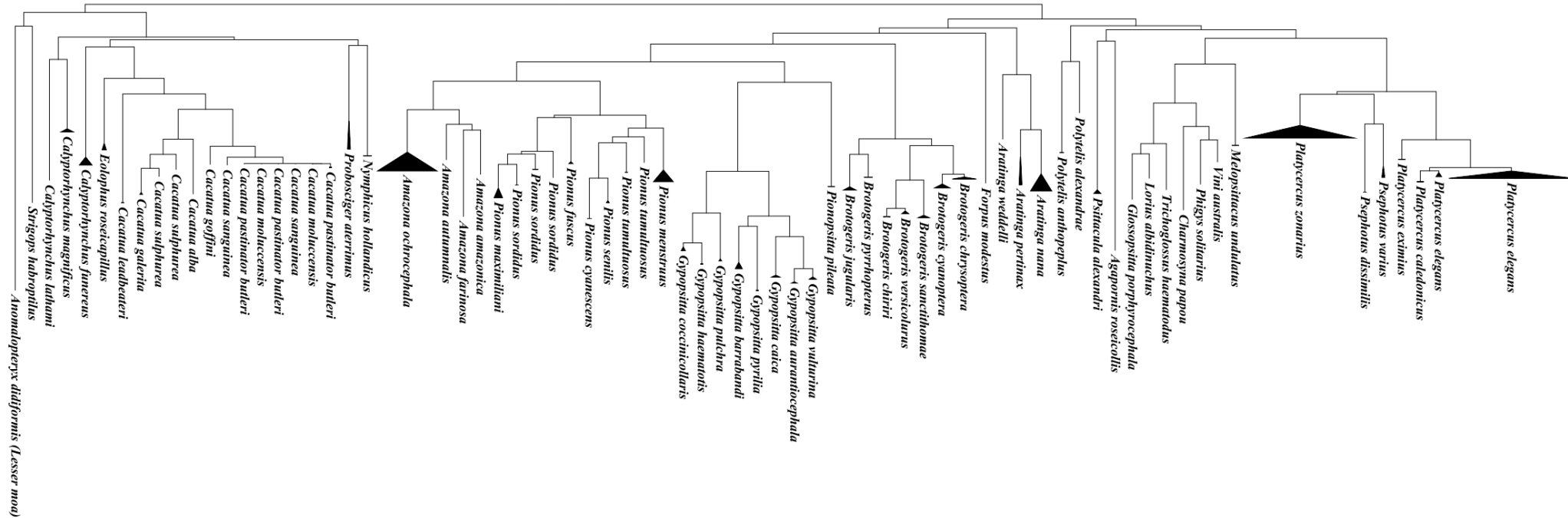
Figure D.10: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND2 gene of parrot and cockatoo species using Neighbor-Joining method, Kimura 2-parameter model in MEGA 5 program.
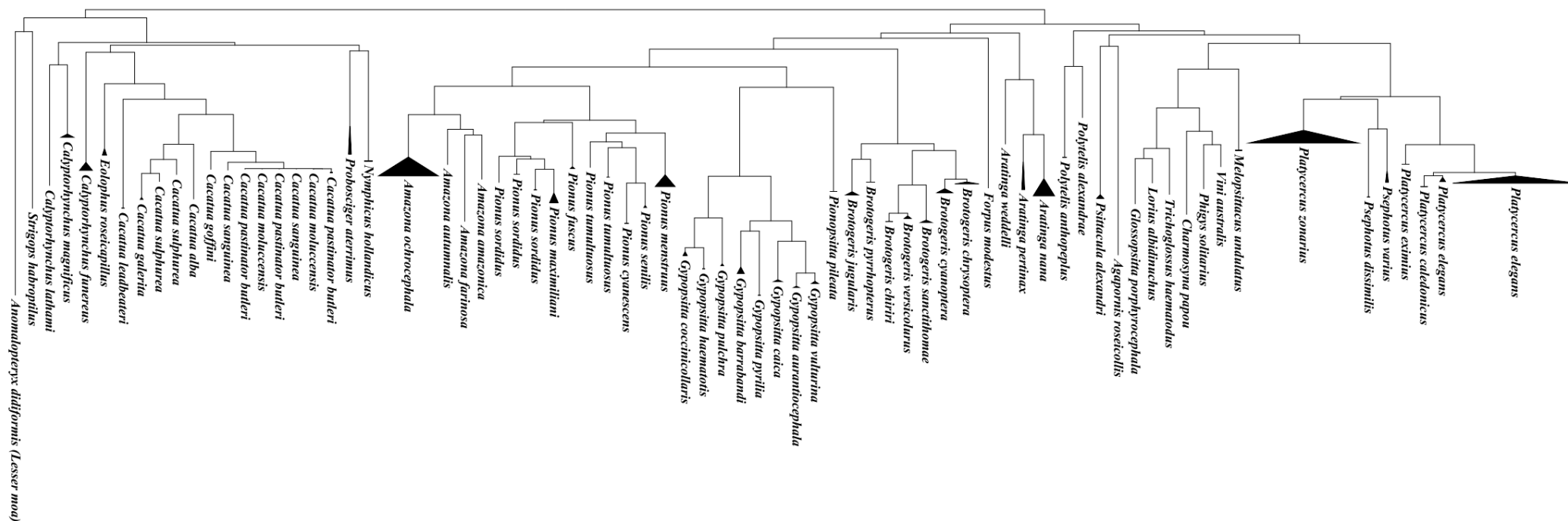
Figure D.11: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND2 gene of parrot and cockatoo species using Neighbor-Joining method, Tajima-Nei model in MEGA 5 program.
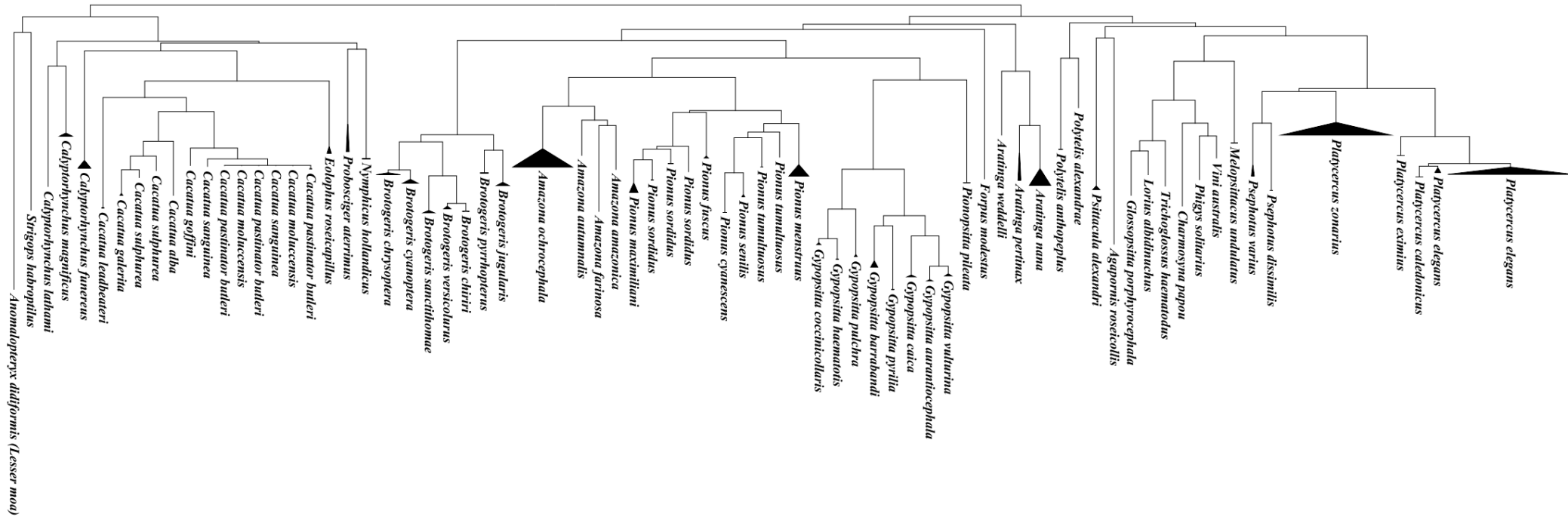
Figure D.12: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND2 gene of parrot and cockatoo species using Neighbor-Joining method, Tamura 3-parameter model in MEGA 5 program.

Figure D.13: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND2 gene of parrot and cockatoo species using Neighbor-Joining method, Tamura-Nei model in MEGA 5 program.
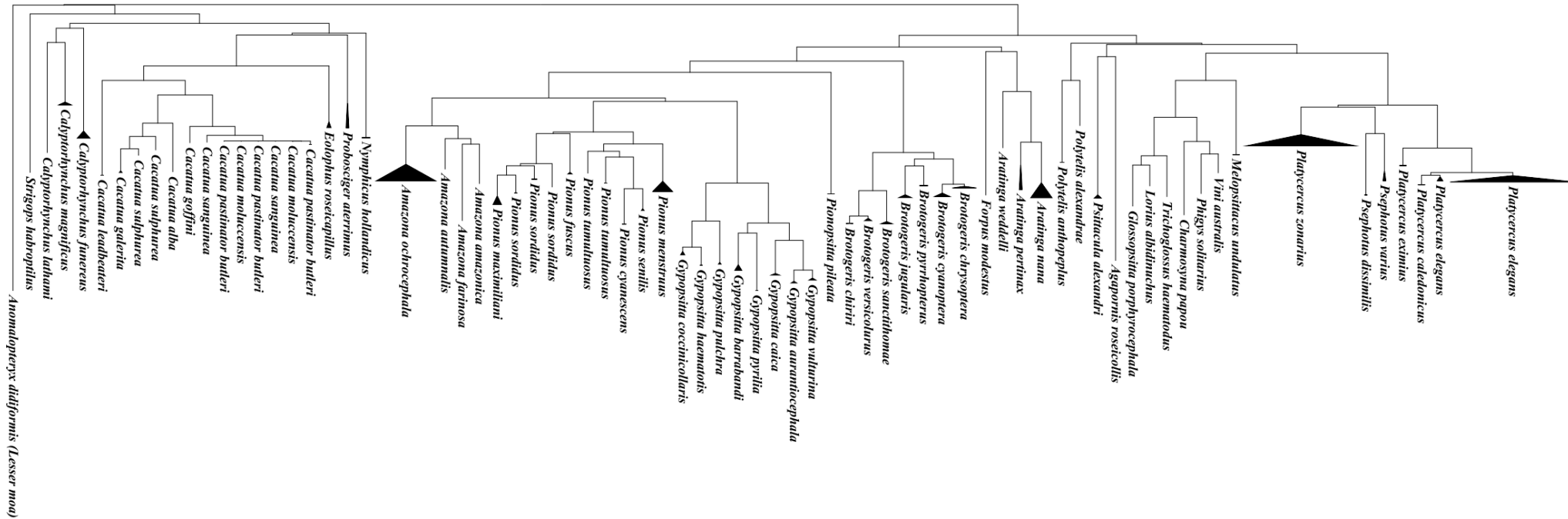
Figure D.14: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND2 gene of parrot and cockatoo species using Neighbor-Joining method, Maximum Composite Likelihood model in MEGA 5 program.
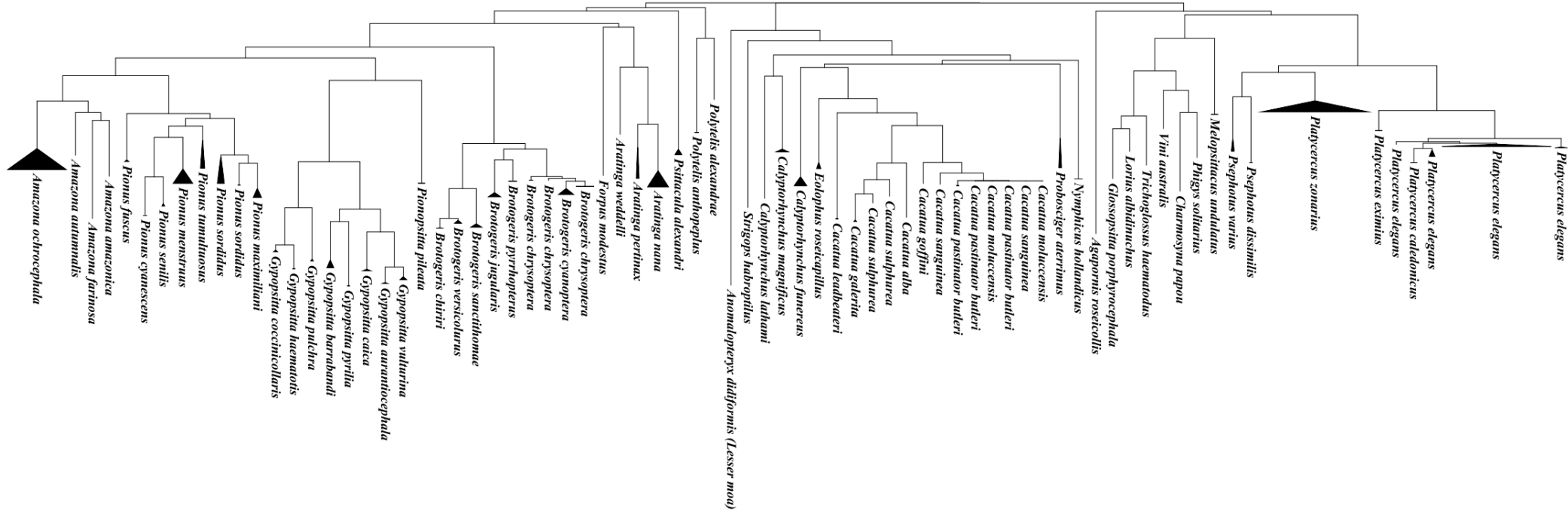
Figure D.15: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND2 gene of parrot and cockatoo species using Neighbor-Joining method, LogDet (Tamura-Kumar) model in MEGA 5 program.
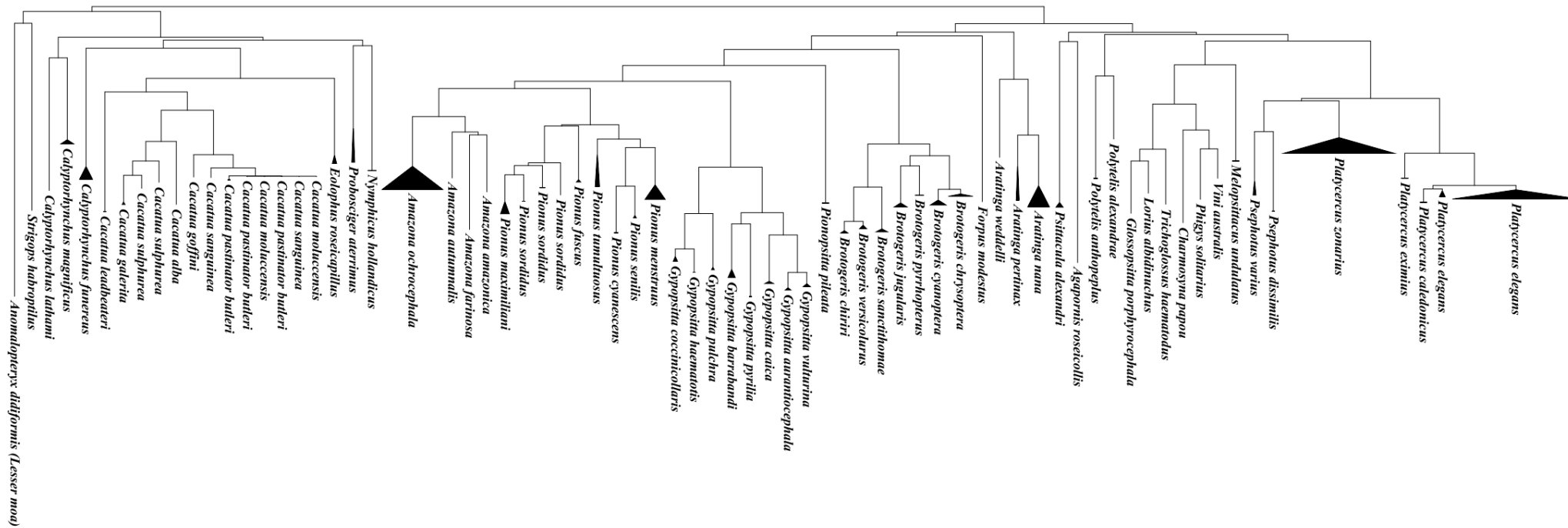
Figure D.16: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND2 gene of parrot and cockatoo species using Minimum-Evolution method, No. of differences model in MEGA 5 program.
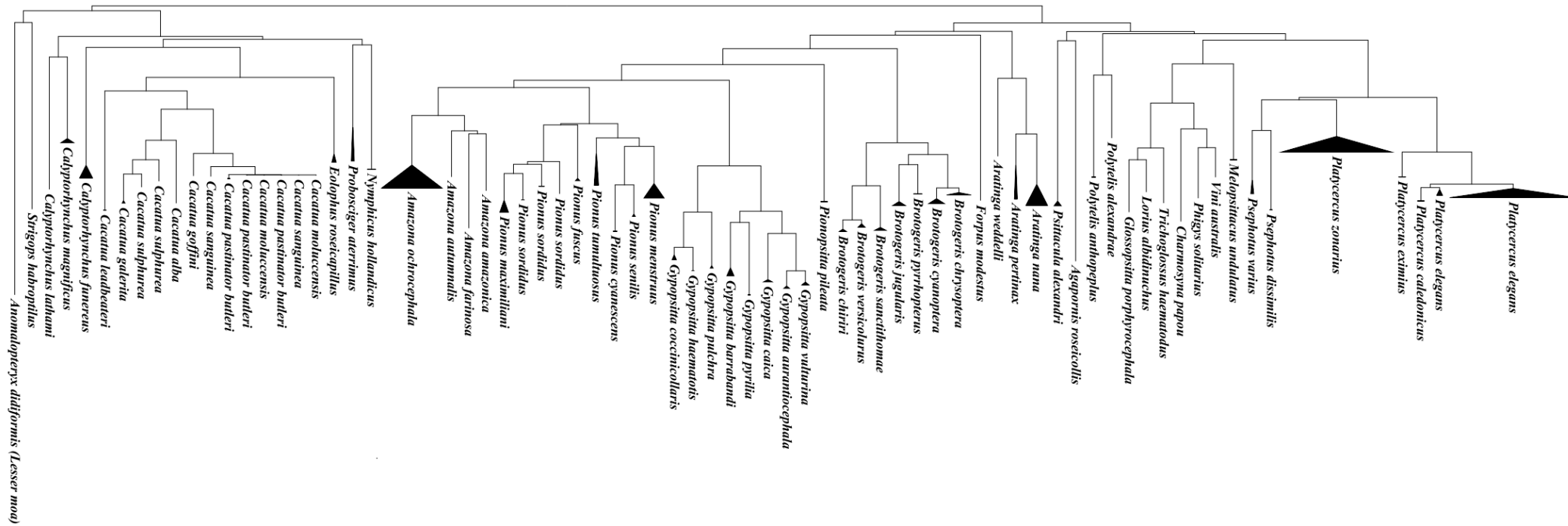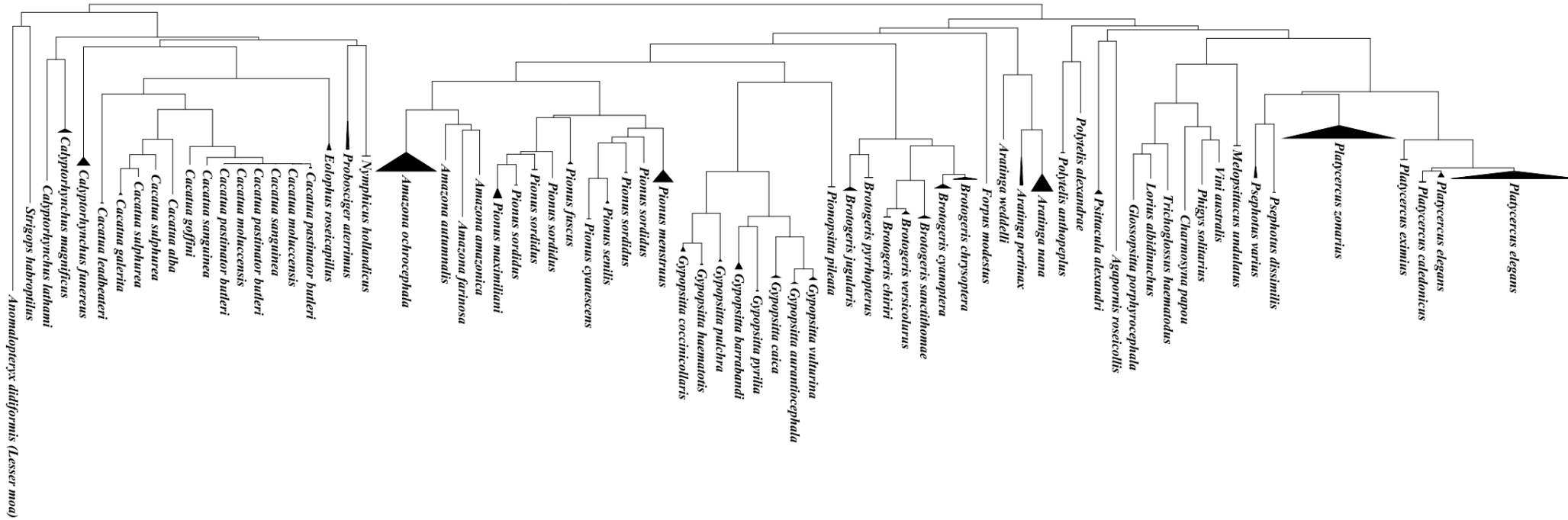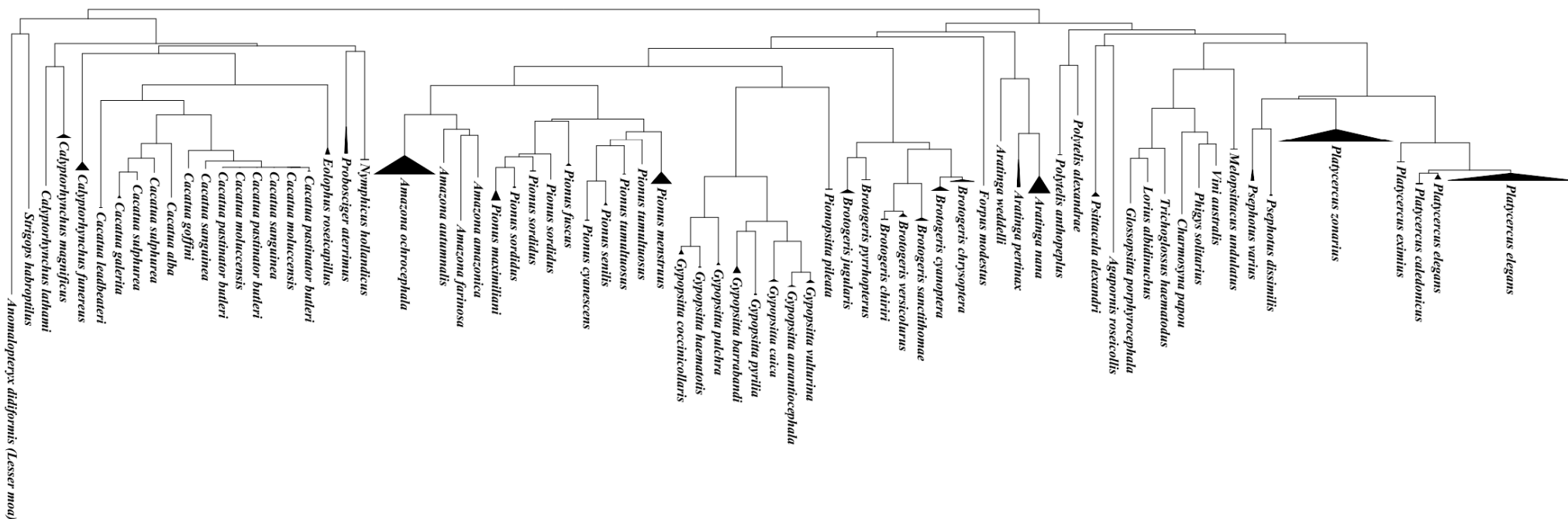
Figure D.17: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND2 gene of parrot and cockatoo species using Minimum-Evolution method, p-distance model in MEGA 5 program.

