Phylogeny estimation of *Nannizziopsiacea* spp. infecting chelonians
Dataset

• Fungal Internal Transcribed Spacer (ITS) Region
• 57 Sequences Total
  • 11 from turtle cases
  • 45 published sequences from GenBank
  • 1 outgroup – Coccidioides immitis
• Sequence length heterogeneity
  • 418 – 590 bp
Multiple Sequence Alignment

- Two MSA methods
- MAFFT
  - v7.273
  - FFN-NS-2 Strategy
- Clustal Omega
  - Dealign Input Sequences: No
  - MBED-Like Clustering Guide Tree: Yes
  - MBED-Like Clustering Iteration: Yes
  - Number of Combined Iterations: default(0)
  - Max Guide Tree Iterations: Default
  - Max HMM Iterations: Default
  - Order: Aligned
Tree Estimation

- RAxML
  - v7.7.1
  - GTR-Gamma model
  - 100 rapid bootstrap inferences

- Tree comparison
  - Dendropy4
  - 10 FN, 10 FP
  - Normalized RF Score 0.185185
MAFFT Alignment