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T. interdigitale H6 CCTGCGGAAGGATCATTAA CGCGCAGGCCGGAGGCTGGCCCCCACGATAGGGCCAAACGTCCGT CAGGGGTGAGCAGATGTG
T. interdigitale MR816 CCTGCGGAAGGATCATTAA CGCGCAGGCCGGAGGCTGGCCCCCACGATAGGGCCAAACGTCCGT CAGGGGTGAGCAGATGTG
T. interdigitale AF168124 CCTGCGGAAGGATCATTAA CGCGCAGGCCGGAGGCTGGCCCCCACGATAGGGCCAAACGTCCGT CAGGGGTGAGCAGATGTG
T. interdigitale AY062119 CCTGCGGAAGGATCATTAA CGCGCAGGCCGGAGGCTGGCCCCCACGATAGGGCCAAACGTCCGT CAGGGGTGAGCAGATGTG

T. interdigitale H6 CGCCGGCCGTACCGCCCCATTCTTGCTAC TTACTCGGTTGCCTCGGCGGGCCGCGCTCTCCAGGAGAGCCGTT CGGCGAG
T. interdigitale MR816 CGCCGGCCGTACCGCCCCATTCTTGCTAC TTACTCGGTTGCCTCGGCGGGCCGCGCTCTCCAGGAGAGCCGTT CGGCGAG
T. interdigitale AF168124 CGCCGGCCGTACCGCCCCATTCTTGCTAC TTACTCGGTTGCCTCGGCGGGCCGCGCTCTCCAGGAGAGCCGTT CGGCGAG
T. interdigitale AY062119 CGCCGGCCGTACCGCCCCATTCTTGCTAC TTACTCGGTTGCCTCGGCGGGCCGCGCTCTCCAGGAGAGCCGTT CGGCGAG

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Figure S1. ITS sequence variation in *T. interdigitale*. Aligned ITS sequence is shown for four isolates, including the two for which whole genomes were sequenced (H6 and MR816) and two previously characterized isolates (AF168124 and AY062119). Isolate AY062119 has been re-classified as *T. mentagrophytes*. Variant sites are highlighted.