Figure D.18: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND2 gene of parrot and cockatoo species using Minimum-Evolution method, Jukes-Cantor model in MEGA 5 program.

Figure D.19: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND2 gene of parrot and cockatoo species using Minimum-Evolution method, Kimura 2-parameter model in MEGA 5 program.

Figure D.20: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND2 gene of parrot and cockatoo species using Minimum-Evolution method, Tajima-Nei model in MEGA 5 program.

Figure D.21: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND2 gene of parrot and cockatoo species using Minimum-Evolution method, Tamura 3-parameter model in MEGA 5 program.
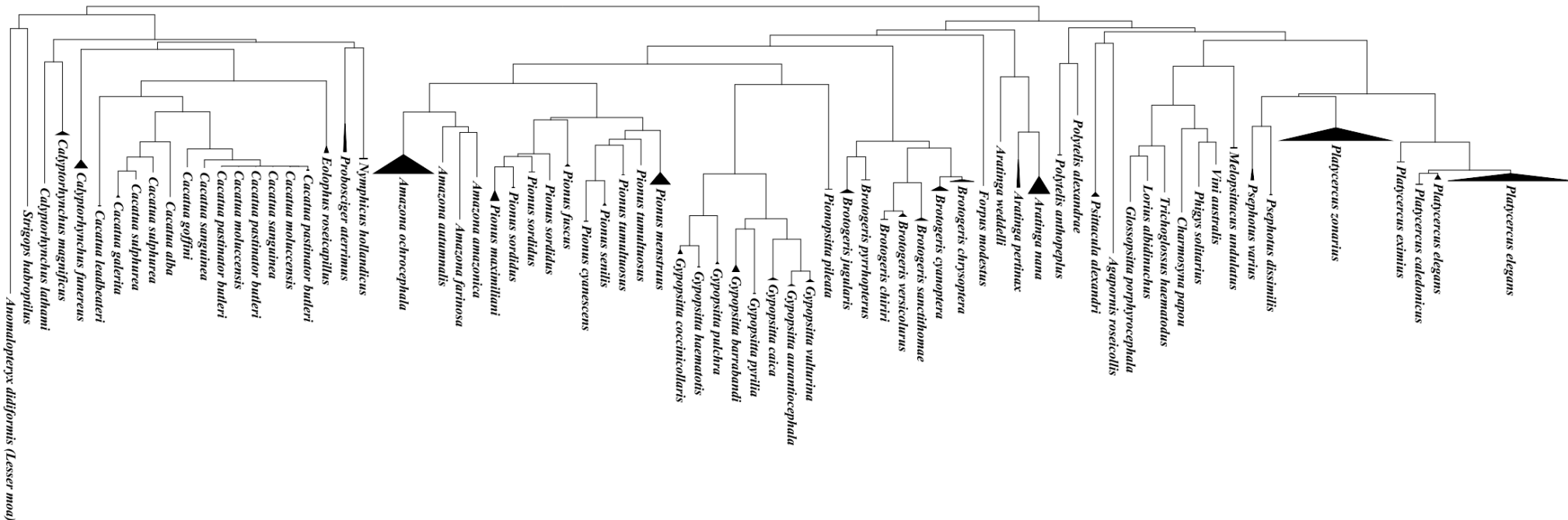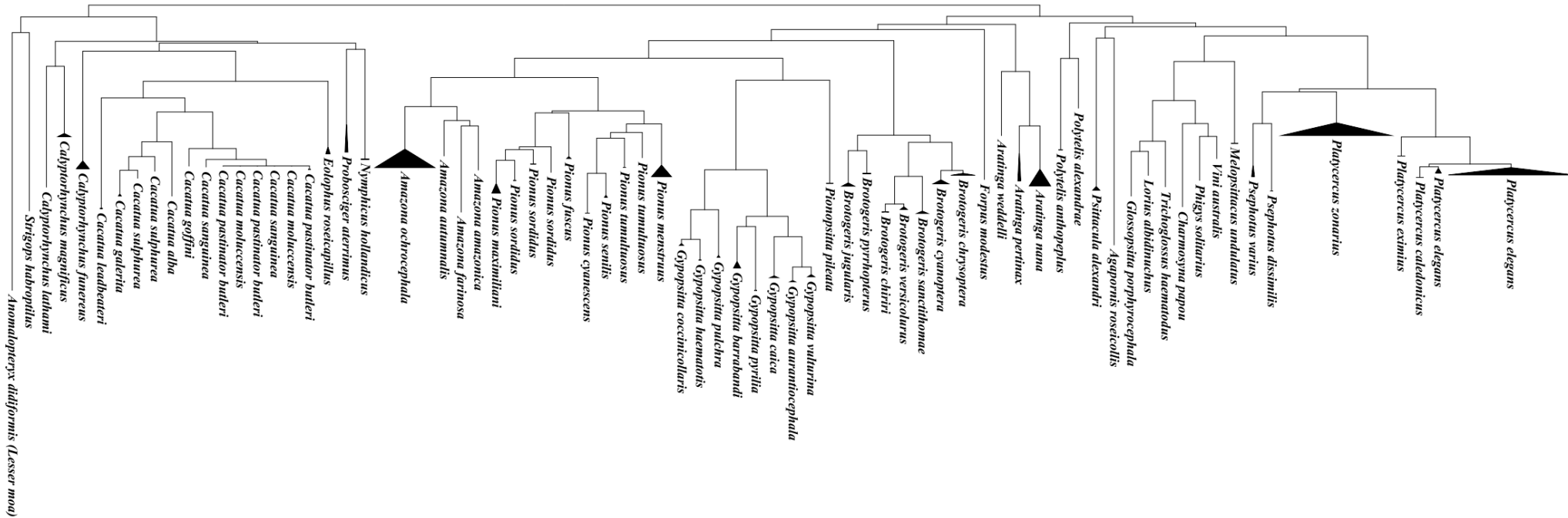
Figure D.22: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND2 gene of parrot and cockatoo species using Minimum-Evolution method, Tamura-Nei model in MEGA 5 program.
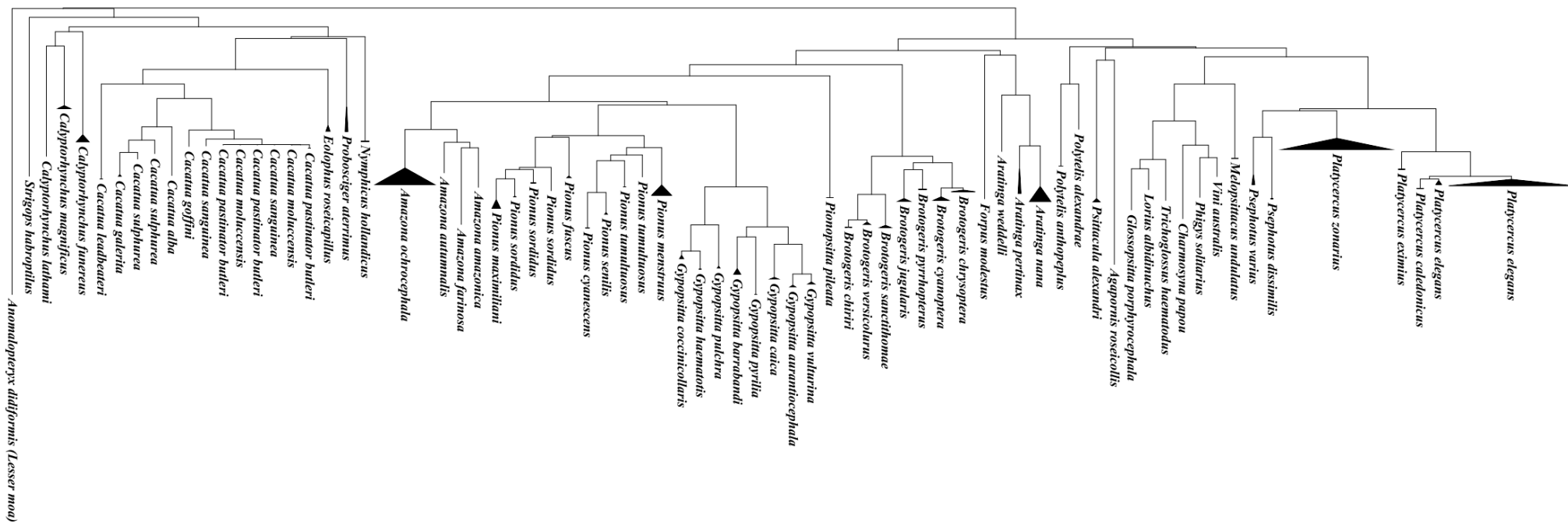
Figure D.23: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND2 gene of parrot and cockatoo species using Minimum-Evolution method, Maximum Composite Likelihood model in MEGA 5 program.

Figure D.24: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND2 gene of parrot and cockatoo species using Minimum-Evolution method, LogDet (Tamura-Kumar) model in MEGA 5 program.
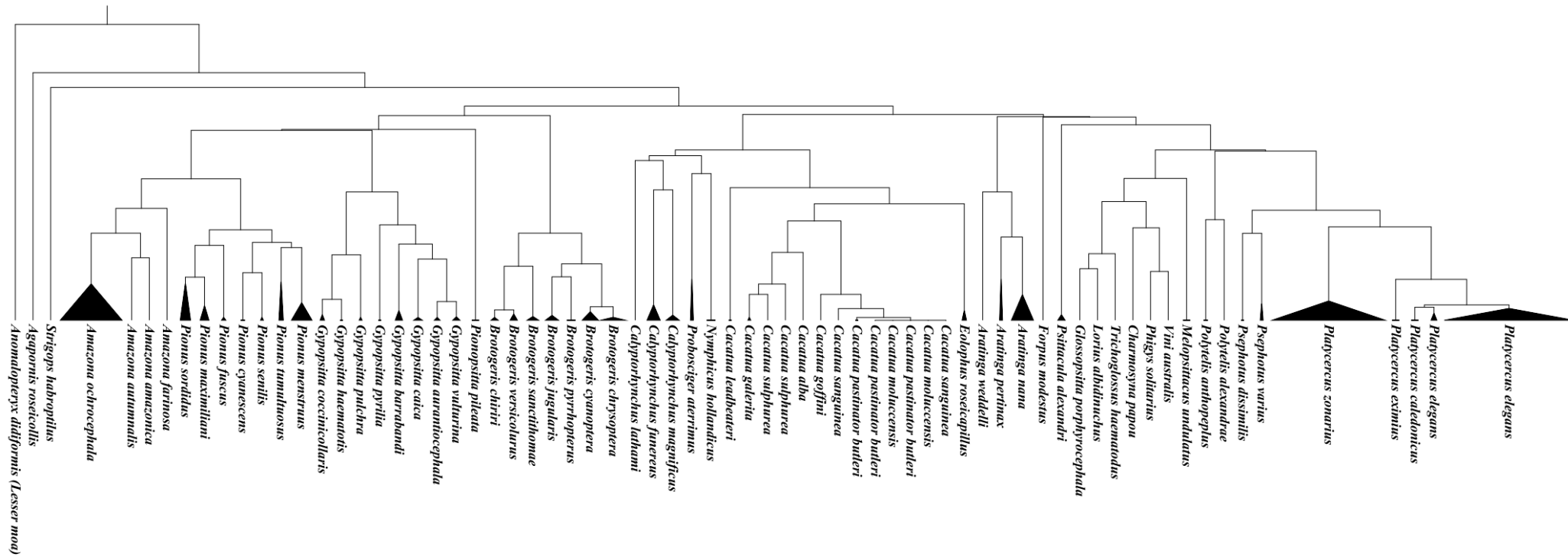
Figure D.25: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND2 gene of parrot and cockatoo species using UPGMA method, No. of differences model in MEGA 5 program.

Figure D.26: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND2 gene of parrot and cockatoo species using UPGMA method, p-distance model in MEGA 5 program.
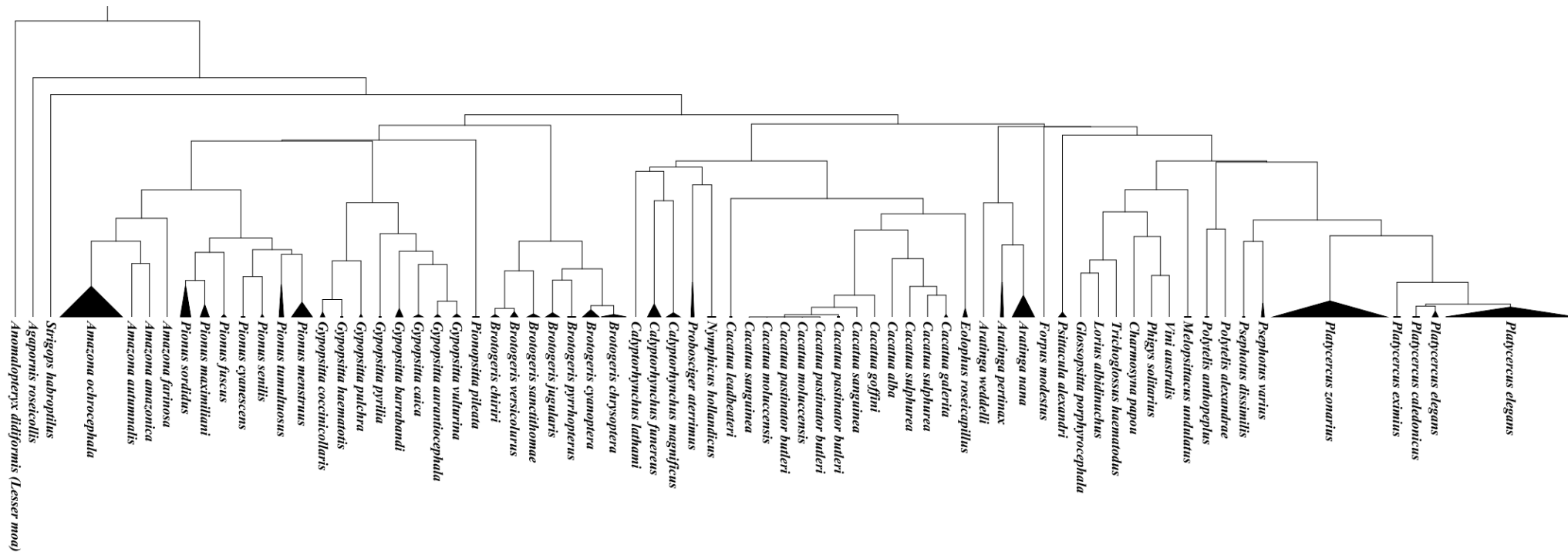
Figure D.27: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND2 gene of parrot and cockatoo species using UPGMA method, Jukes-Cantor model in MEGA 5 program.
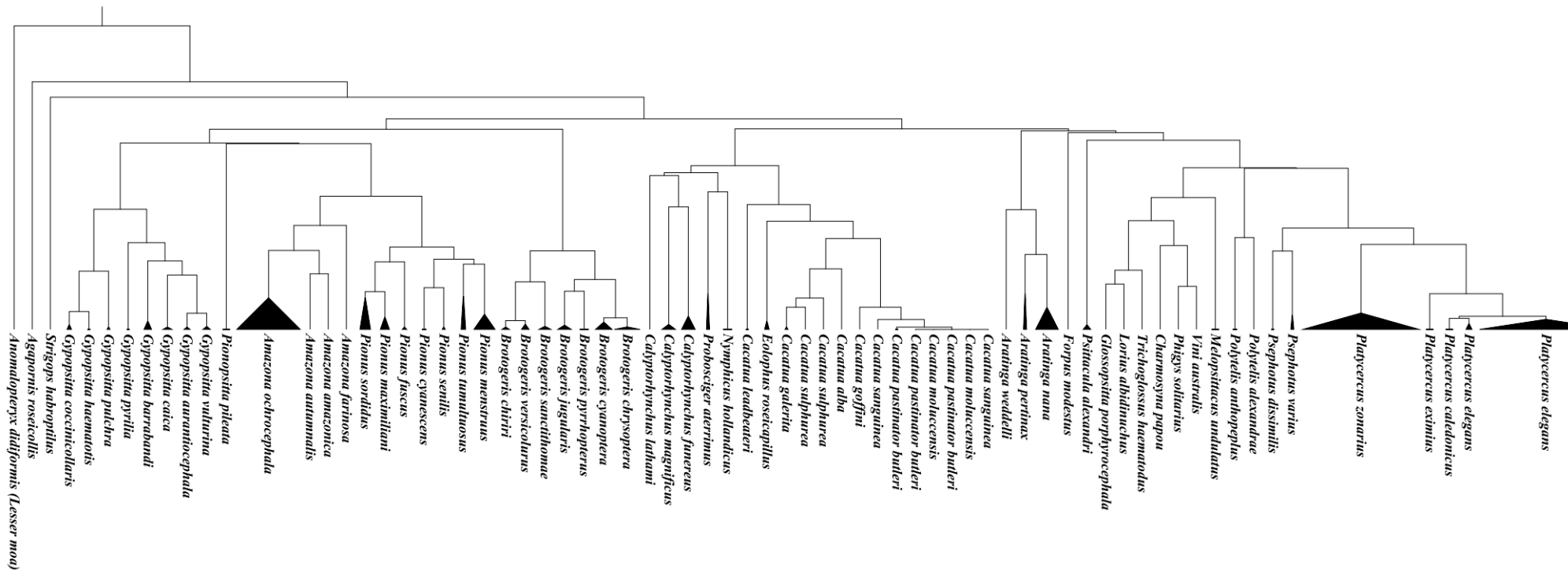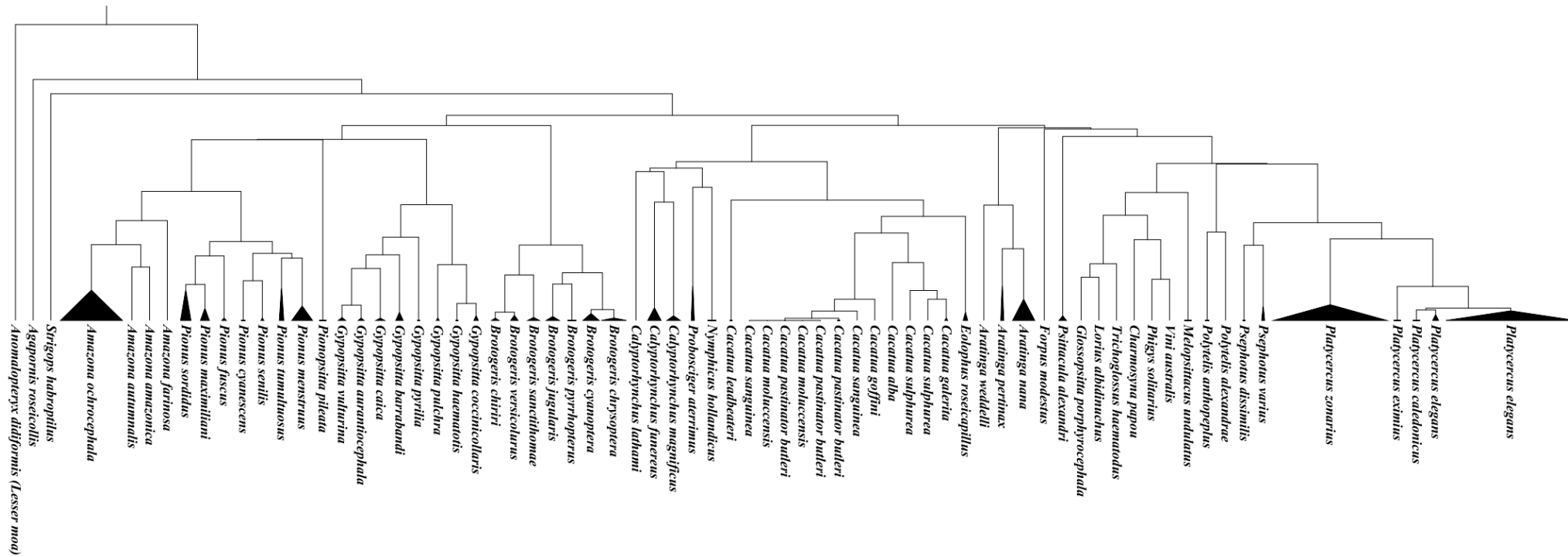
Figure D.28: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND2 gene of parrot and cockatoo species using UPGMA method, Kimura 2-parameter model in MEGA 5 program.

Figure D.29: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND2 gene of parrot and cockatoo species using UPGMA method, Tajima-Nei model in MEGA 5 program.

