- **Species: Cinnamomum Capparu Coronde**
- **Data size: 1GB**
- **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 four sequences were blasted against the NCBI nr/nt database.

   - The BLAST results for three sequences contained the ITS regions of fungal species (Colletotrichum scovillei, Colletotrichum eriobotryae, Colletotrichum indonesiense, Colletotrichum sp., Acaromyces ingoldii, Laurobasidium hachijoense)

   - The BLAST results for only one sequence contained the ITS regions of Cinnamomum species. (Cinnamomum verum, Cinnamomum multiflorum)

   - 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%**

2. **ITSxpress - Output (ITSxpress_outptut.fastq)**

   - Only one sequence found in the output.

   - The BLAST results for only one sequence contained the ITS regions of Cinnamomum species. (Cinnamomum verum, Cinnamomum multiflorum)

   - 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.
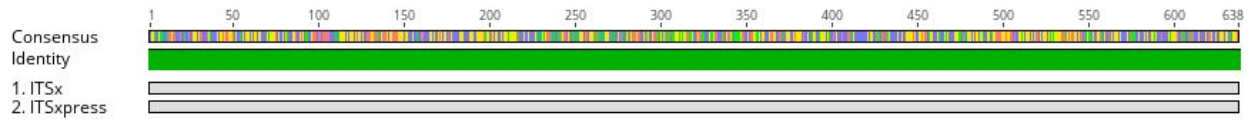
Figure2: Alignment view

Distance matrix

	ITSx	ITSxpress
ITSx		0
ITSxpress	0	

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