

- **Species: Cinnamomum Capparum Coronde**
- **Data size: 3GB**
- **Comparison between ITSx and ITSxpress output obtained using contigs as input**

1. ITSx - Output (ITSx_outptut.full.fasta)

- There are four sequences found in the output.

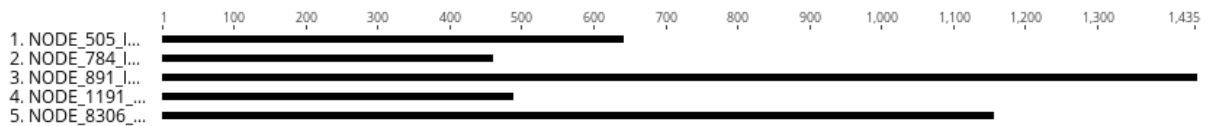


Figure1: ITSx output sequence view

- All five sequences were blasted against the NCBI nr/nt database.
- The BLAST results for two sequences contained the ITS regions of fungal species (Diaporthaceae sp., Phomopsis sp., Acaromyces ingoldii)
- The BLAST results for two sequences contained the ITS regions of animal species (Aceria sp., Phyllocoptes gracilis)
- The BLAST results for only one sequence contained the ITS regions of Cinnamomum species. (Cinnamomum verum)
- 98.7 % similarity found for Cinnamomum verum in the blast results.
- **GC content : 68.4% - 71.8%**

2. ITSxpress - Output (ITSxpress_output.fastq)

- Only three sequences were found in the output.



Figure2: ITSxpress output sequence view

- The BLAST results for one sequence contained the ITS regions of fungal species (*Acaromyces ingoldii*)
- The BLAST results for one sequence contained the ITS regions of animal species (*Aceria* sp.)
- The BLAST results for only one sequence contained the ITS regions of *Cinnamomum* species. (*Cinnamomum verum*)
- 98.7 % similarity found for *Cinnamomum verum* and 97.4% similarity found for *Cinnamomum multiflorum* in the blast results.
- **GC content : 68.4% - 71.8%**

3. Comparison done using multiple alignment

- The only ITSx output sequence that contained the ITS regions of *Cinnamomum* species when blasting and the only ITSxpress output sequence that contained the ITS regions of *Cinnamomum* species when blasting were aligned using the MAFFT algorithm.

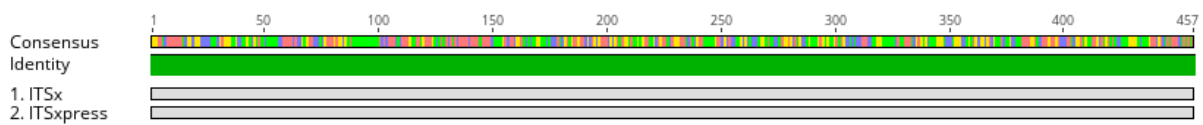


Figure3: Alignment view

Distance matrix

	ITSx	ITSxpress
ITSx	0	0
ITSxpress	0	0

- According to the above distance matrix, there is no difference in the results obtained from ITSx and ITSxpress using contigs as input.