Figure D.30: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND2 gene of parrot and cockatoo species using UPGMA method, Tamura 3-parameter model in MEGA 5 program.
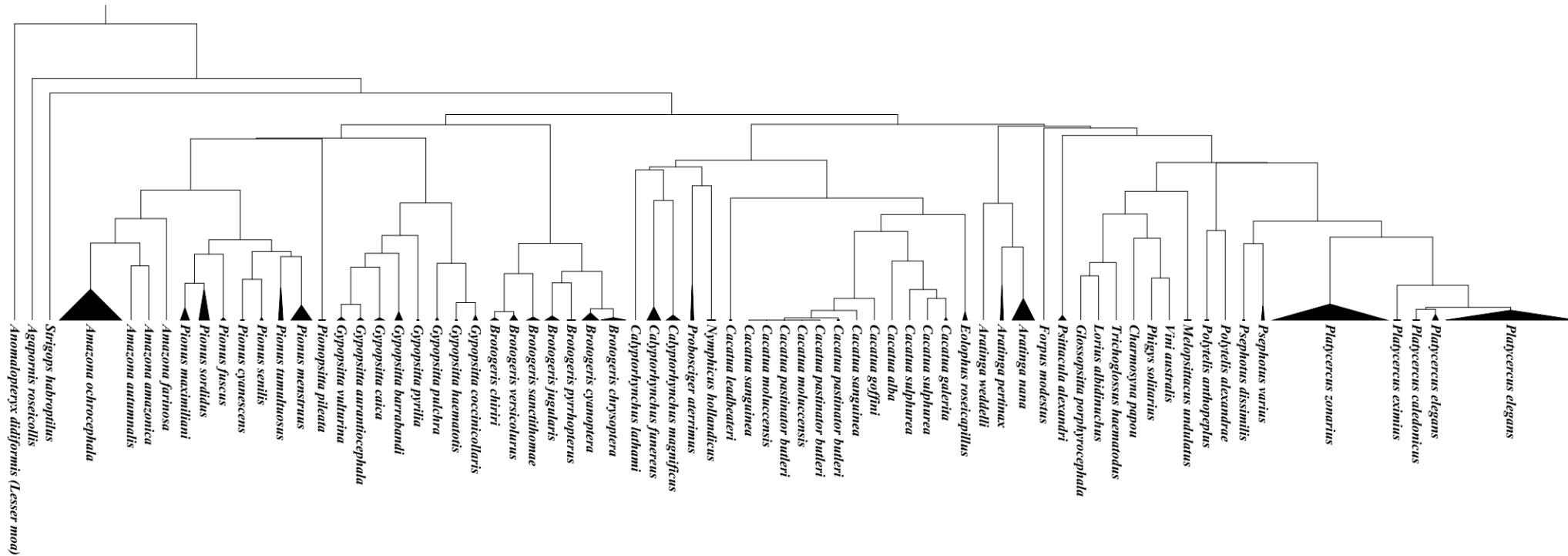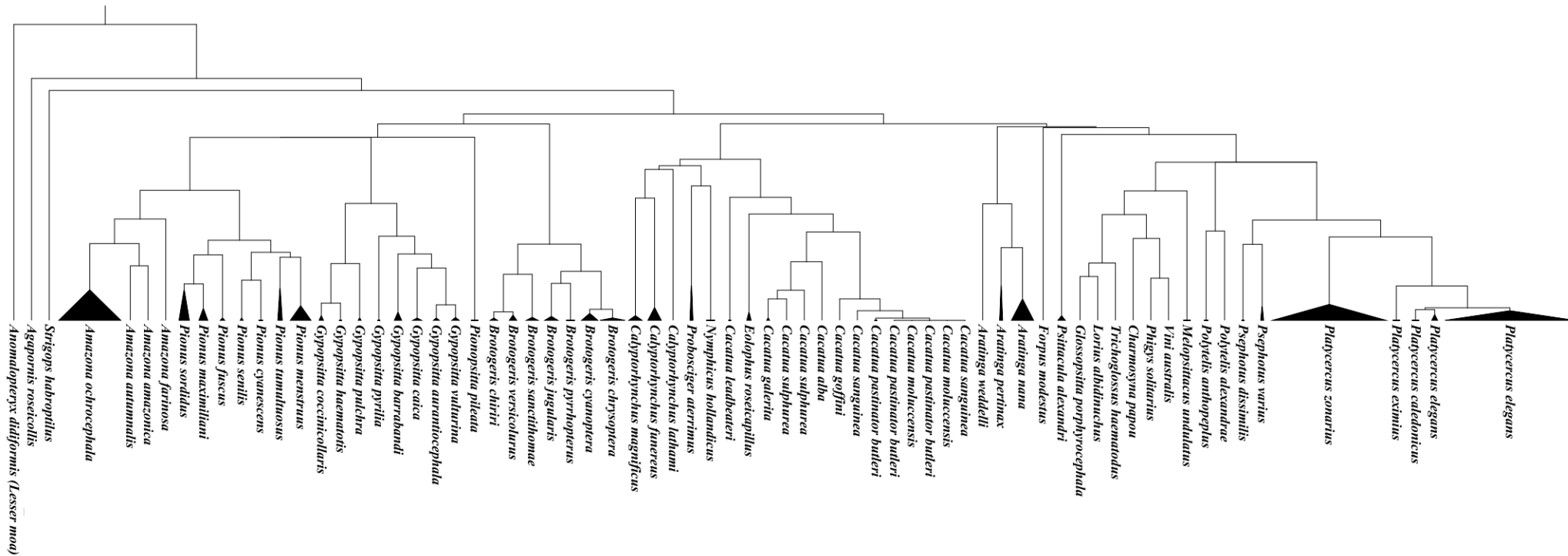
Figure D.31: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND2 gene of parrot and cockatoo species using UPGMA method, Tamura-Nei model in MEGA 5 program.
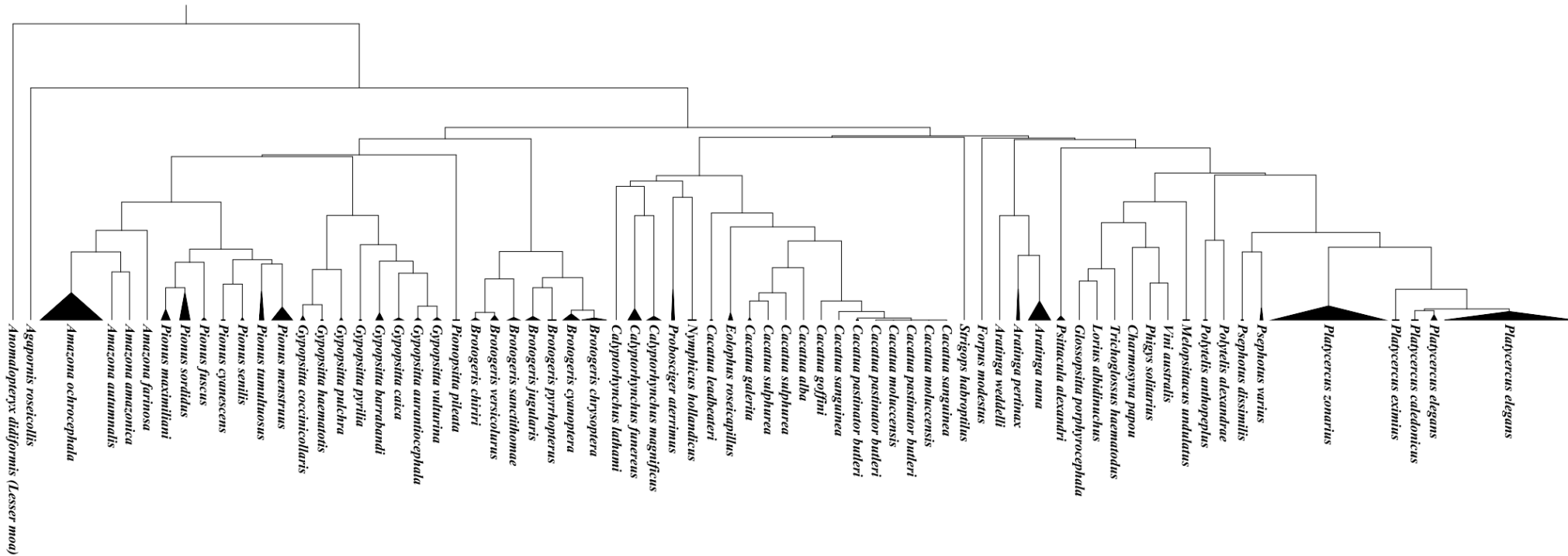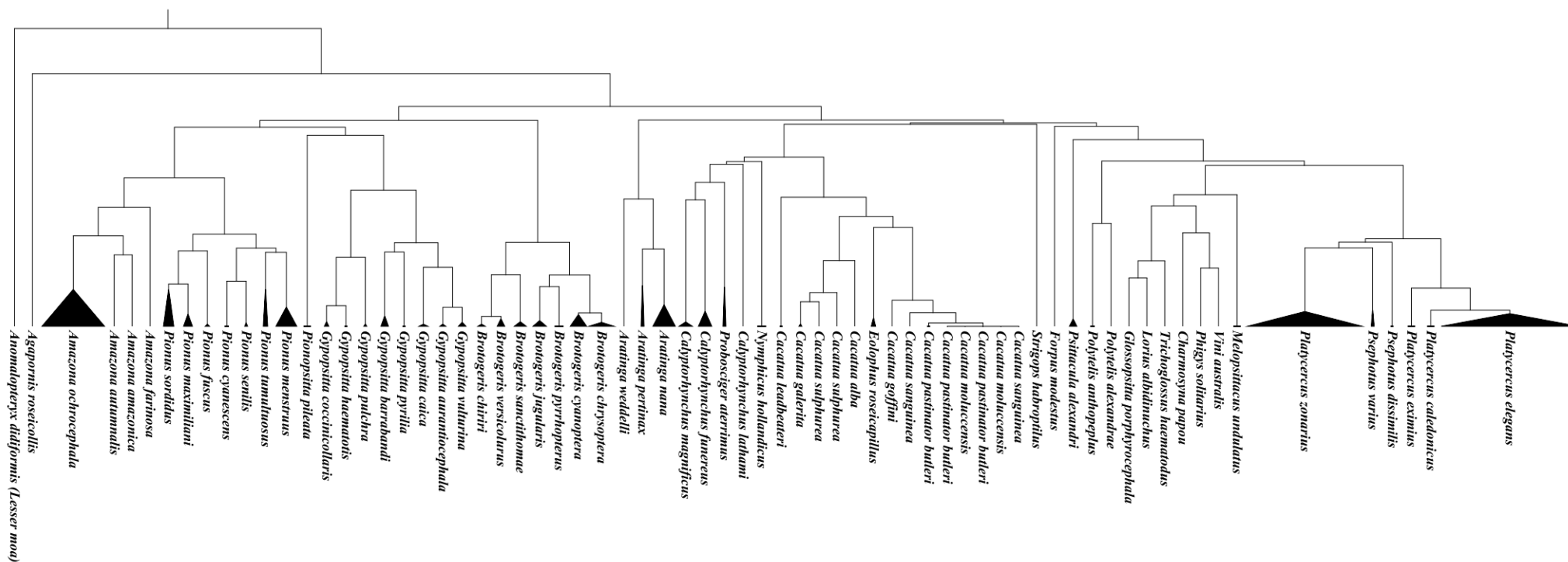
Figure D.32: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND2 gene of parrot and cockatoo species using UPGMA method, Maximum Composite Likelihood model in MEGA 5 program.
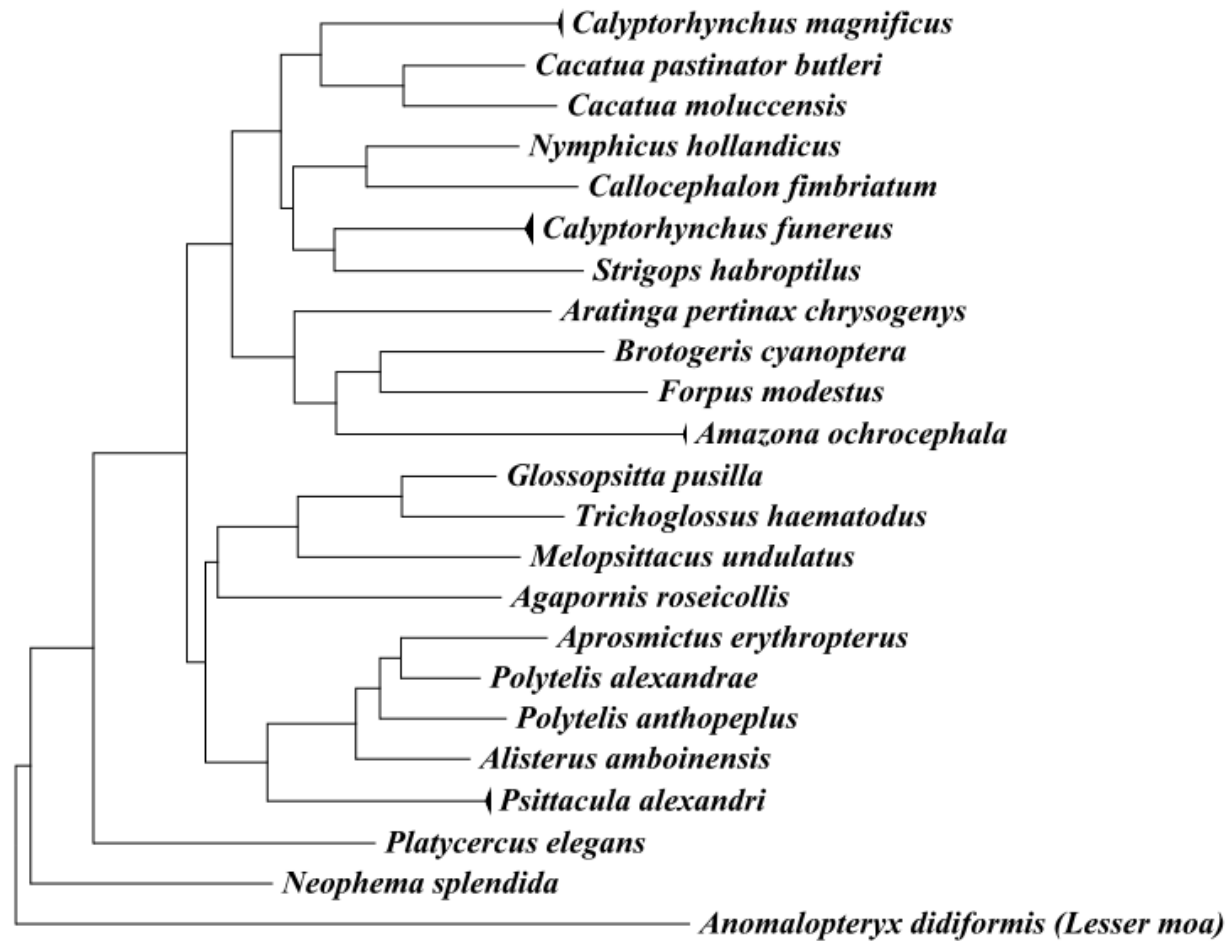
Figure D.33: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND2 gene of parrot and cockatoo species using UPGMA method, LogDet (Tamura-Kumar) model in MEGA 5 program.

Figure D.34: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND2 gene of parrot and cockatoo species using Maximum Parsimony method in MEGA 5 program.
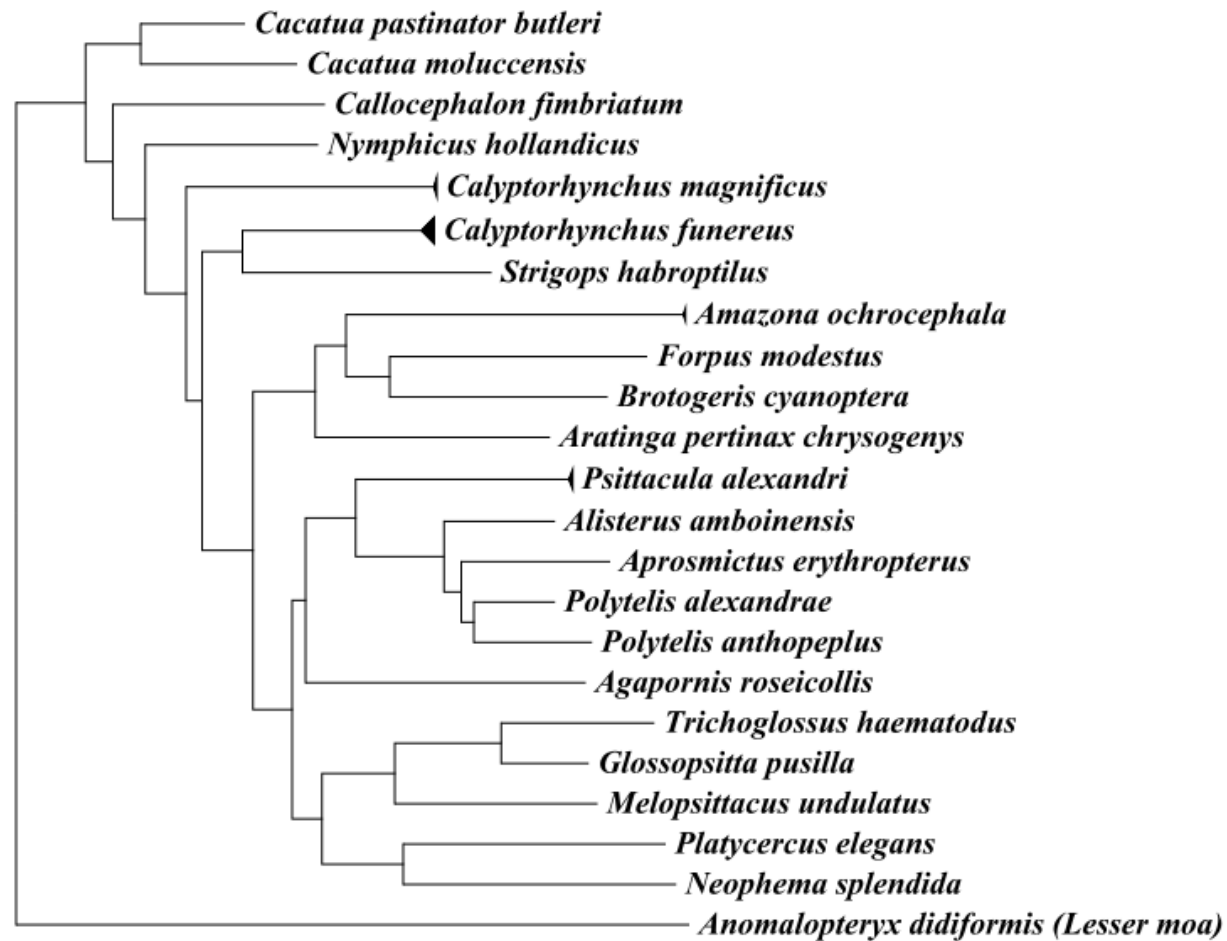
Figure D.35: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND2 gene of parrot and cockatoo species using MrBayes.

Figure D.36: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND5 gene of parrot and cockatoo species using Maximum Likelihood method, Jukes-Cantor model in MEGA 5 program.
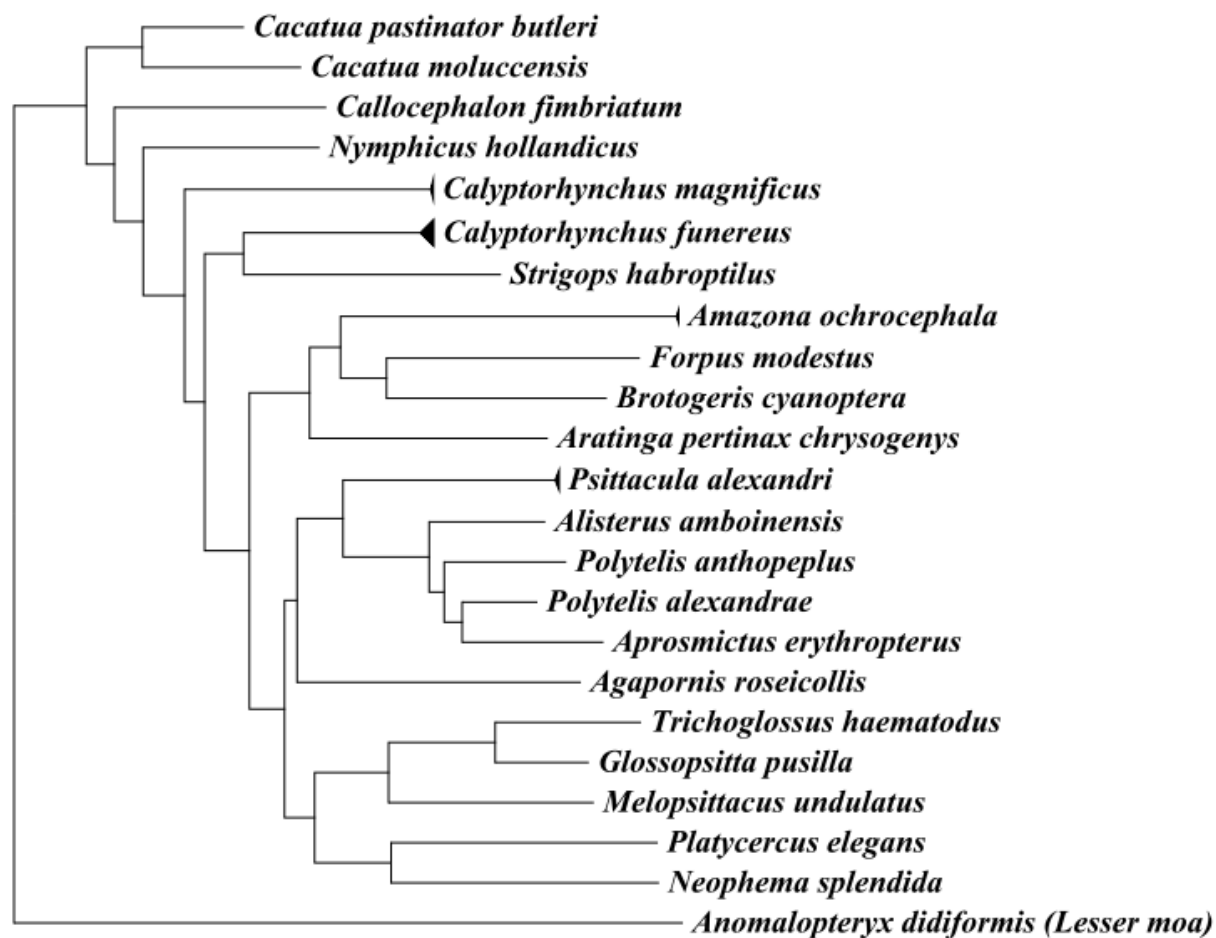
Figure D.37: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND5 gene of parrot and cockatoo species using Maximum Likelihood method, Kimura 2-parameter model in MEGA 5 program.

Figure D.38: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND5 gene of parrot and cockatoo species using Maximum Likelihood method, Tamura 3-parameter model in MEGA 5 program.
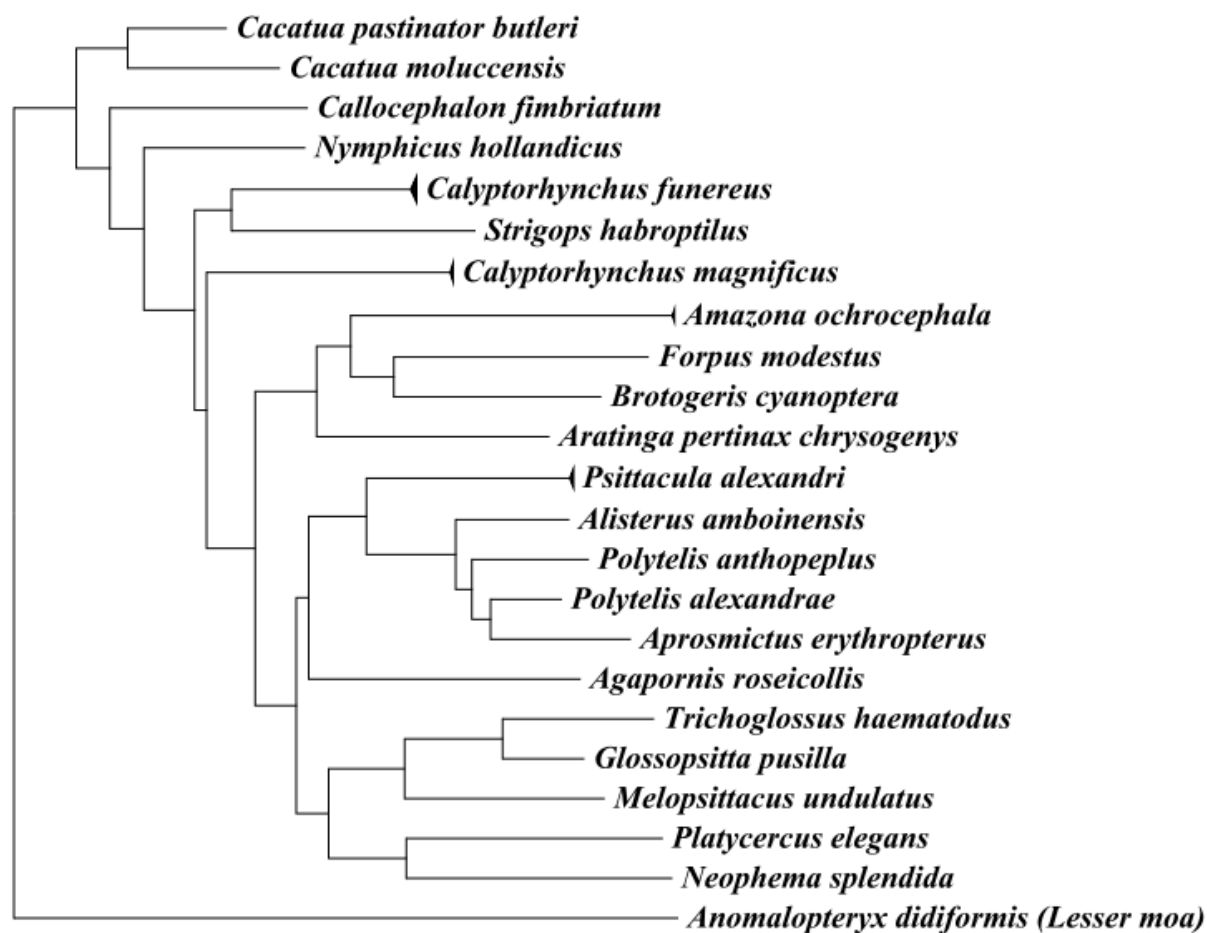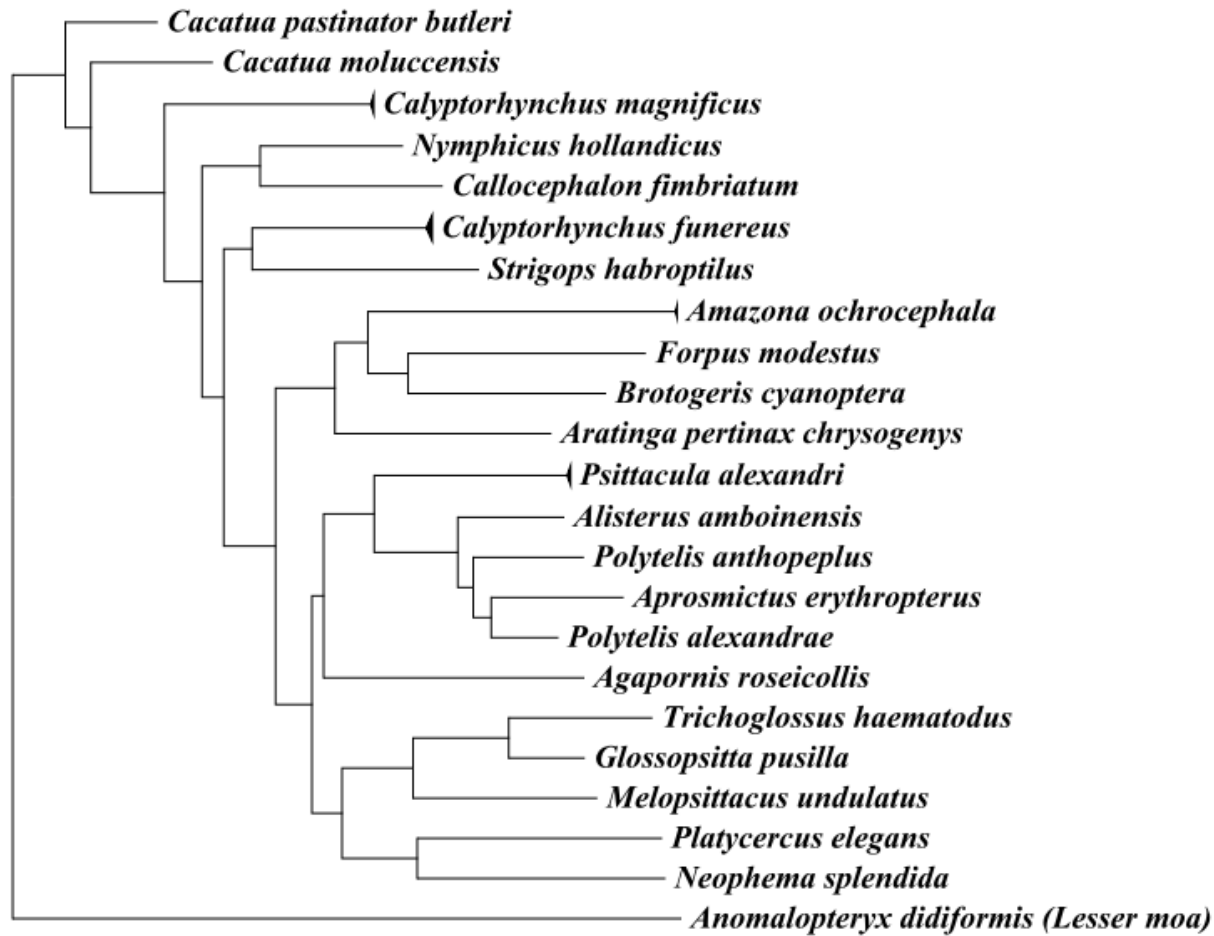
Figure D.39: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND5 gene of parrot and cockatoo species using Maximum Likelihood method, Hasegawa-Kishino-Yano model in MEGA 5 program.

Figure D.40: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND5 gene of parrot and cockatoo species using Maximum Likelihood method, Tamura-Nei model in MEGA 5 program.
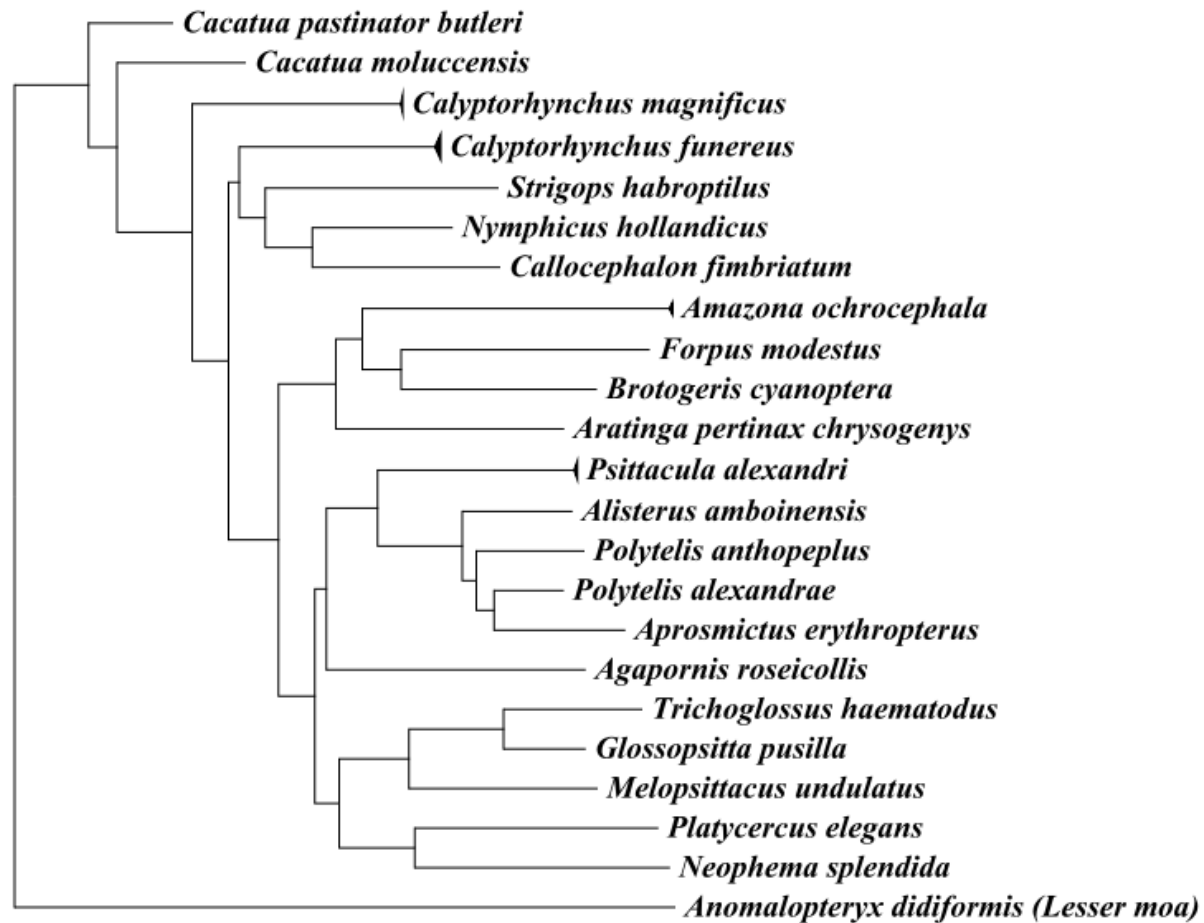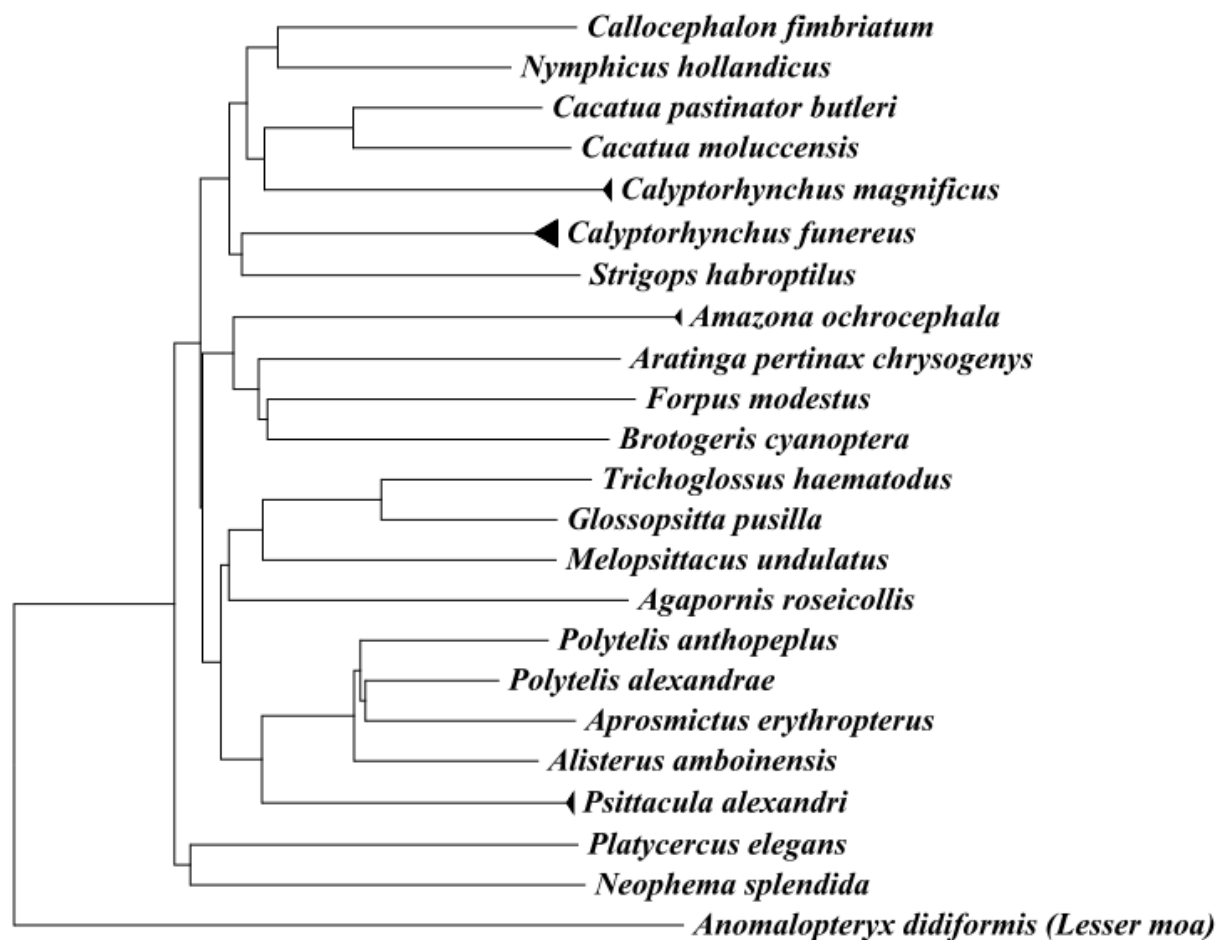
Figure D.41: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND5 gene of parrot and cockatoo species using Maximum Likelihood method, General Time Reversible model in MEGA 5 program.

Figure D.42: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND5 gene of parrot and cockatoo species using Neighbor-Joining method, No. of differences model in MEGA 5 program.
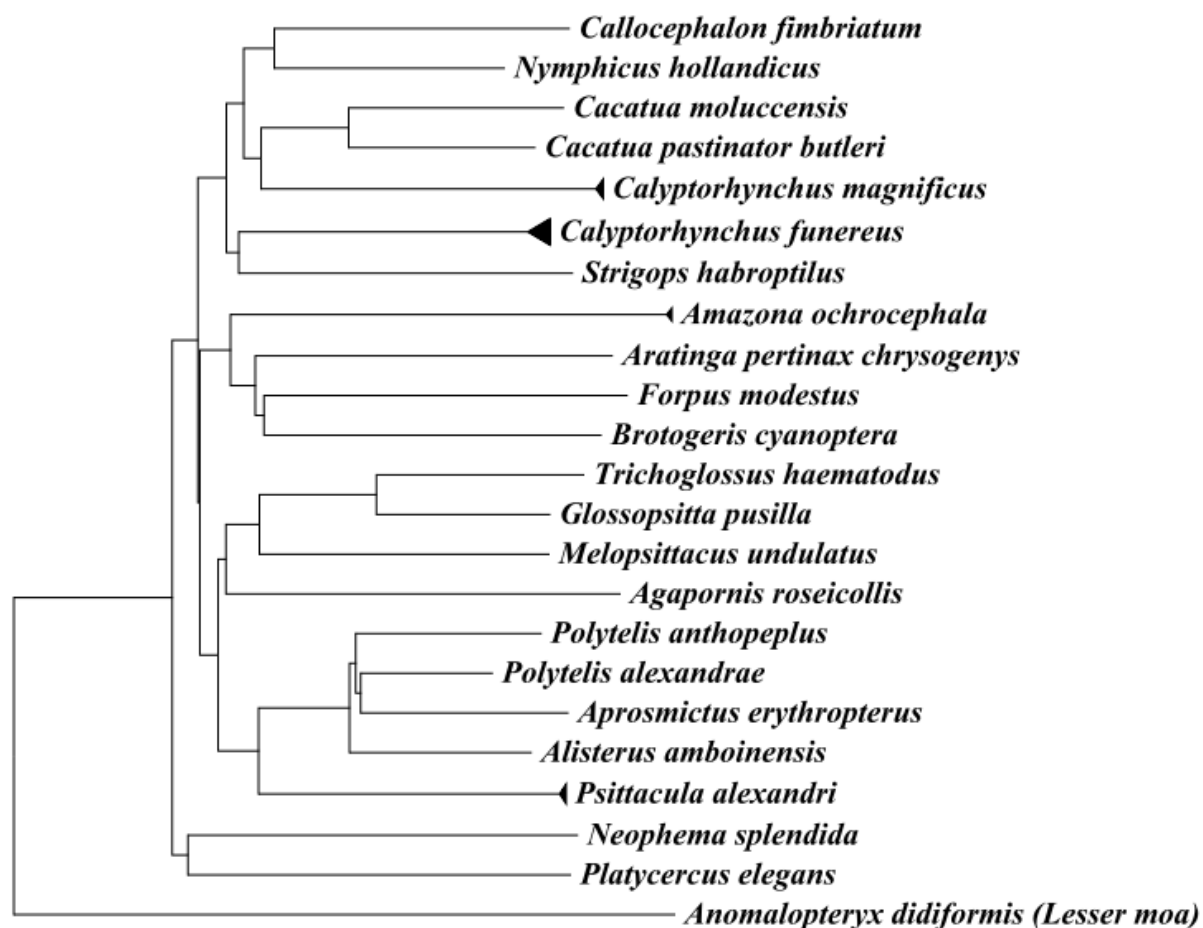
Figure D.43: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND5 gene of parrot and cockatoo species using Neighbor-Joining method, p-distance model in MEGA 5 program.

Figure D.44: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND5 gene of parrot and cockatoo species using Neighbor-Joining method, Jukes-Cantor model in MEGA 5 program.

Figure D.45: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND5 gene of parrot and cockatoo species using Neighbor-Joining method, Kimura 2-parameter model in MEGA 5 program.
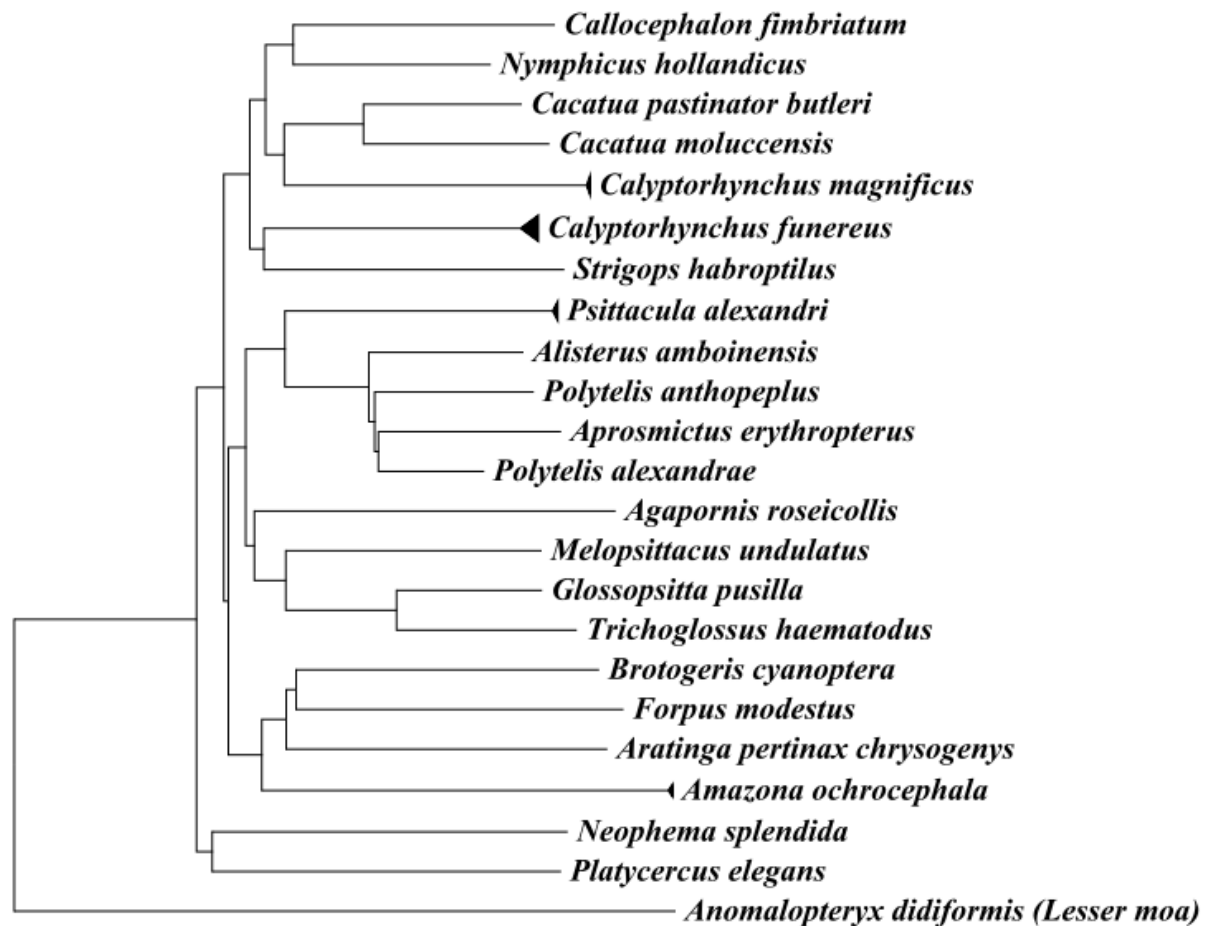
Figure D.46: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND5 gene of parrot and cockatoo species using Neighbor-Joining method, Tajima-Nei model in MEGA 5 program.

Figure D.47: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND5 gene of parrot and cockatoo species using Neighbor-Joining method, Tamura 3-parameter model in MEGA 5 program.
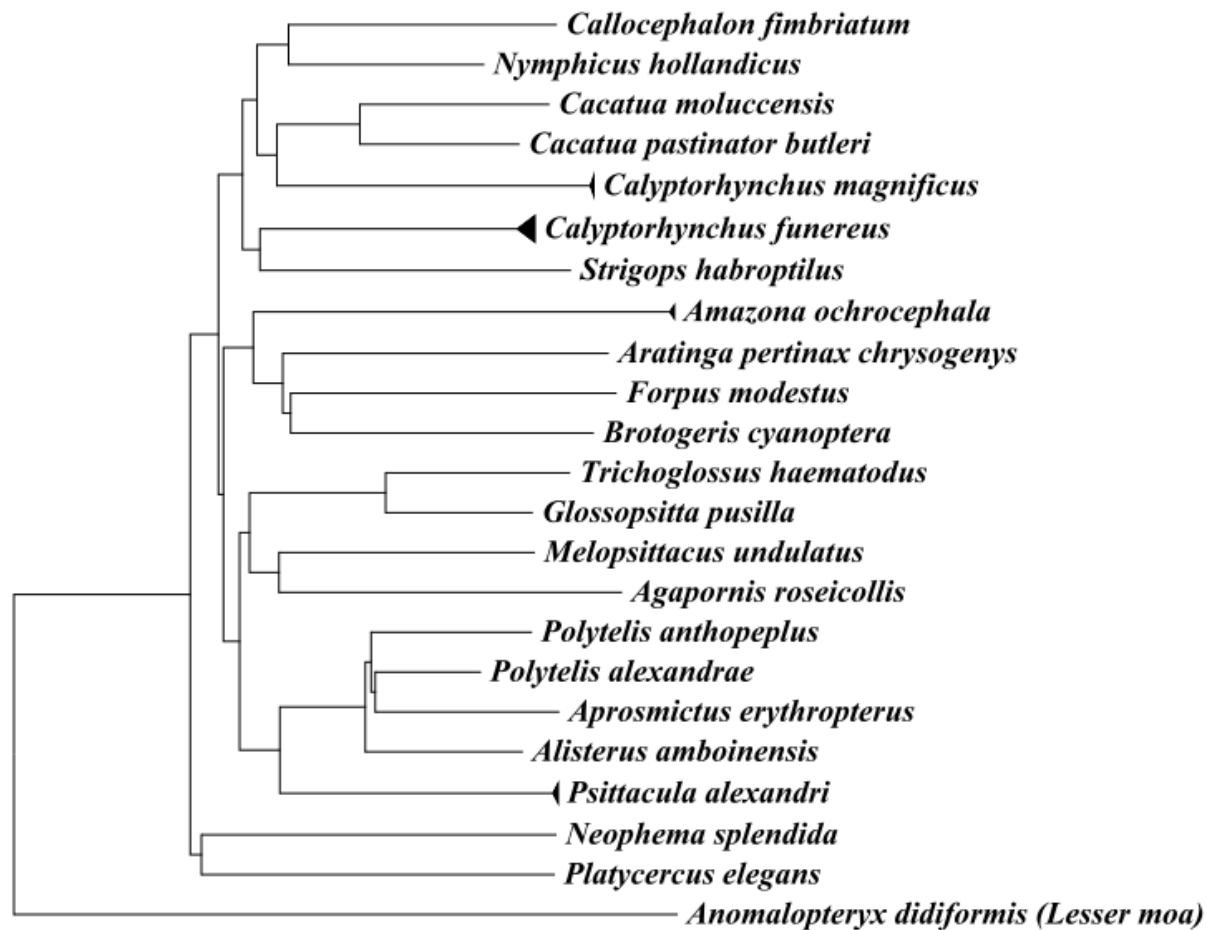
Figure D.48: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND5 gene of parrot and cockatoo species using Neighbor-Joining method, Tamura-Nei model in MEGA 5 program.
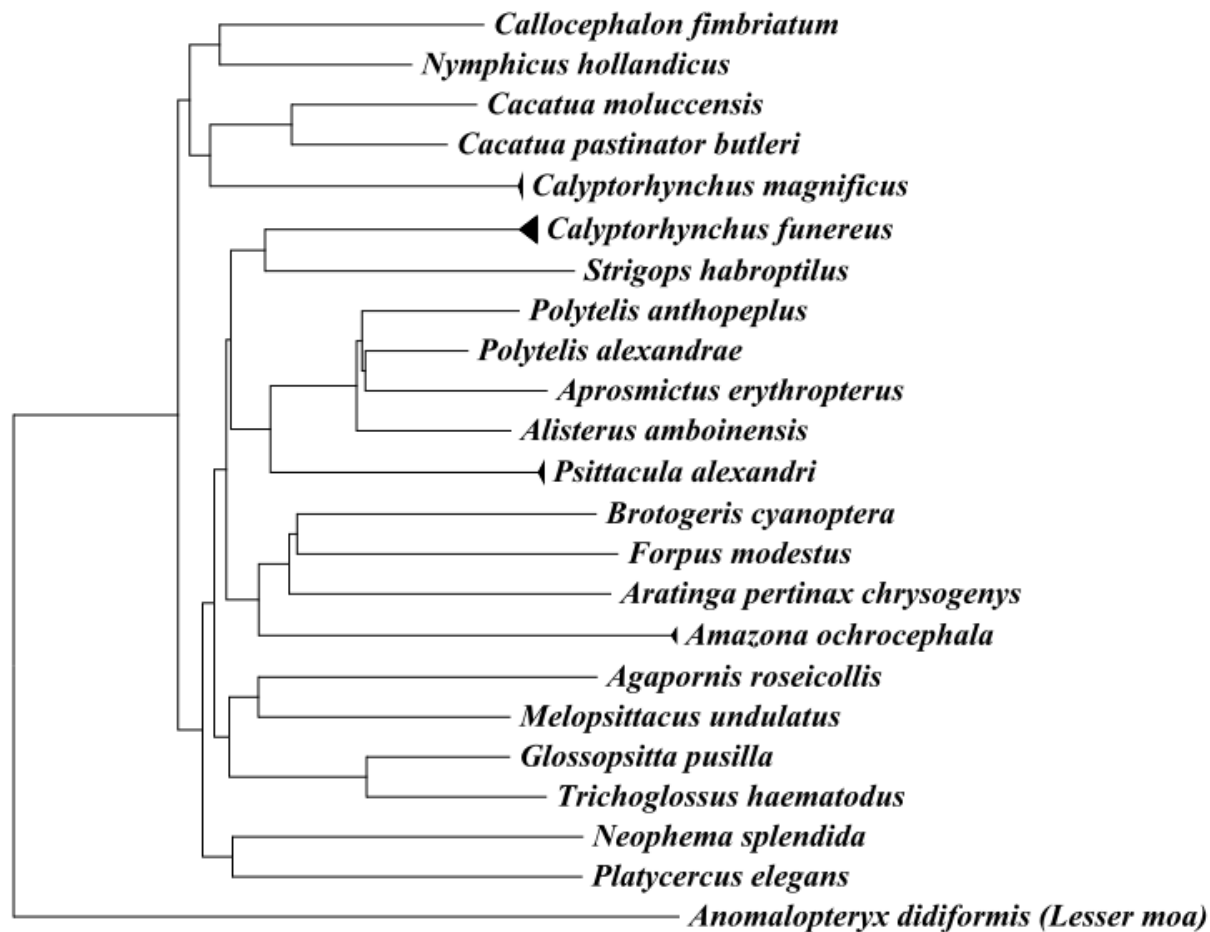
Figure D.49: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND5 gene of parrot and cockatoo species using Neighbor-Joining method, Maximum Composite Likelihood model in MEGA 5 program.
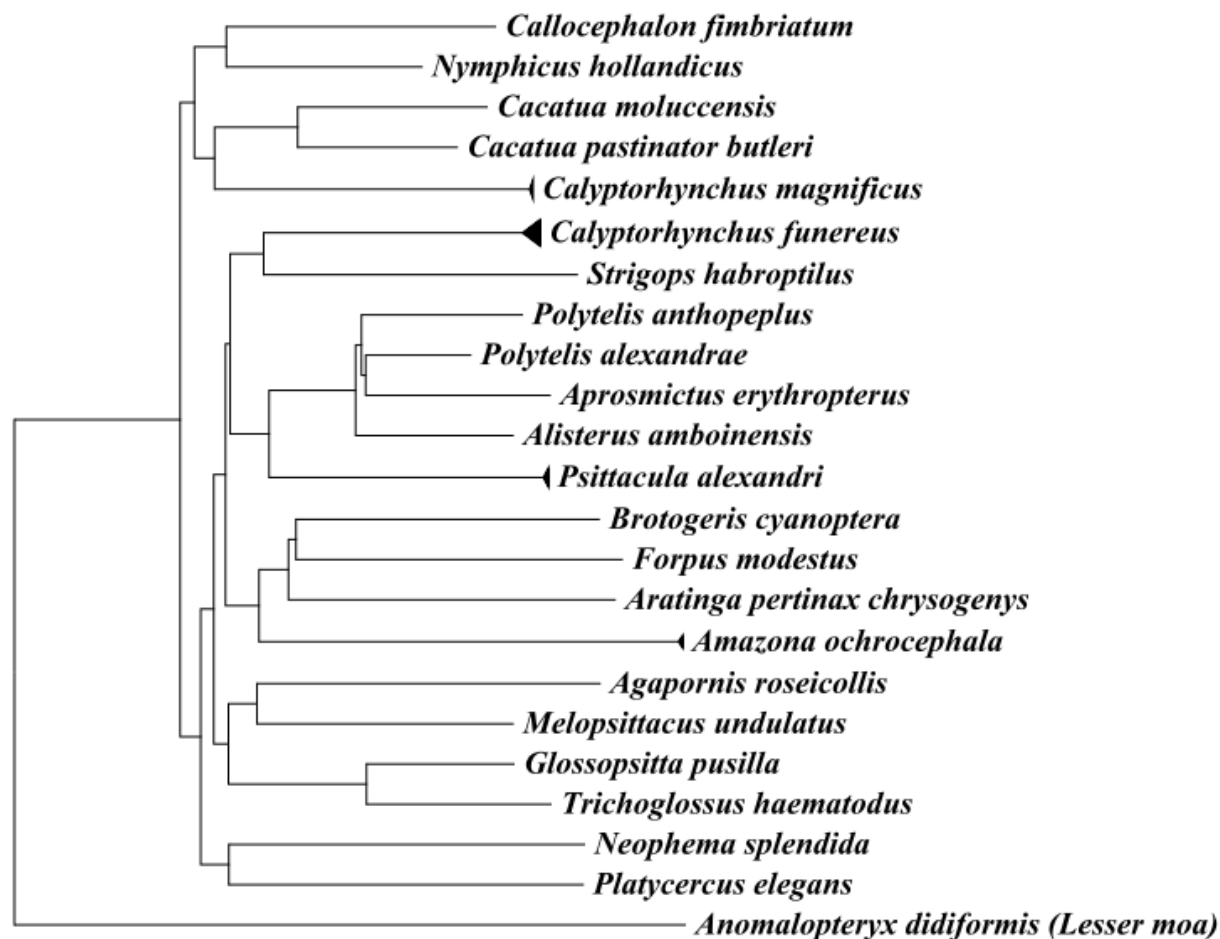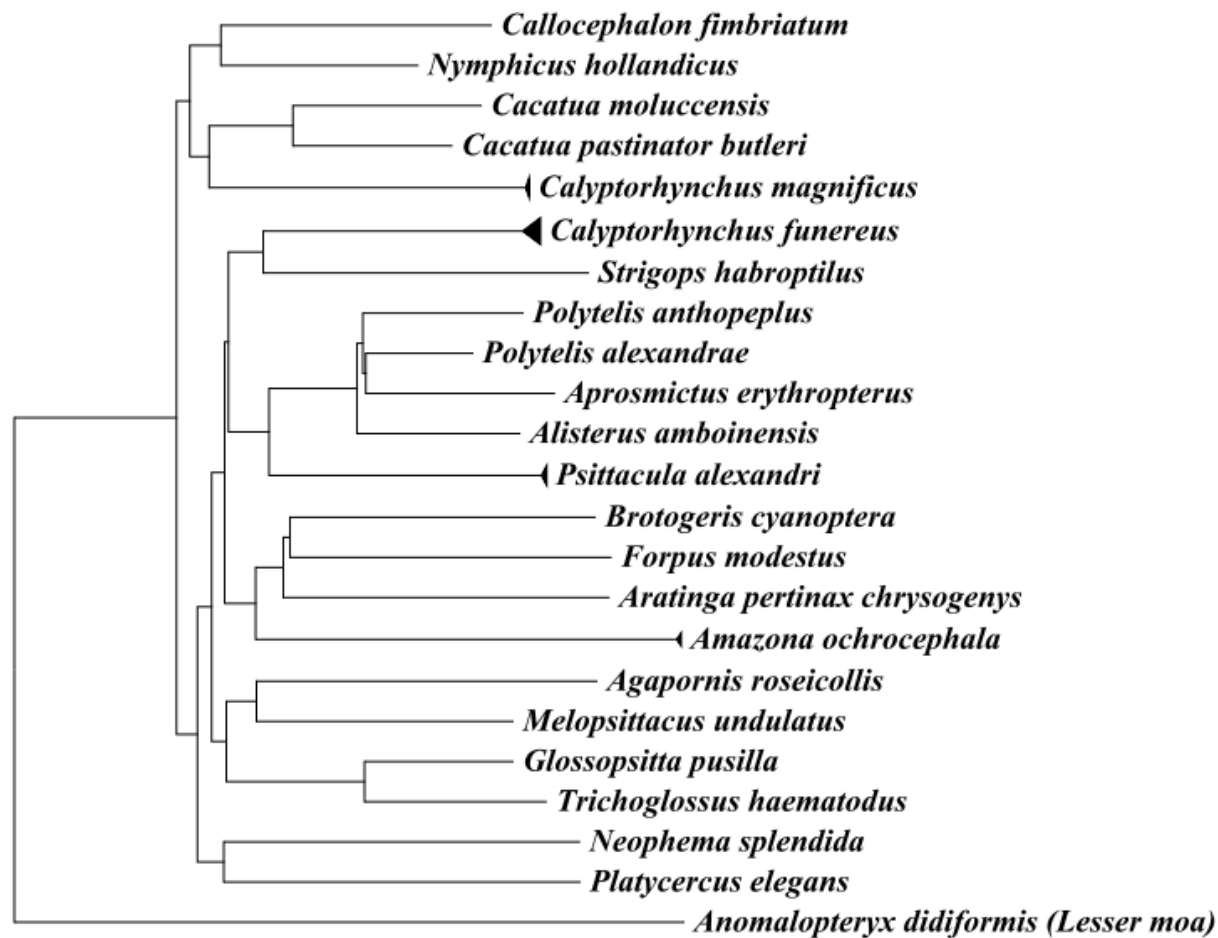
Figure D.50: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND5 gene of parrot and cockatoo species using Neighbor-Joining method, LogDet (Tamura-Kumar) model in MEGA 5 program.

Callocephalon fimbriatum
Nymphicus hollandicus
Cacatua moluccensis
Cacatua pastinator butleri
Calyptorhynchus magnificus
Calyptorhynchus funereus
Strigops habroptilus
Amazona ochrocephala
Aratinga pertinax chrysogenys
Forpus modestus
Brotogeris cyanoptera
Trichoglossus haematodus
Glossopsitta pusilla
Melopsittacus undulatus
Agapornis roseicollis
Polytelis alexandrae
Aprosmictus erythropterus
Polytelis anthopeplus
Alisterus amboinensis
Psittacula alexandri
Neophema splendida
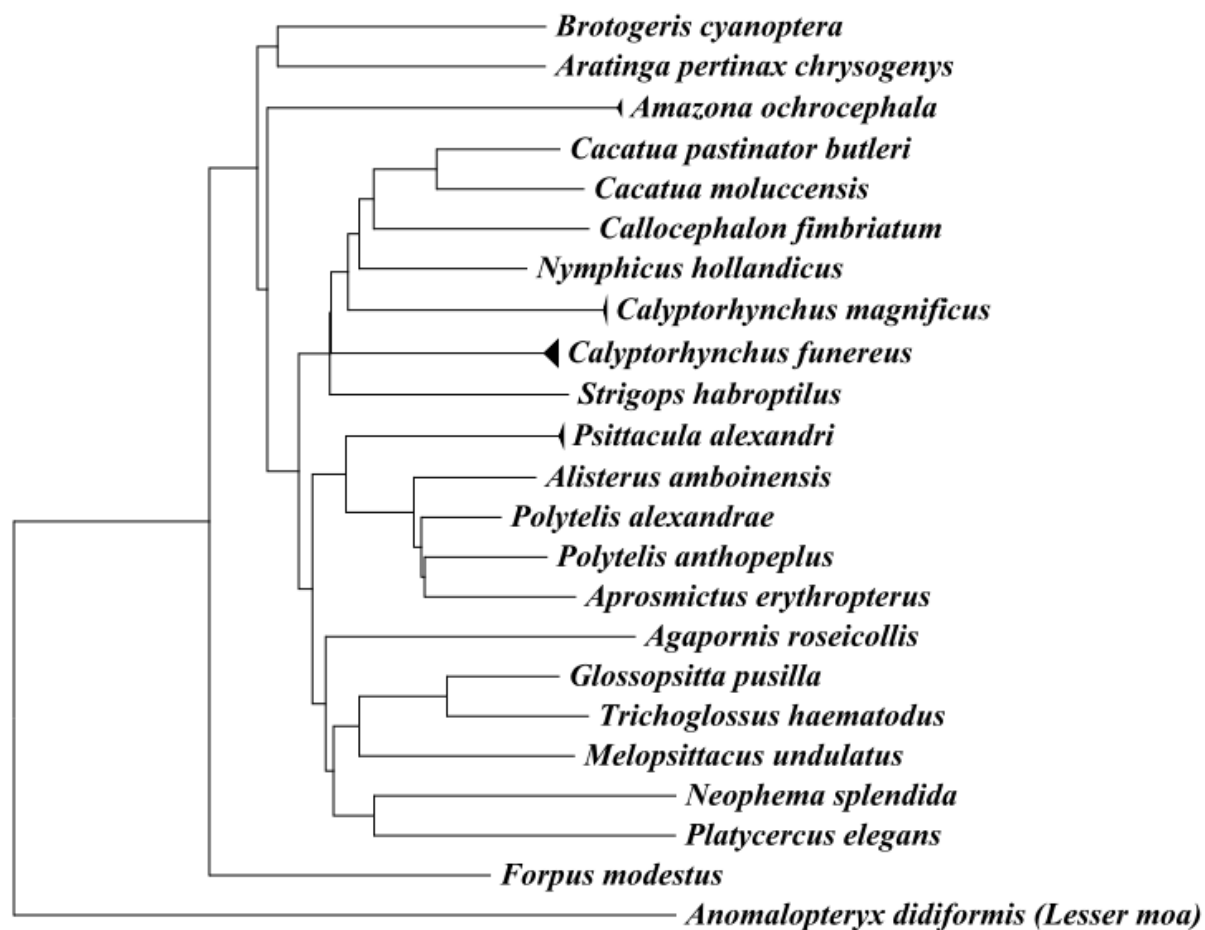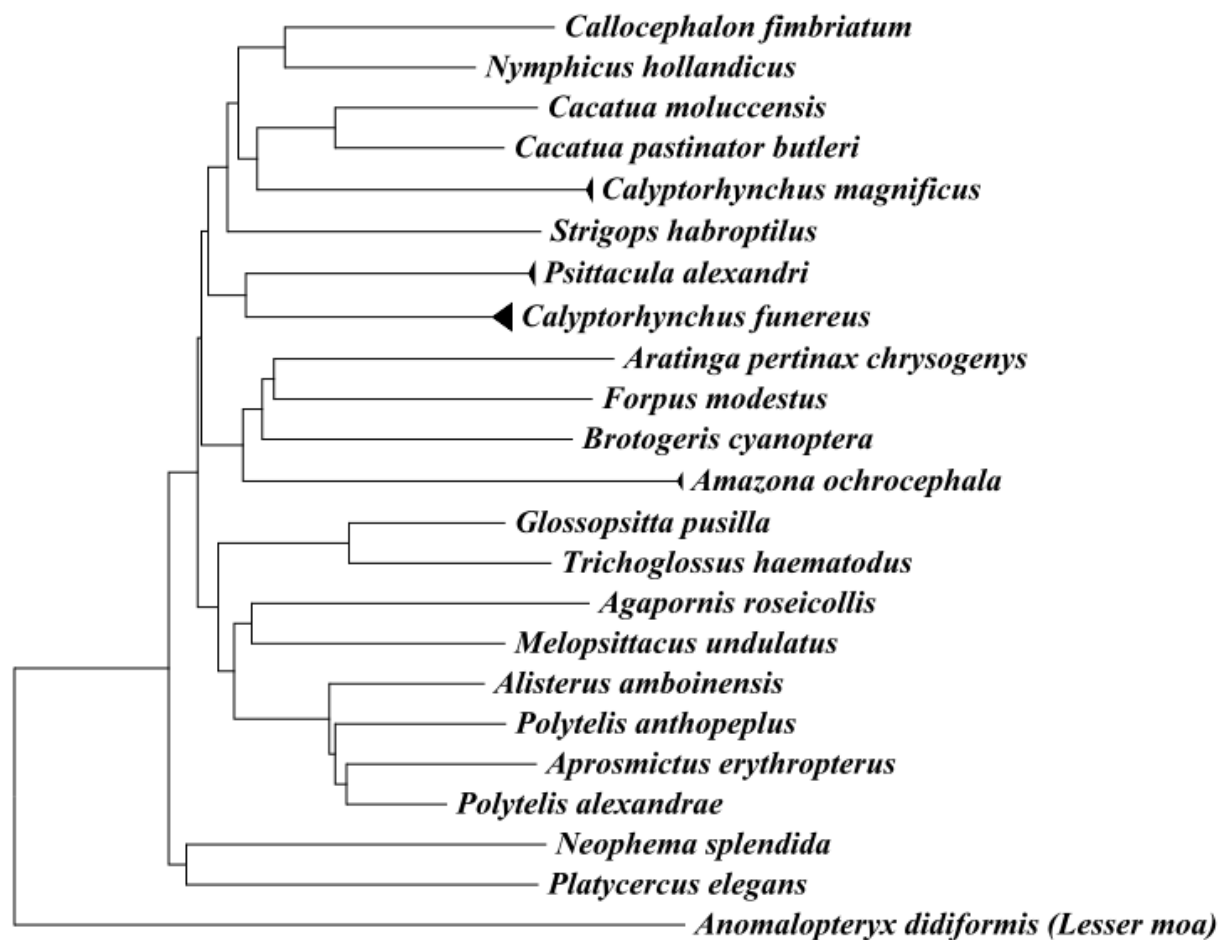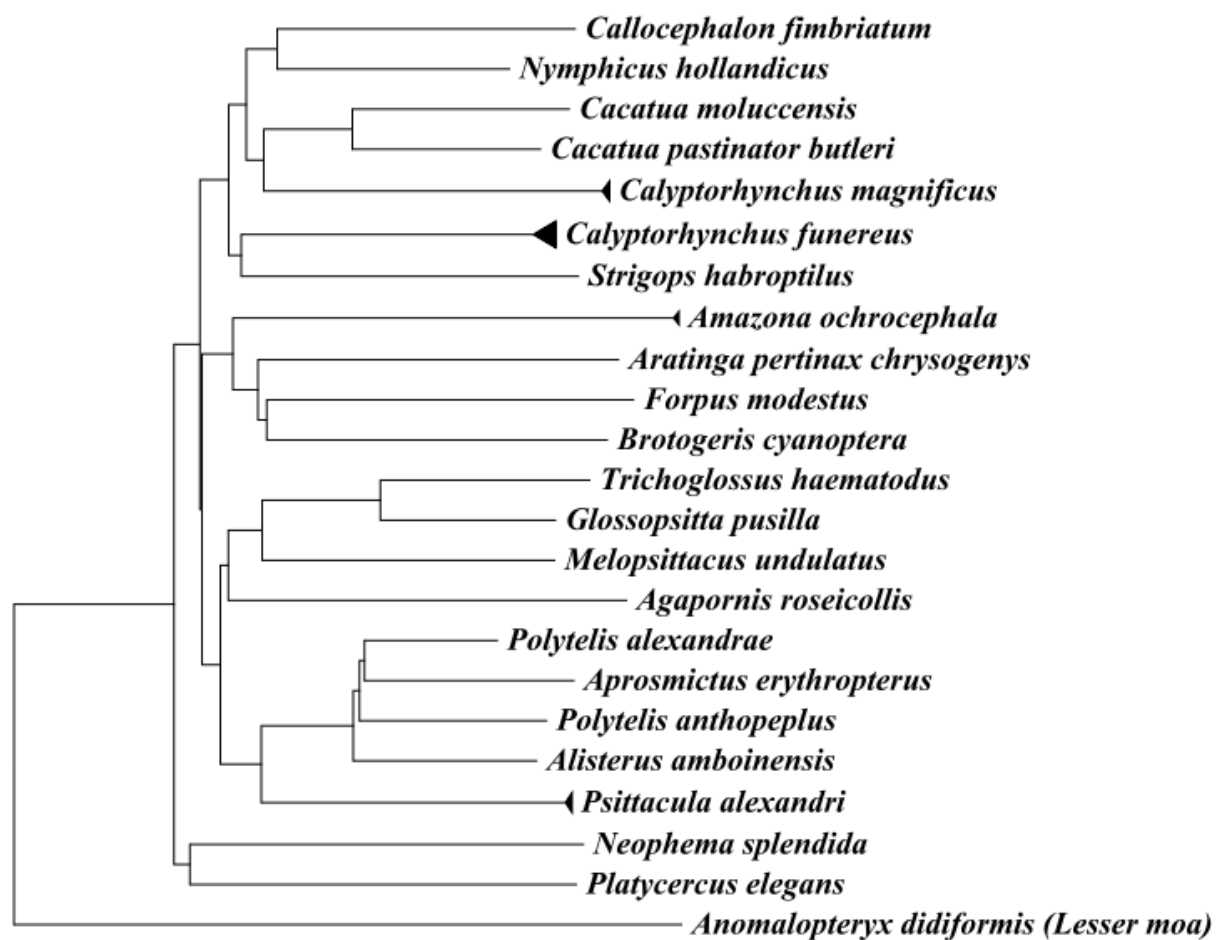Platycercus elegans
Anomalopteryx didiformis (Lesser moa)

Figure D.51: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND5 gene of parrot and cockatoo species using Minimum-Evolution method, No. of differences model in MEGA 5 program.

Figure D.52: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND5 gene of parrot and cockatoo species using Minimum-Evolution method, p-distance model in MEGA 5 program.
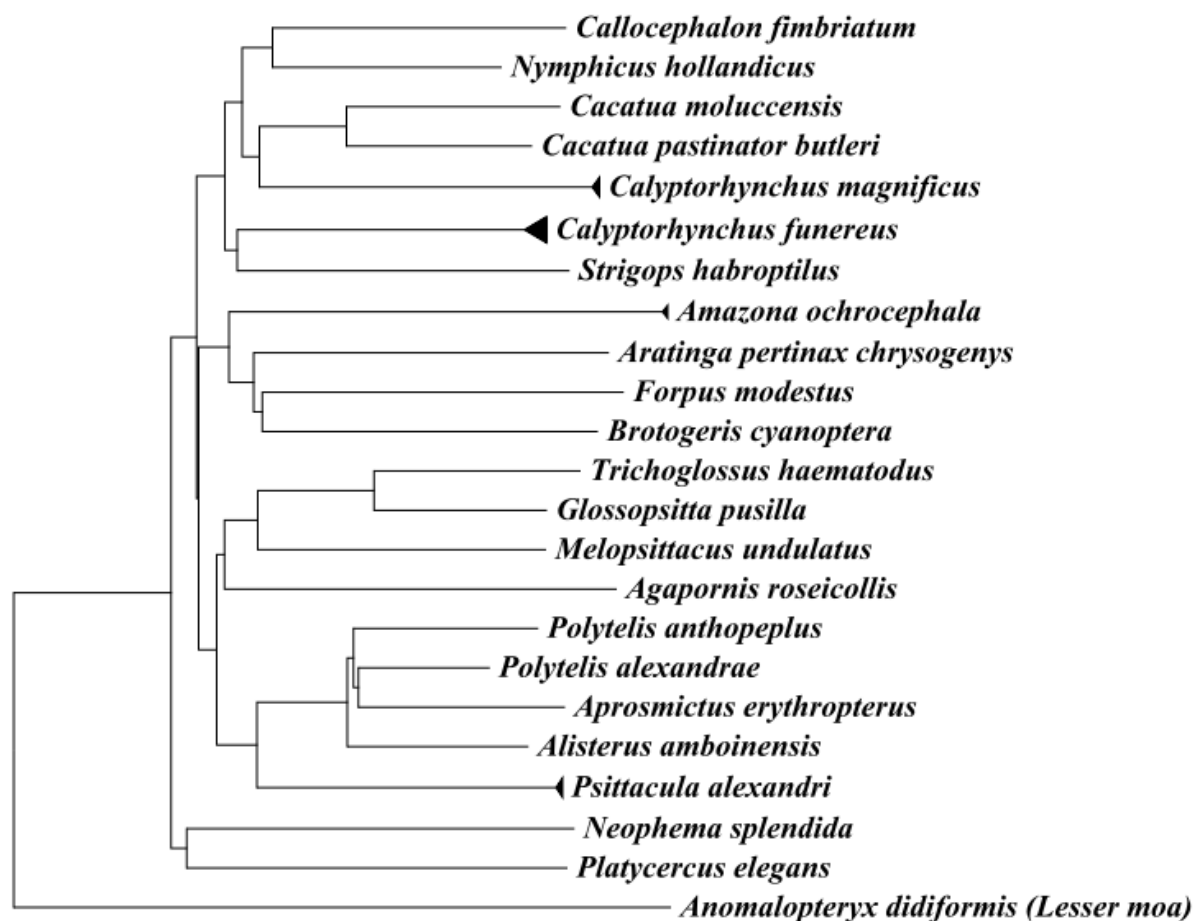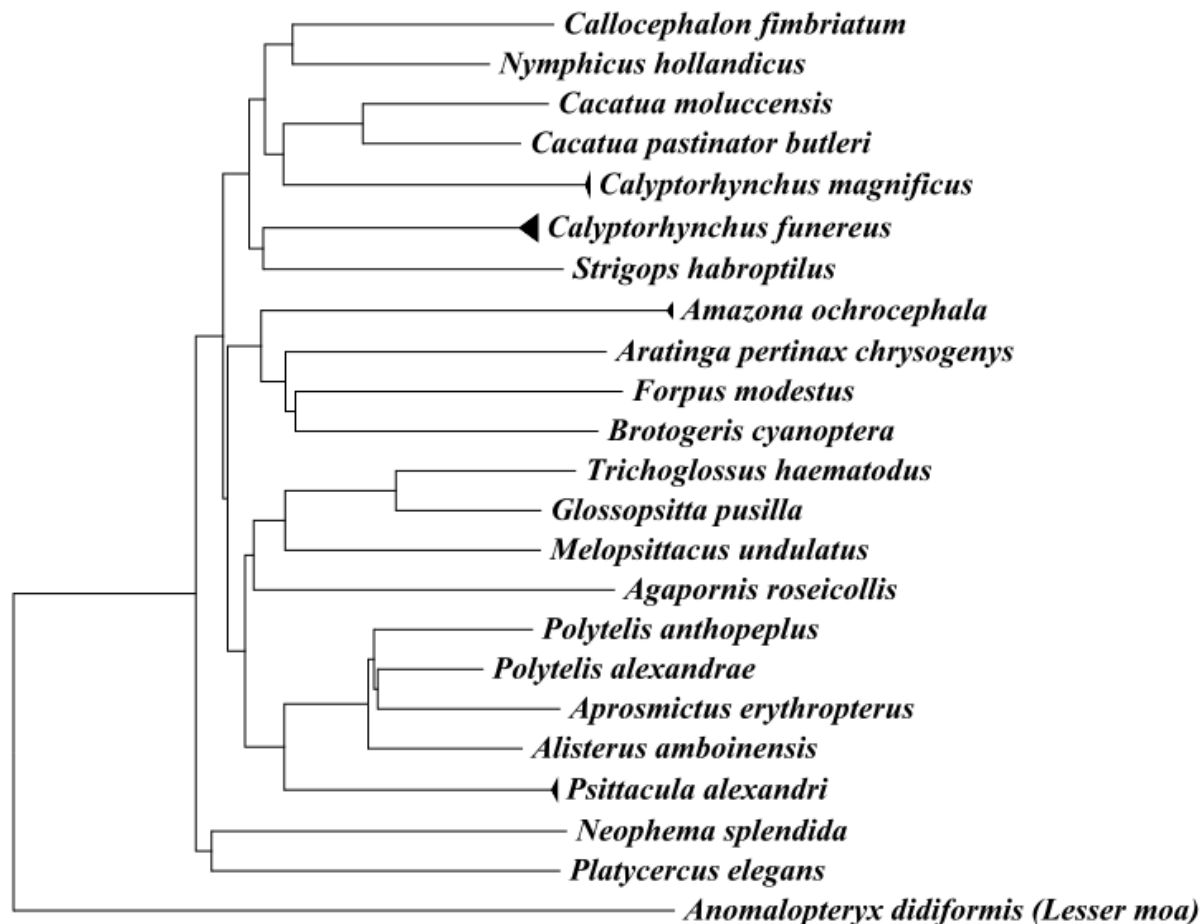
Figure D.53: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND5 gene of parrot and cockatoo species using Minimum-Evolution method, Jukes-Cantor model in MEGA 5 program.

Figure D.54: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND5 gene of parrot and cockatoo species using Minimum-Evolution method, Kimura 2-parameter model in MEGA 5 program.
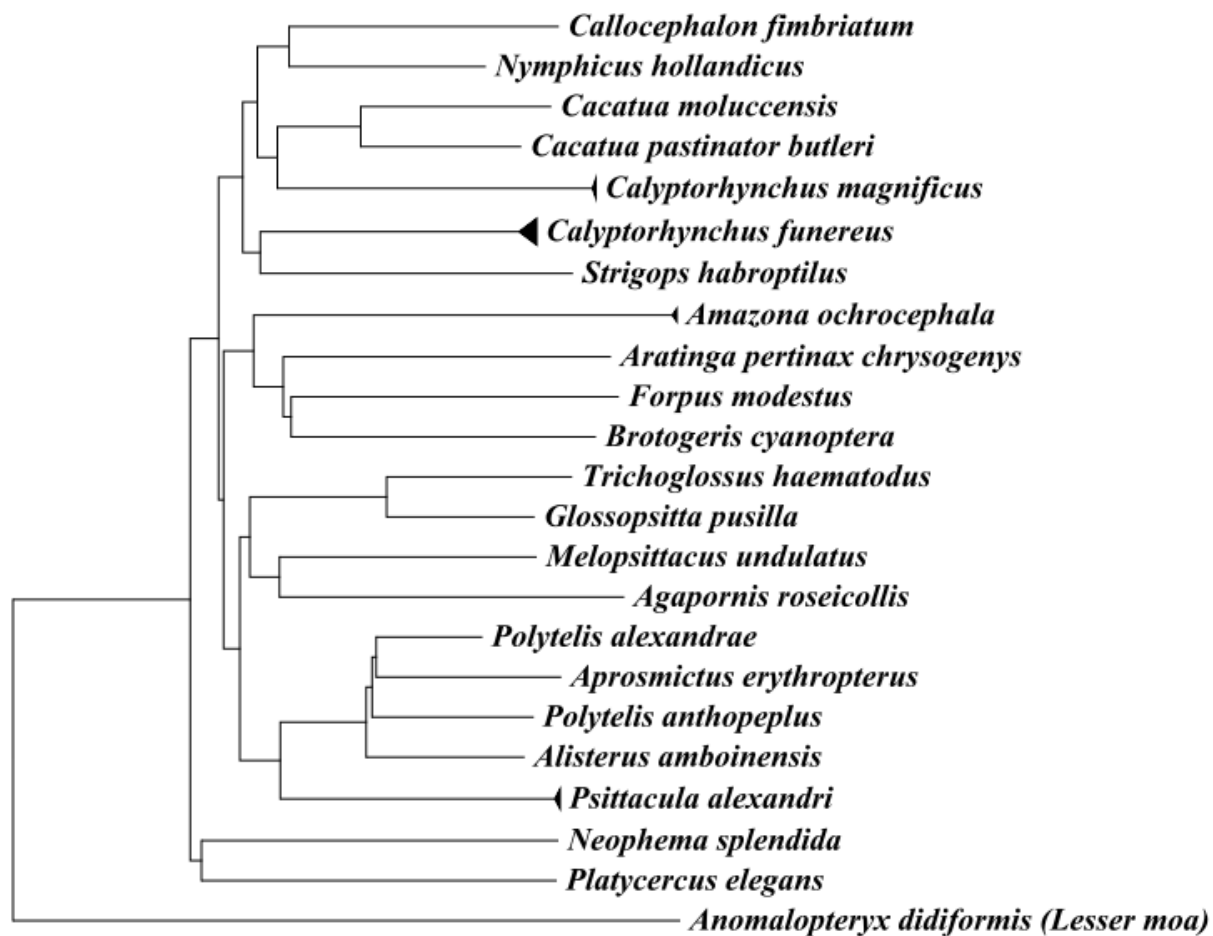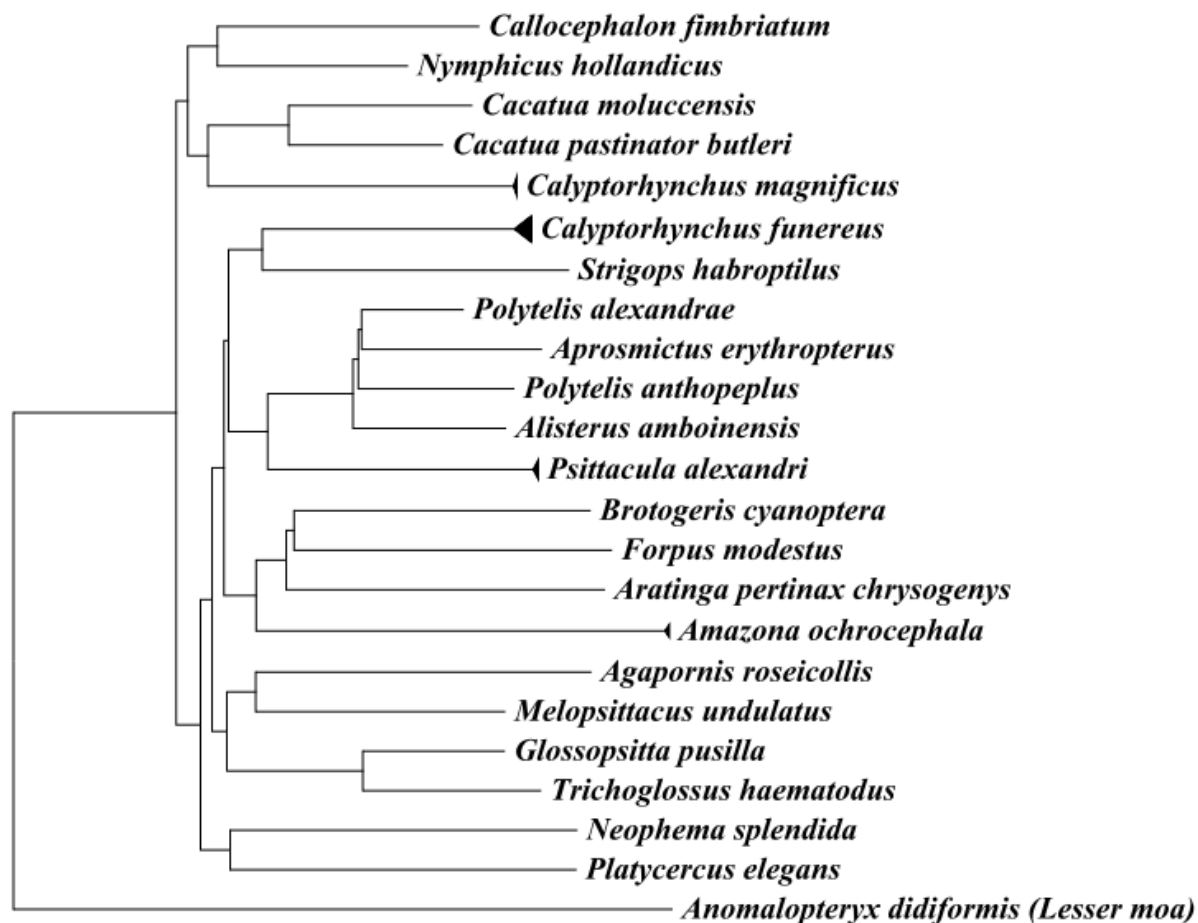
Figure D.55: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND5 gene of parrot and cockatoo species using Minimum-Evolution method, Tajima-Nei model in MEGA 5 program.

Callocephalon fimbriatum
Nymphicus hollandicus
Cacatua moluccensis
Cacatua pastinator butleri
Calyptorhynchus magnificus
Calyptorhynchus funereus
Strigops habroptilus
Polytelis anthopeplus
Polytelis alexandrae
Aprosmictus erythropterus
Alisterus amboinensis
Psittacula alexandri
Brotogeris cyanoptera
Forpus modestus
Aratinga pertinax chrysogenys
Amazona ochrocephala
Agapornis roseicollis
Melopsittacus undulatus
Glossopsitta pusilla
Trichoglossus haematodus
Neophema splendida
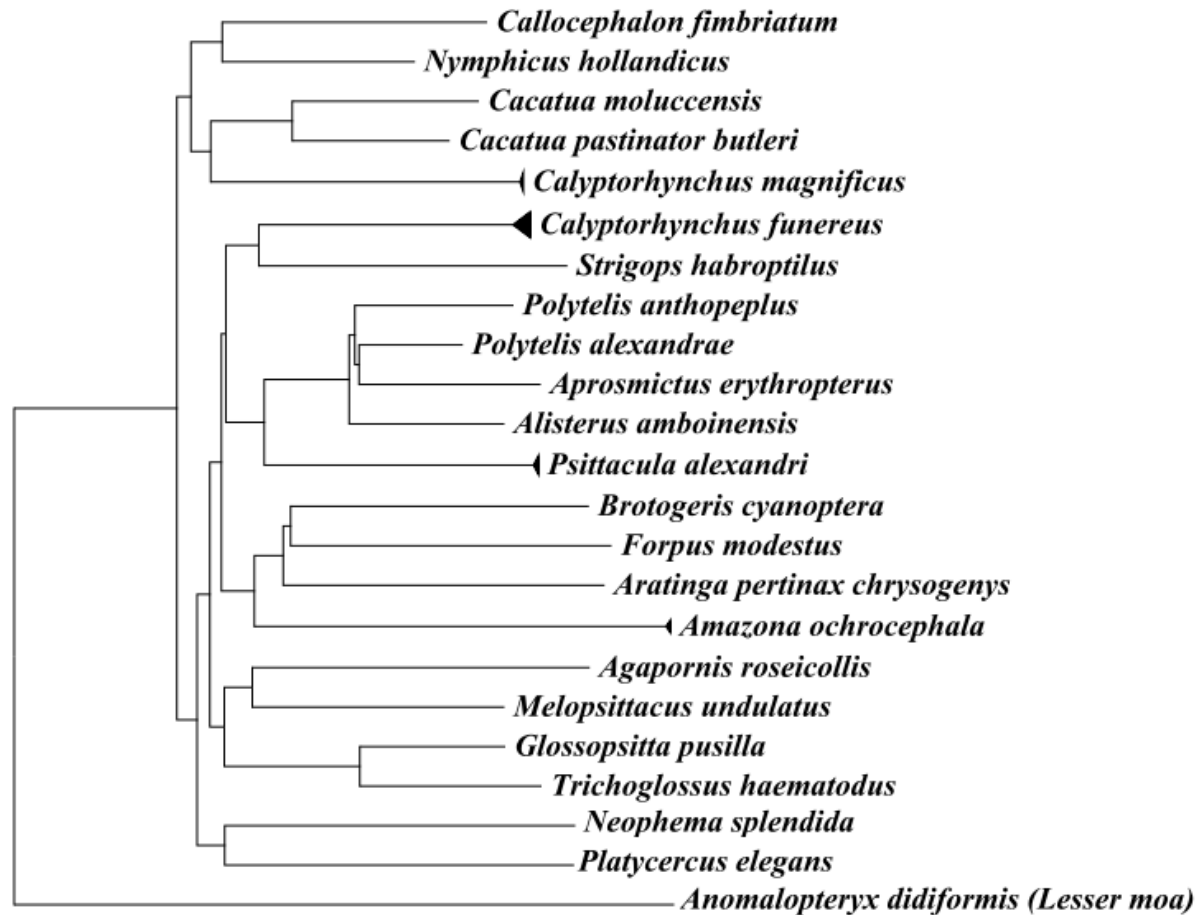Platycercus elegans
Anomalopteryx didiformis (Lesser moa)

Figure D.56: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND5 gene of parrot and cockatoo species using Minimum-Evolution method, Tamura 3-parameter model in MEGA 5 program.
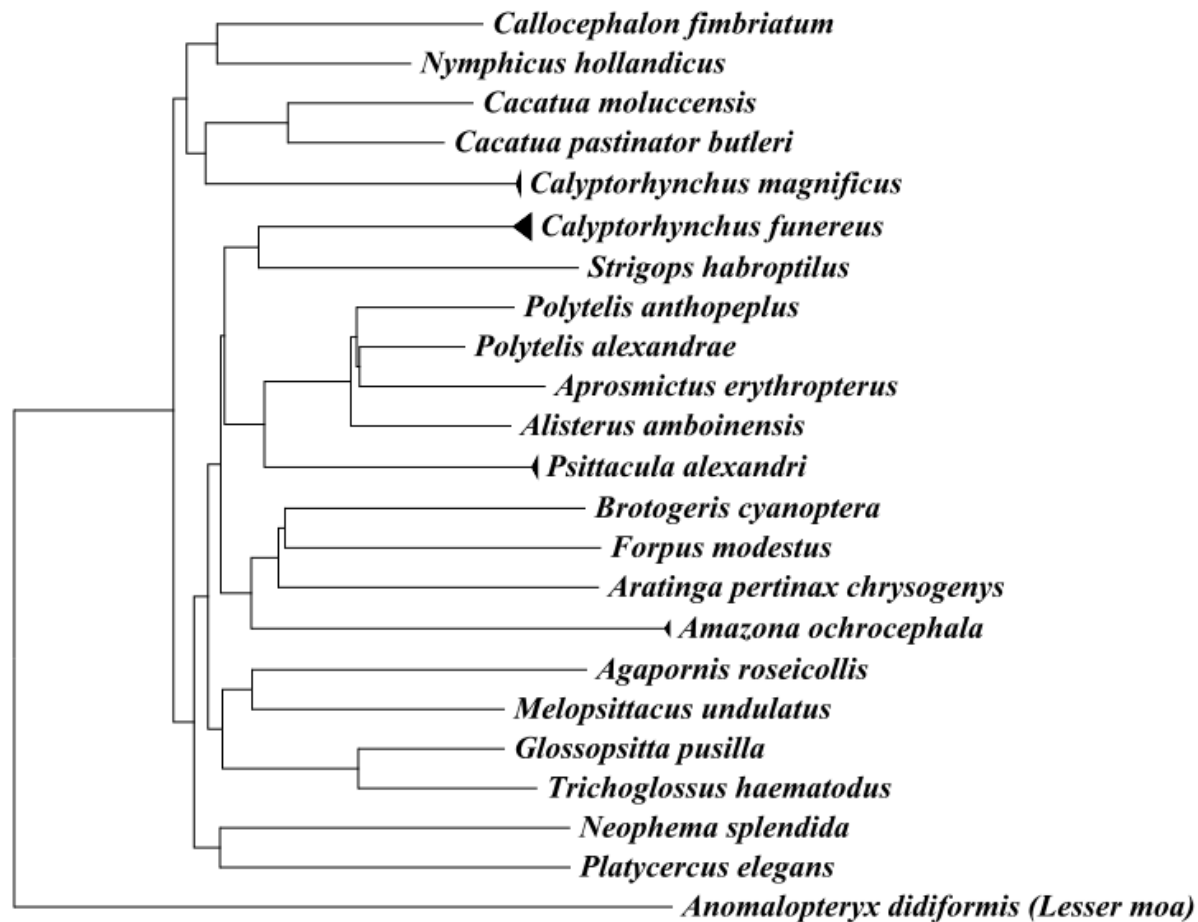
Figure D.57: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND5 gene of parrot and cockatoo species using Minimum-Evolution method, Tamura-Nei model in MEGA 5 program.
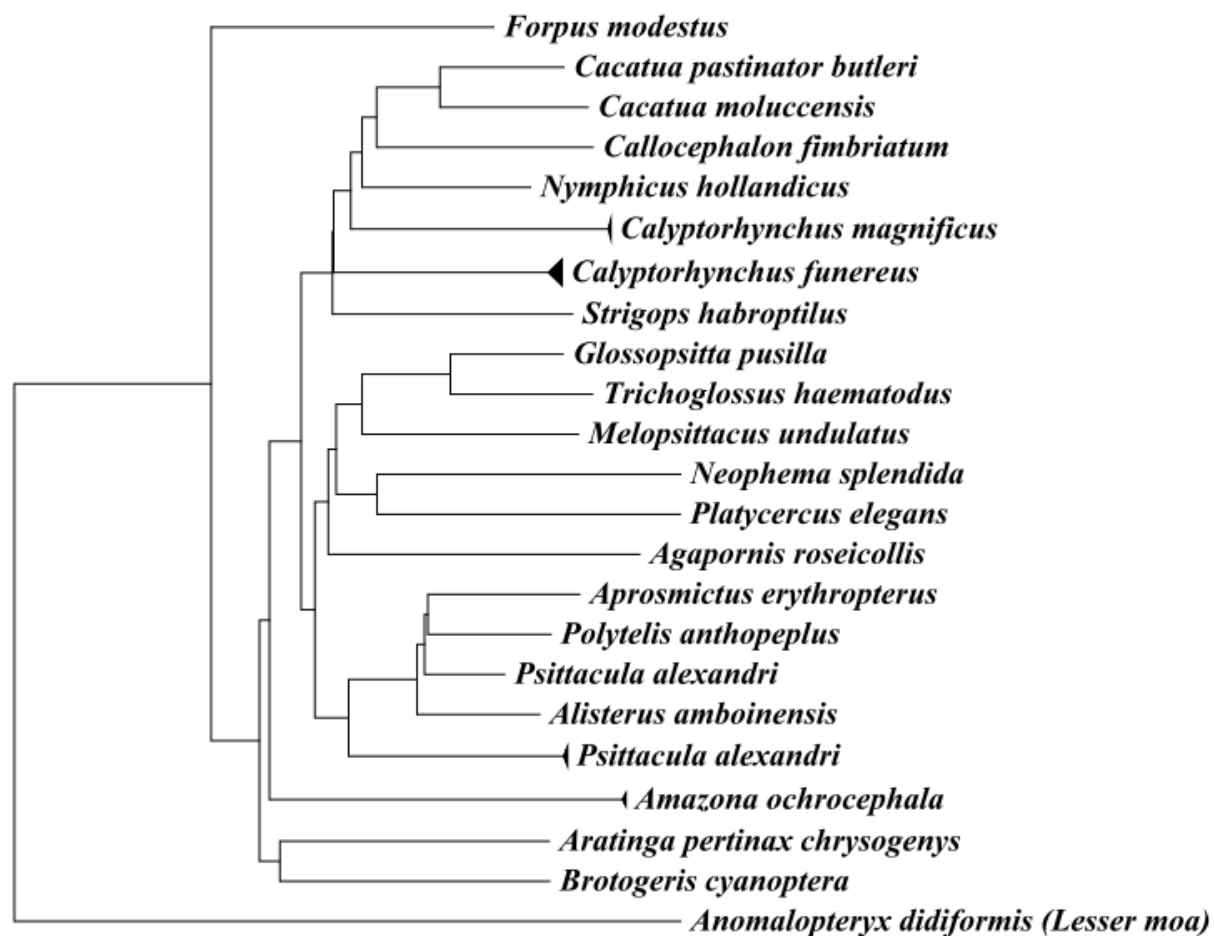
Figure D.58: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND5 gene of parrot and cockatoo species using Minimum-Evolution method, Maximum Composite Likelihood model in MEGA 5 program.
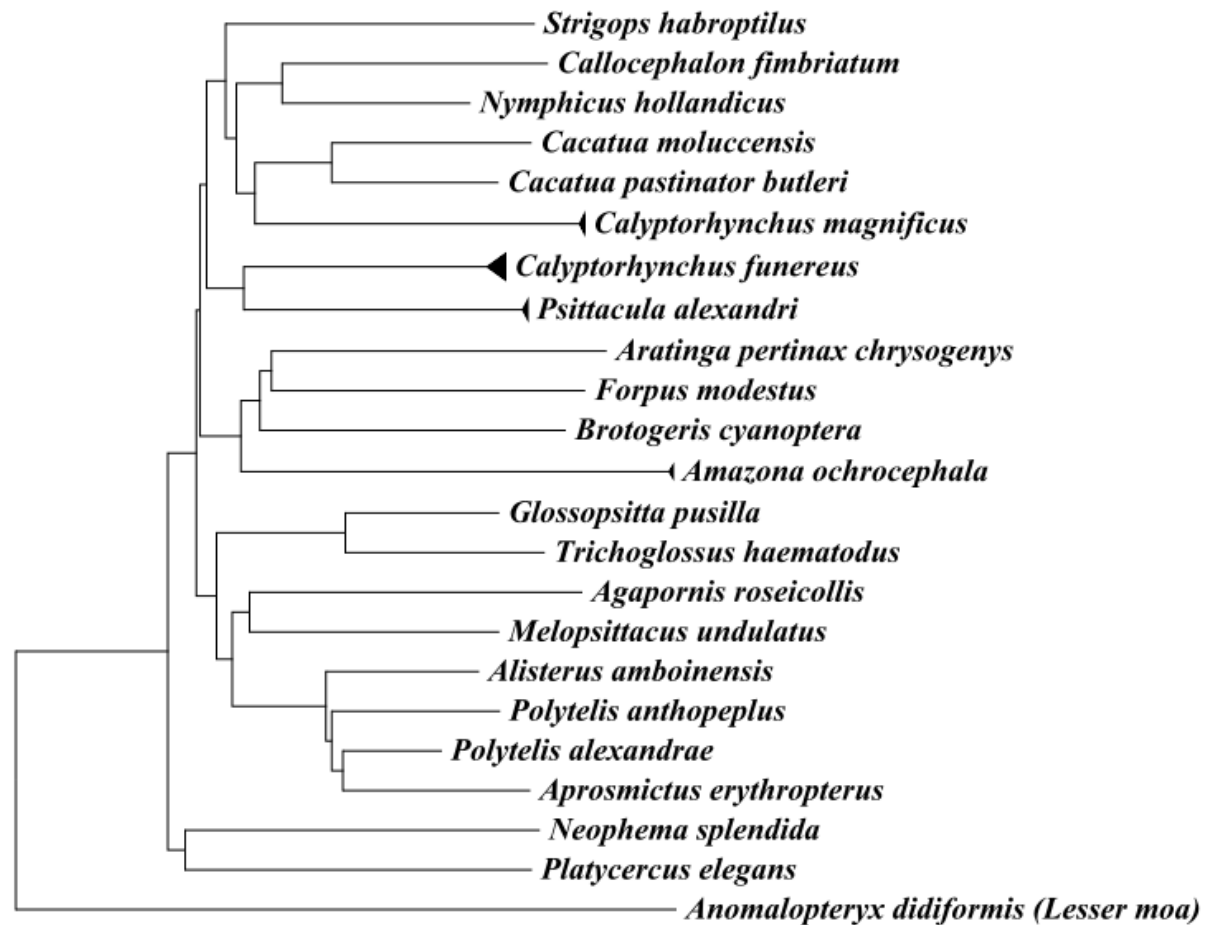
Figure D.59: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND5 gene of parrot and cockatoo species using Minimum-Evolution method, LogDet (Tamura-Kumar) model in MEGA 5 program.
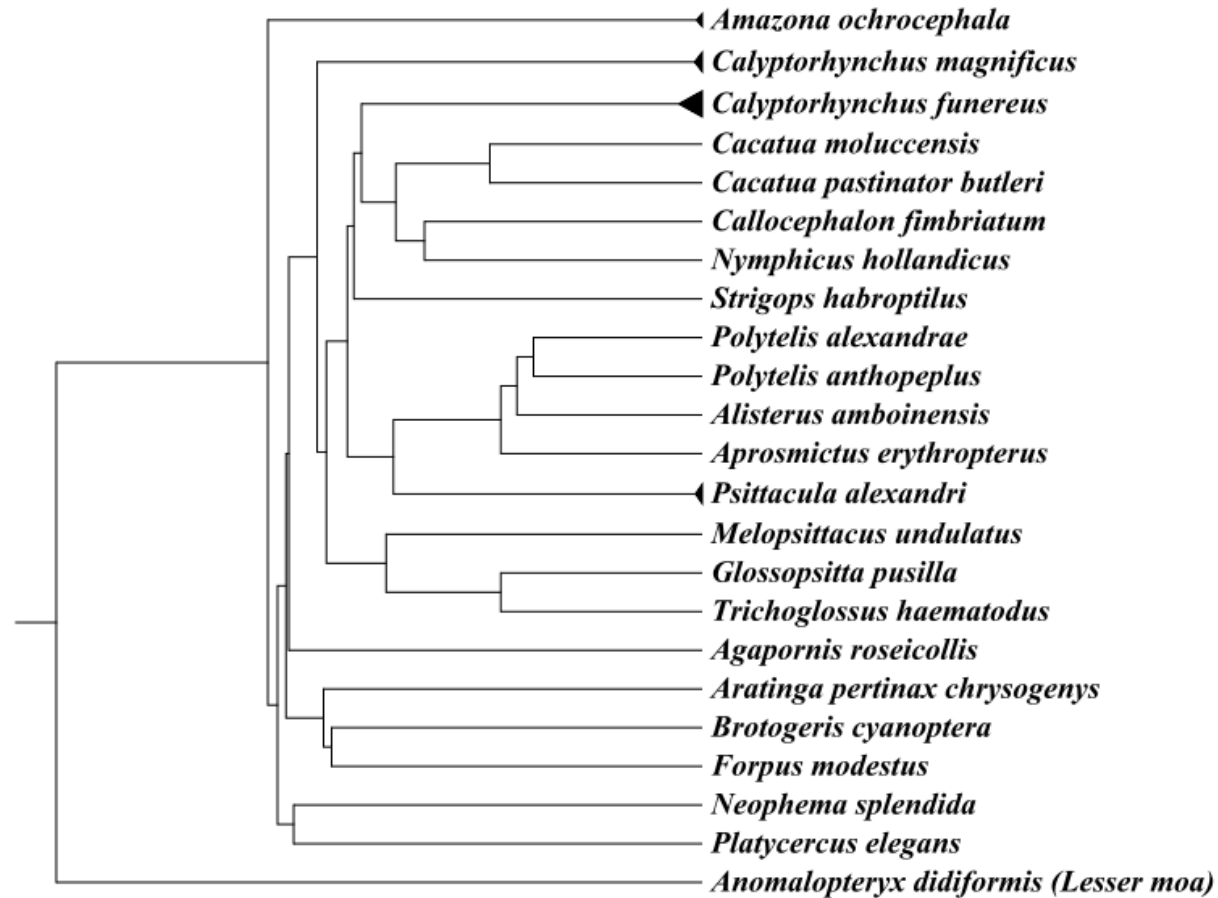
Figure D.60: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND5 gene of parrot and cockatoo species using UPGMA method, No. of differences model in MEGA 5 program.

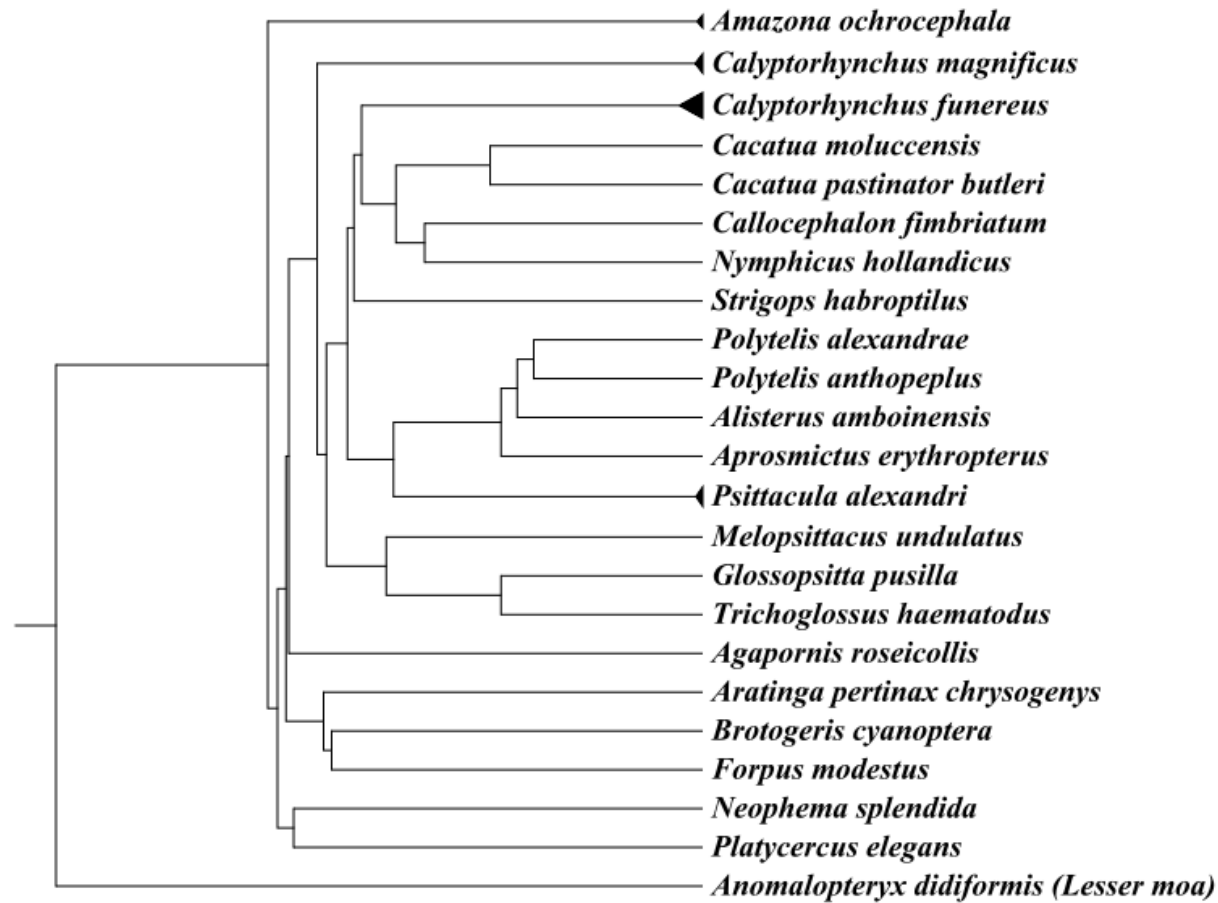**Figure D.61: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND5 gene of parrot and cockatoo species using UPGMA method, p-distance model in MEGA 5 program.**

Figure D.62: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND5 gene of parrot and cockatoo species using UPGMA method, Jukes-Cantor model in MEGA 5 program.
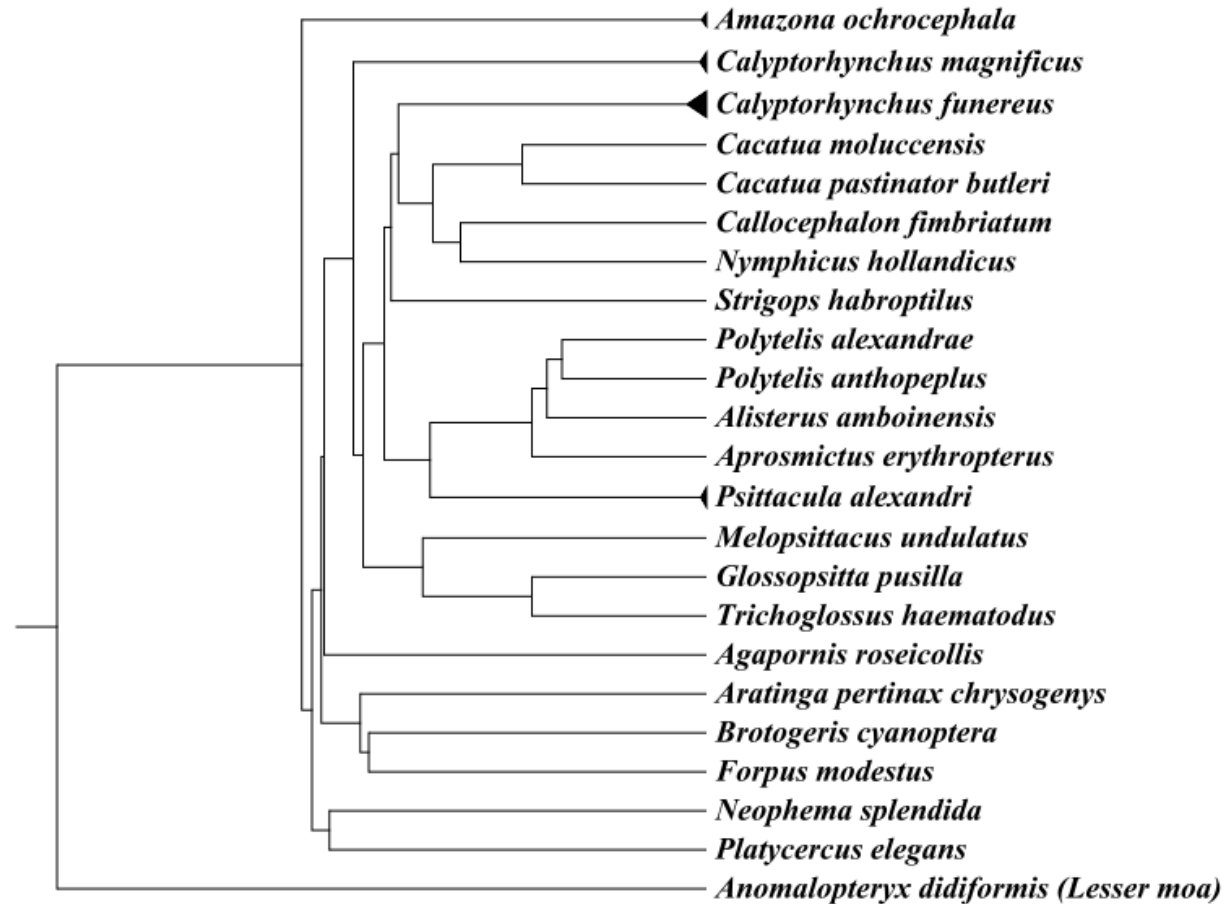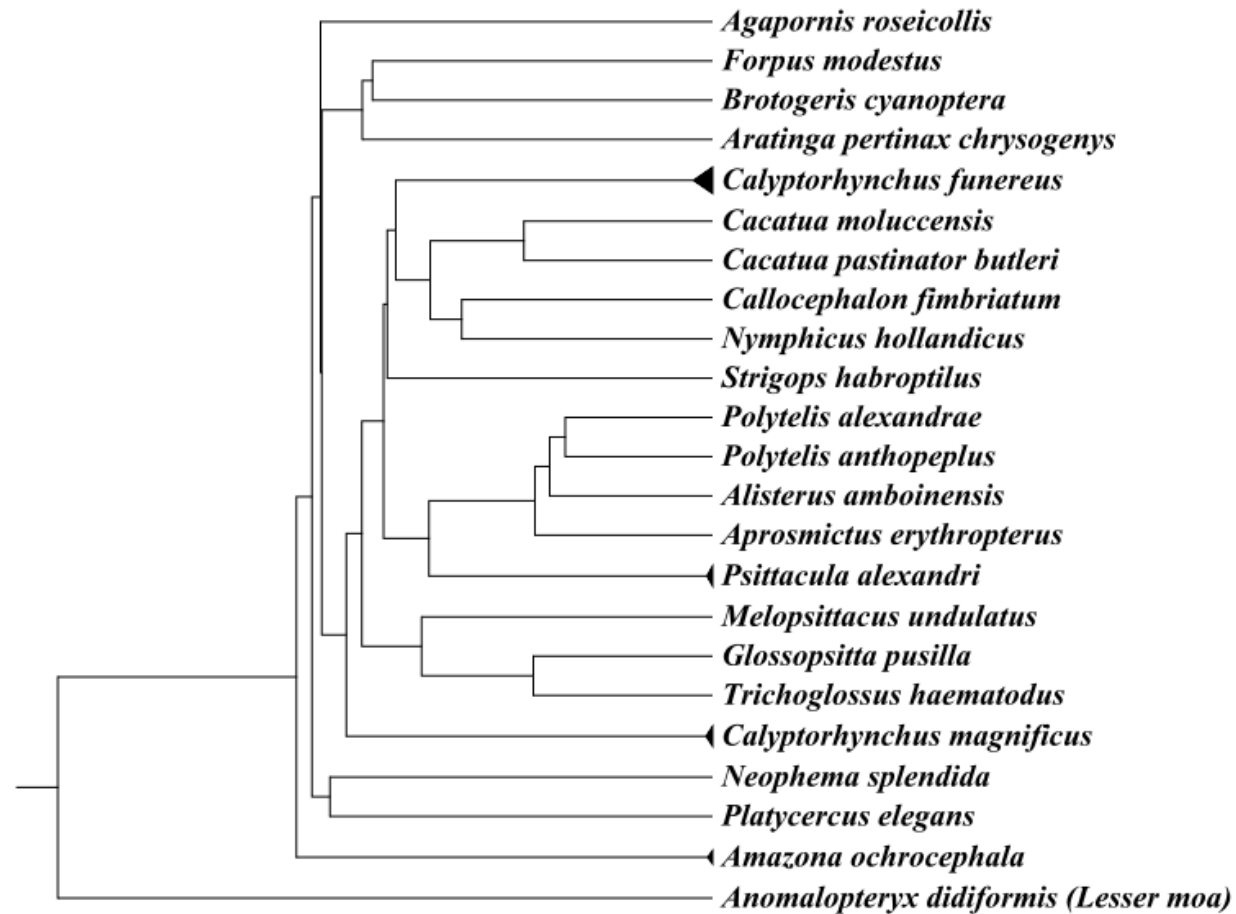
Figure D.63: **The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND5 gene of parrot and cockatoo species using UPGMA method, Kimura 2-parameter model in MEGA 5 program.**

Neophema splendida
Calyptorhynchus magnificus
Trichoglossus haematodus
Glossopsitta pusilla
Melopsittacus undulatus
Calyptorhynchus funereus
Cacatua moluccensis
Cacatua pastinator butleri
Callocephalon fimbriatum
Nymphicus hollandicus
Polytelis alexandrae
Polytelis anthopeplus
Alisterus amboinensis
Aprosmictus erythropterus
Psittacula alexandri
Strigops habroptilus
Aratinga pertinax chrysogenys
Brotogeris cyanoptera
Forpus modestus
Agapornis roseicollis
Platycercus elegans
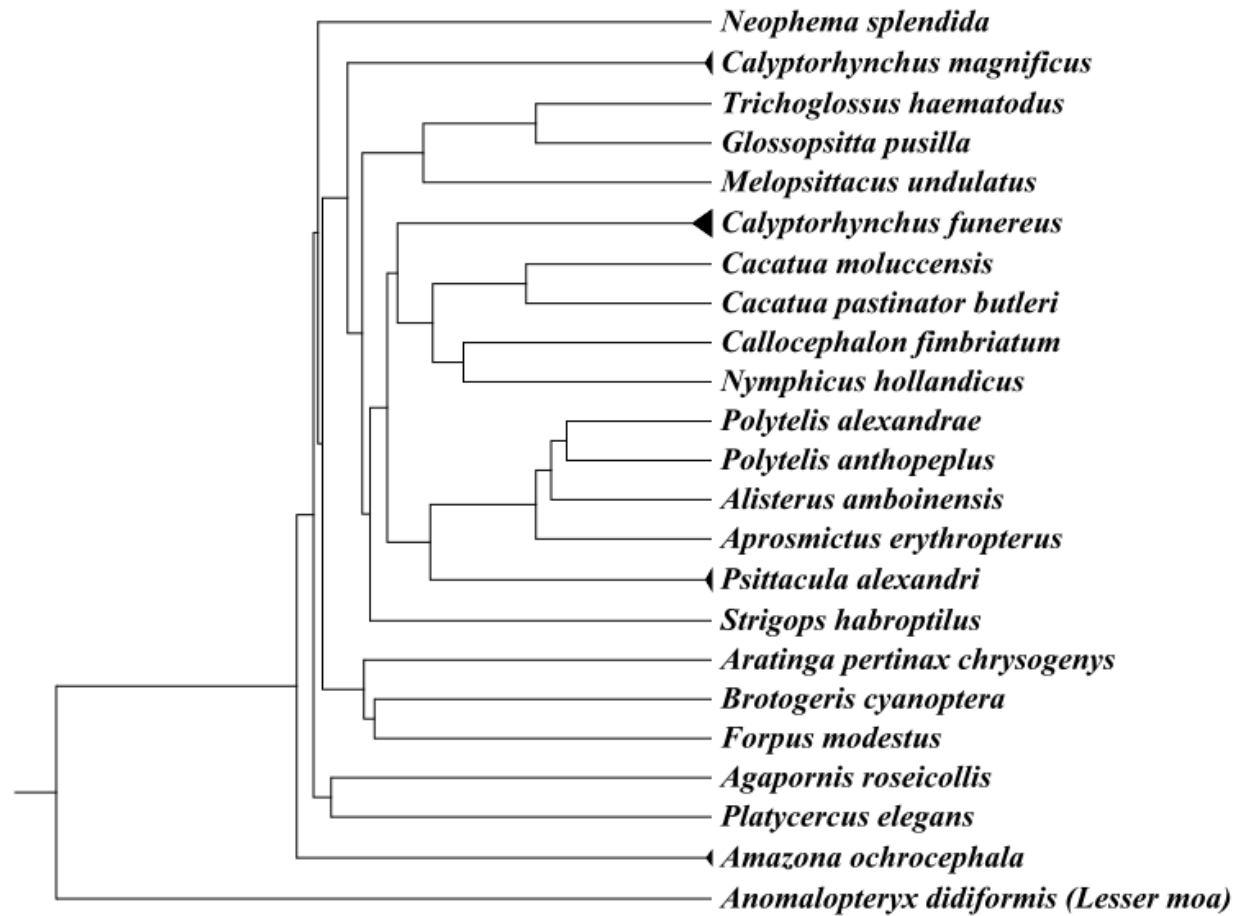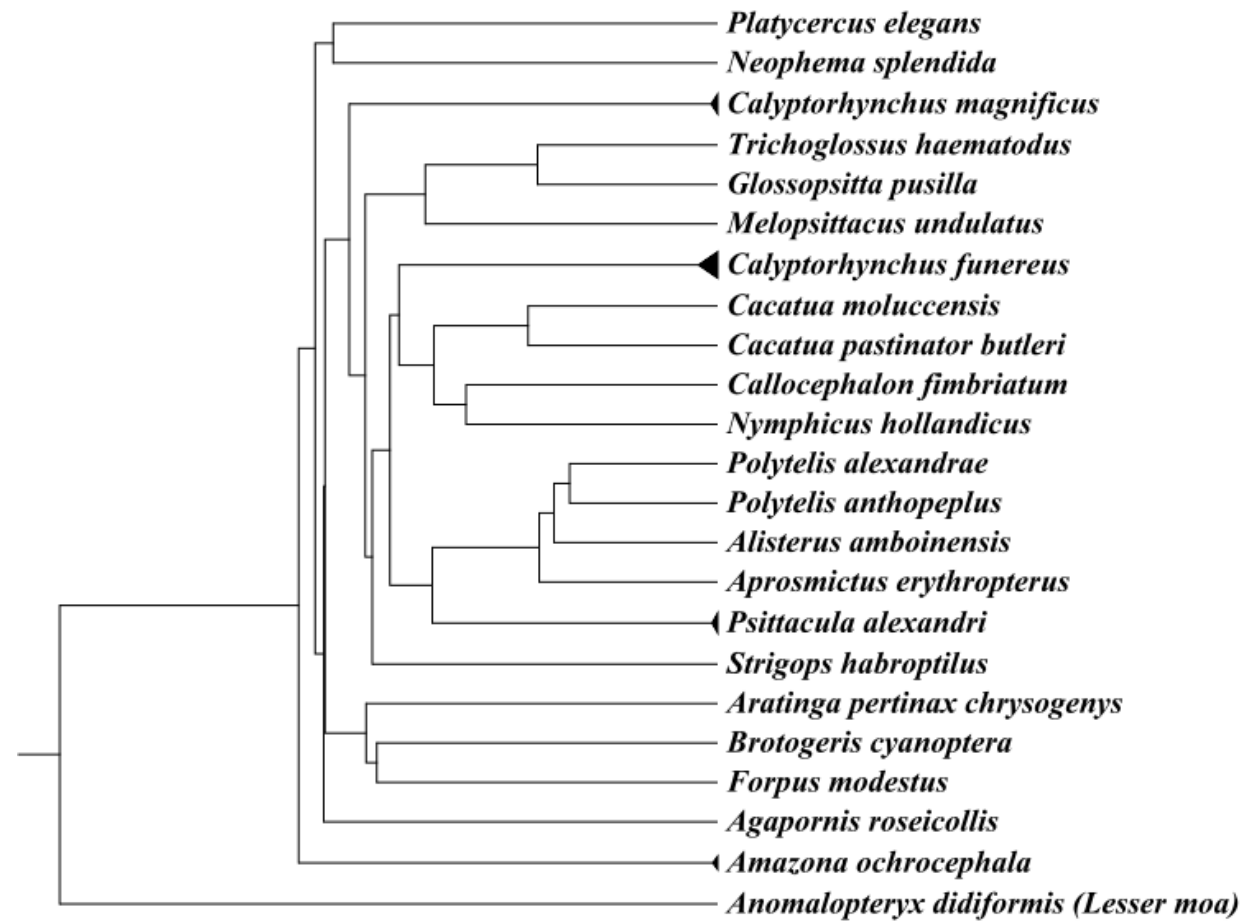*Amazona ochrocephala*
Anomalopteryx didiformis (Lesser moa)

Figure D.64: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND5 gene of parrot and cockatoo species using UPGMA method, Tajima-Nei model in MEGA 5 program.

Figure D.65: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND5 gene of parrot and cockatoo species using UPGMA method, Tamura 3-parameter model in MEGA 5 program.
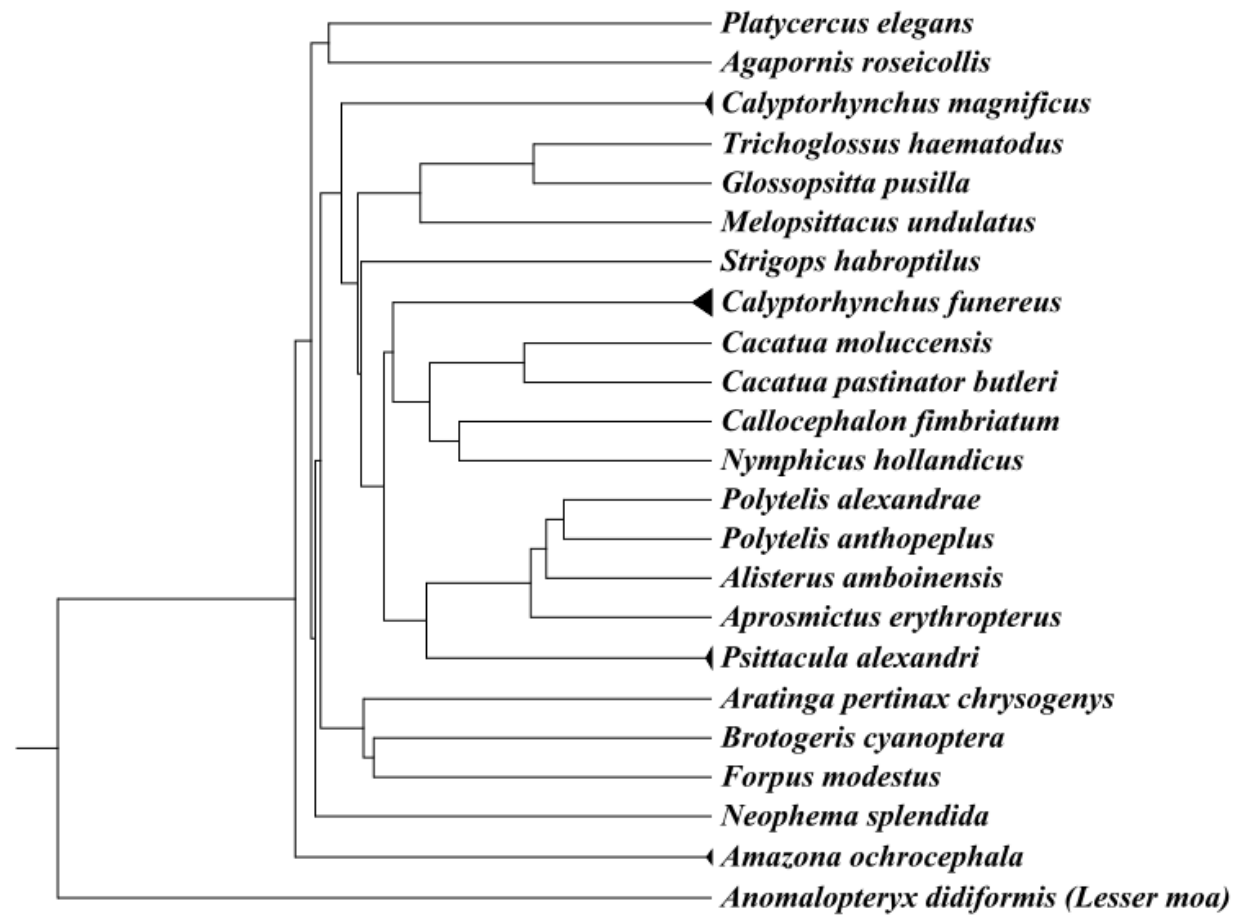
Figure D.66: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND5 gene of parrot and cockatoo species using UPGMA method, Tamura-Nei model in MEGA 5 program.
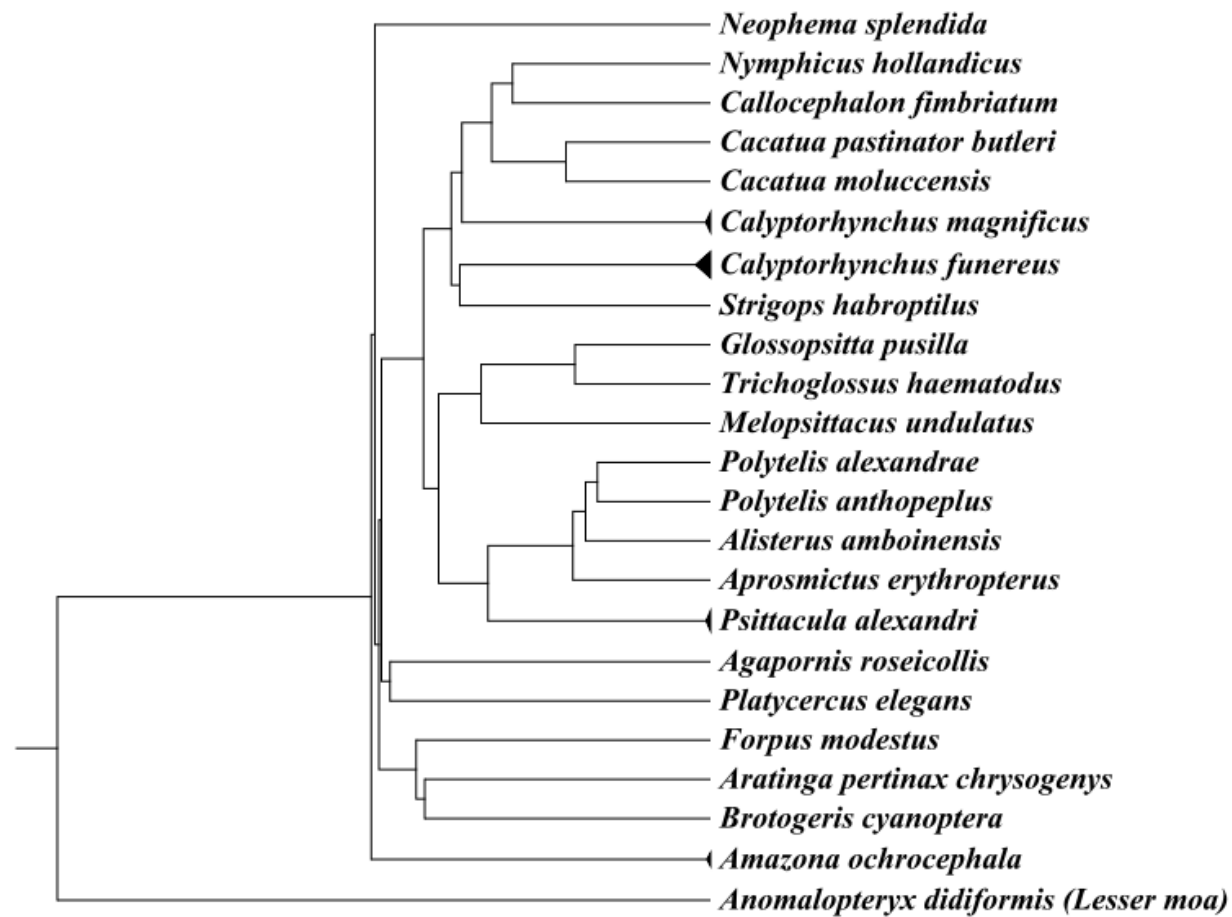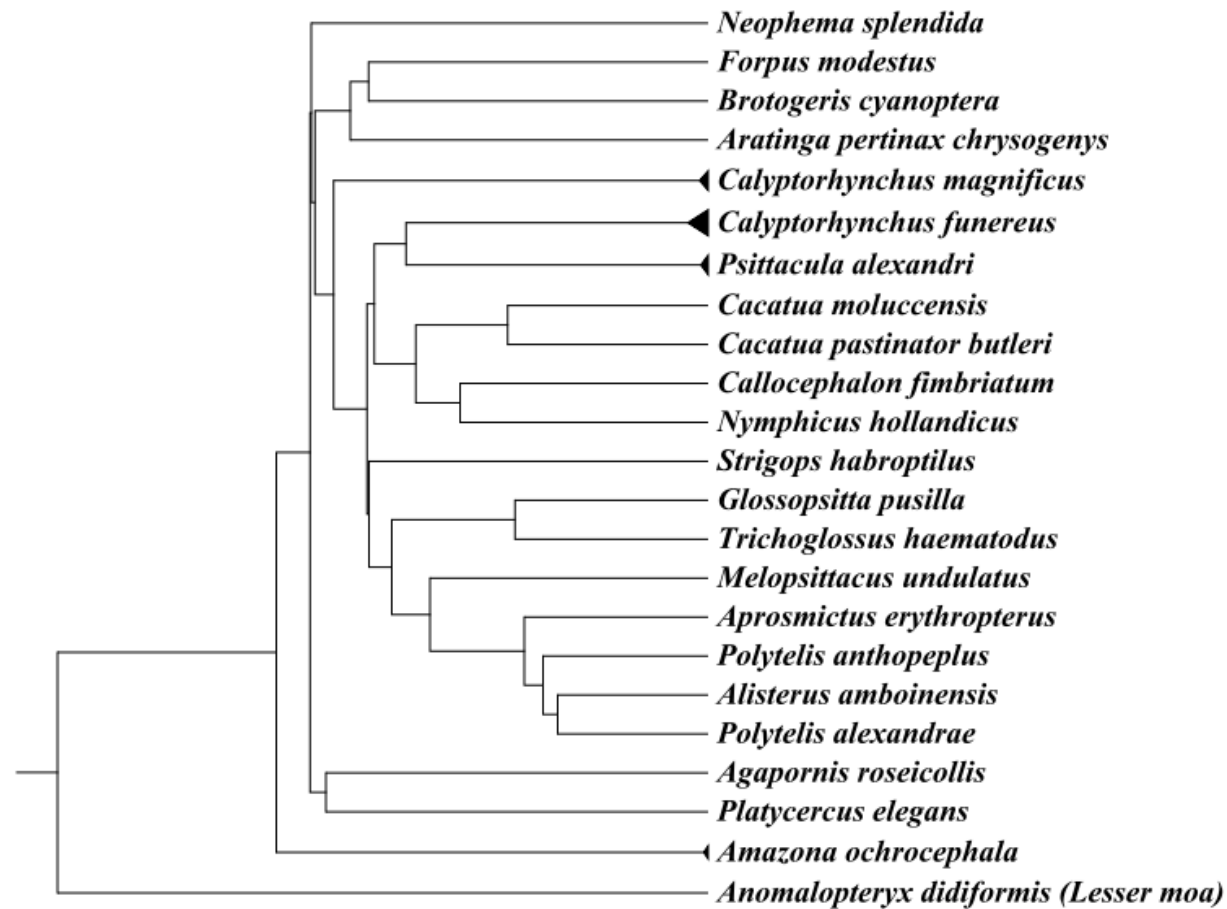
Figure D.67: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND5 gene of parrot and cockatoo species using UPGMA method, Maximum Composite Likelihood model in MEGA 5 program.

Neophema splendida
Forpus modestus
Brotogeris cyanoptera
Aratinga pertinax chrysogenys
Calyptorhynchus magnificus
Calyptorhynchus funereus
Psittacula alexandri
Cacatua moluccensis
Cacatua pastinator butleri
Callocephalon fimbriatum
Nymphicus hollandicus
Strigops habroptilus
Glossopsitta pusilla
Trichoglossus haematodus
Melopsittacus undulatus
Aprosmictus erythropterus
Polytelis anthopeplus
Alisterus amboinensis
Polytelis alexandrae
Agapornis roseicollis
Platycercus elegans
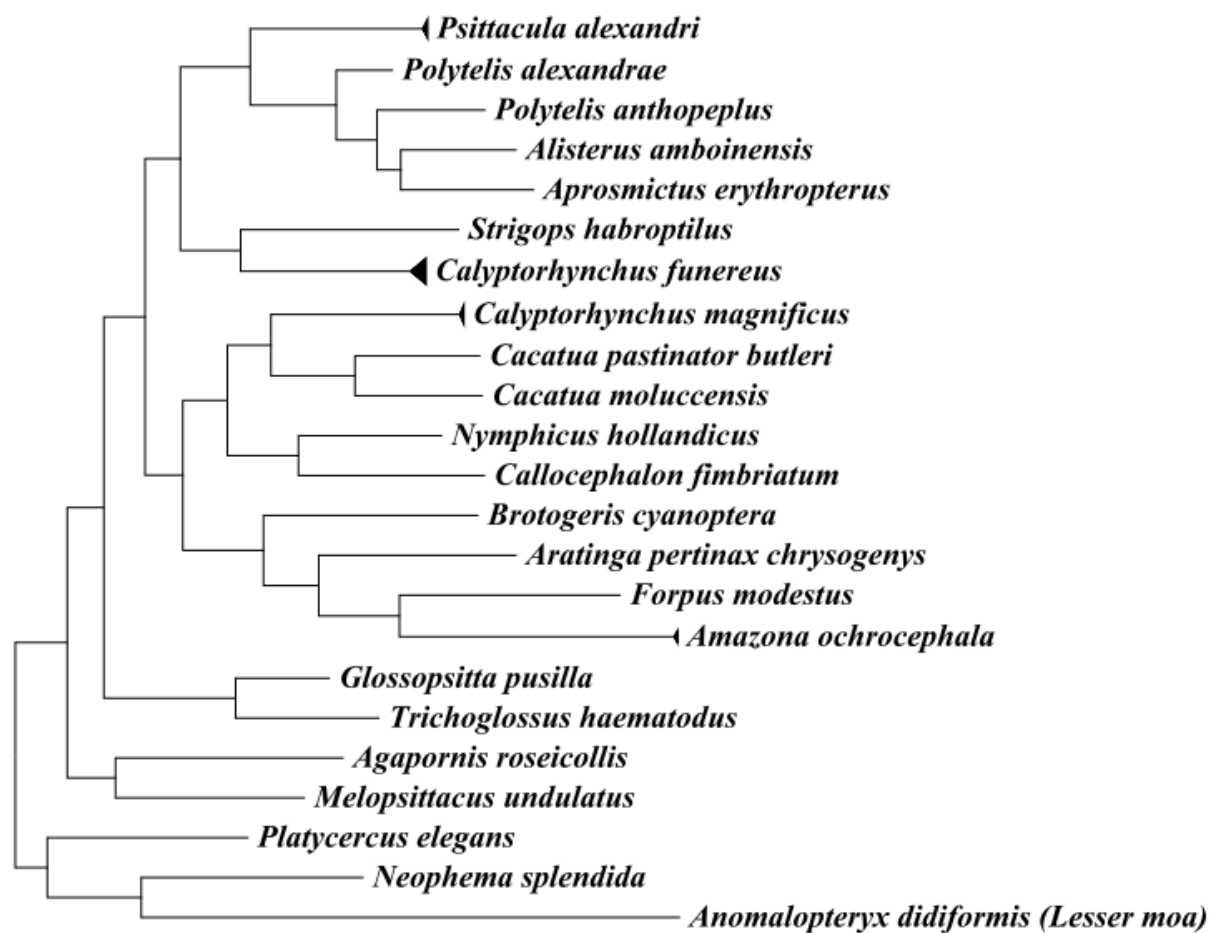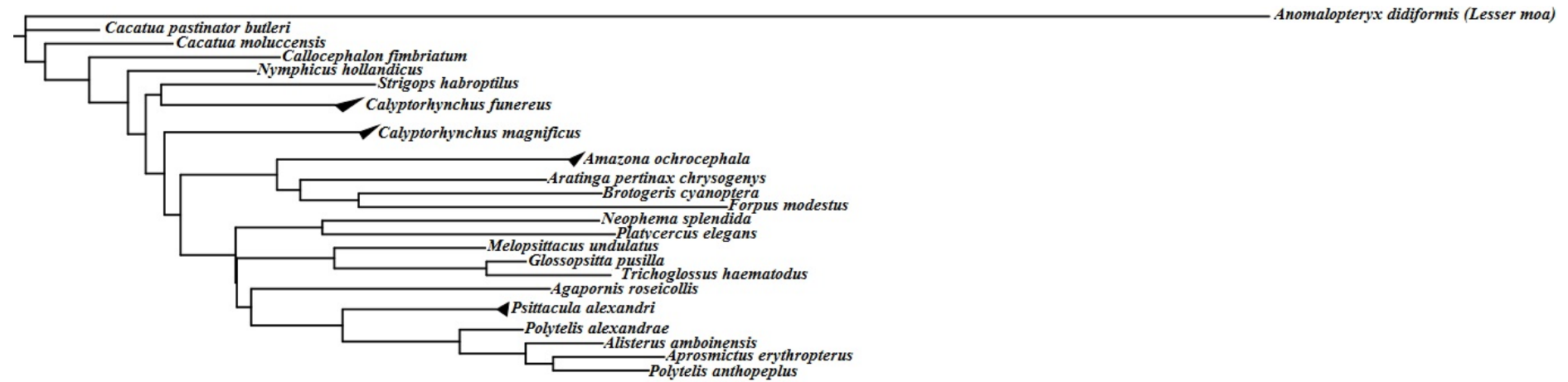Amazona ochrocephala
Anomalopteryx didiformis (Lesser moa)

Figure D.68: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND5 gene of parrot and cockatoo species using UPGMA method, LogDet (Tamura-Kumar) model in MEGA 5 program.

Figure D.69: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND5 gene of parrot and cockatoo species using Maximum Parsimony method in MEGA 5 program.

Figure D.70: The phylogenetic tree was reconstructed using partial sequences at 5' terminus of the ND5 gene of parrot and cockatoo species using MrBayes.