Supplementary Information

The large subunit rDNA sequence of *Plasmodiophora brassicae* does not contain intra-species polymorphism.

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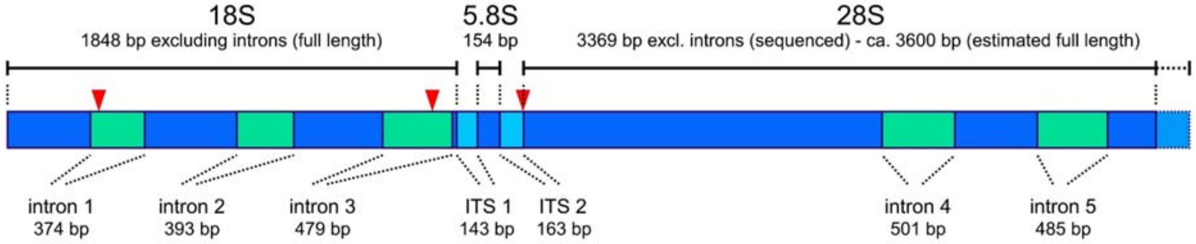
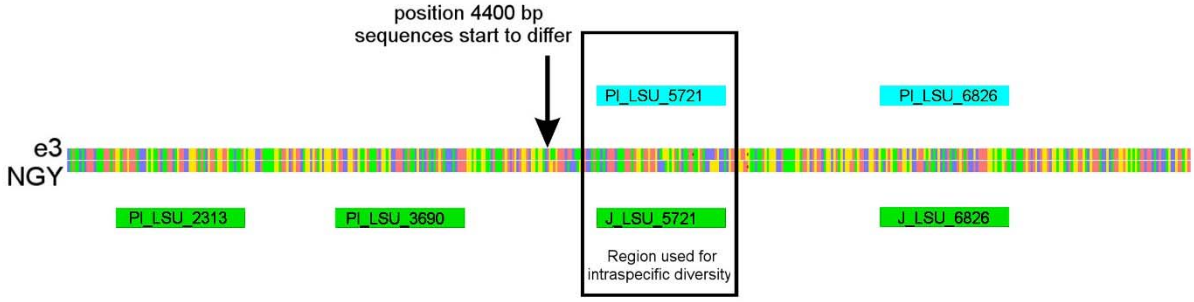
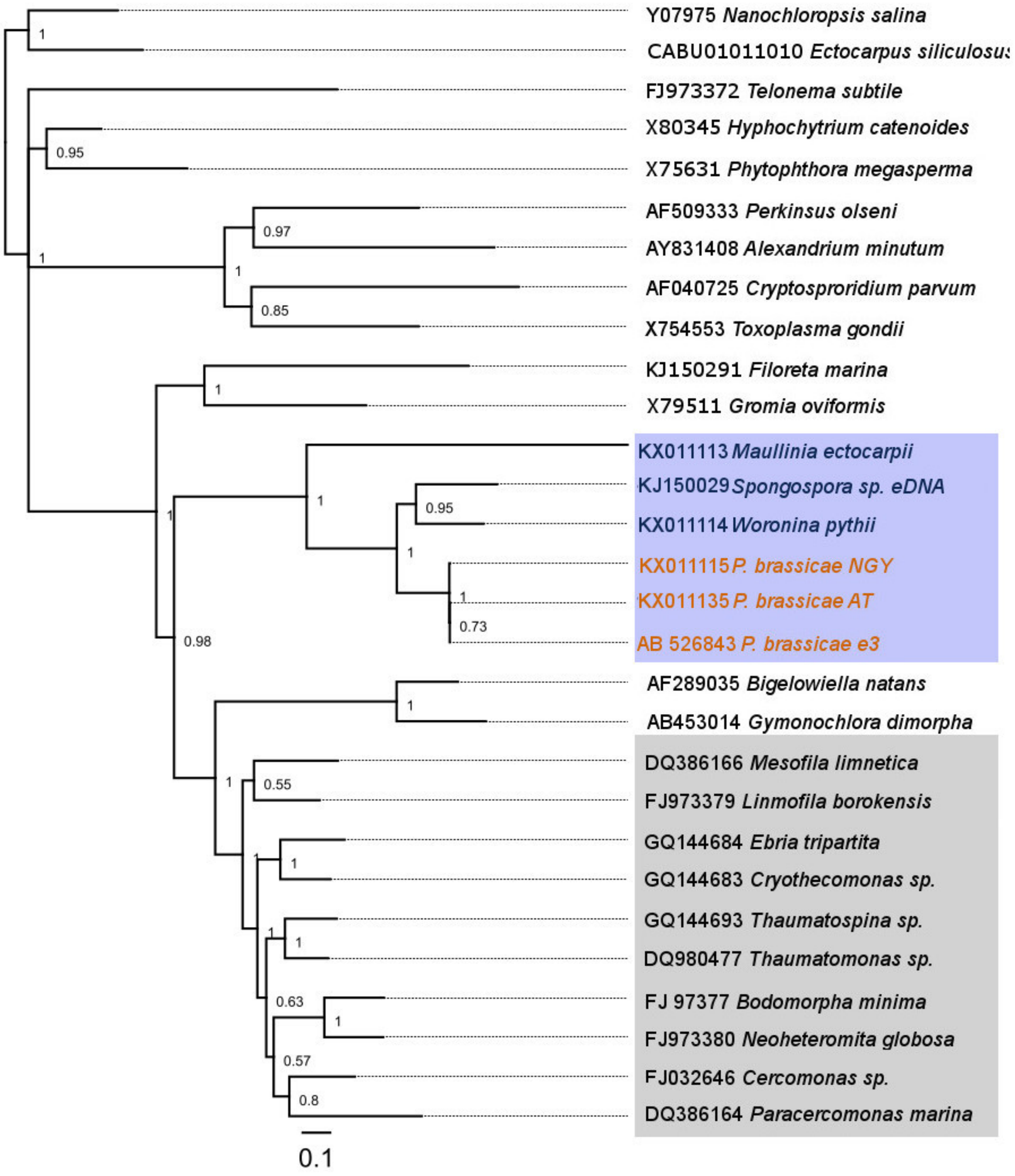
Contents:



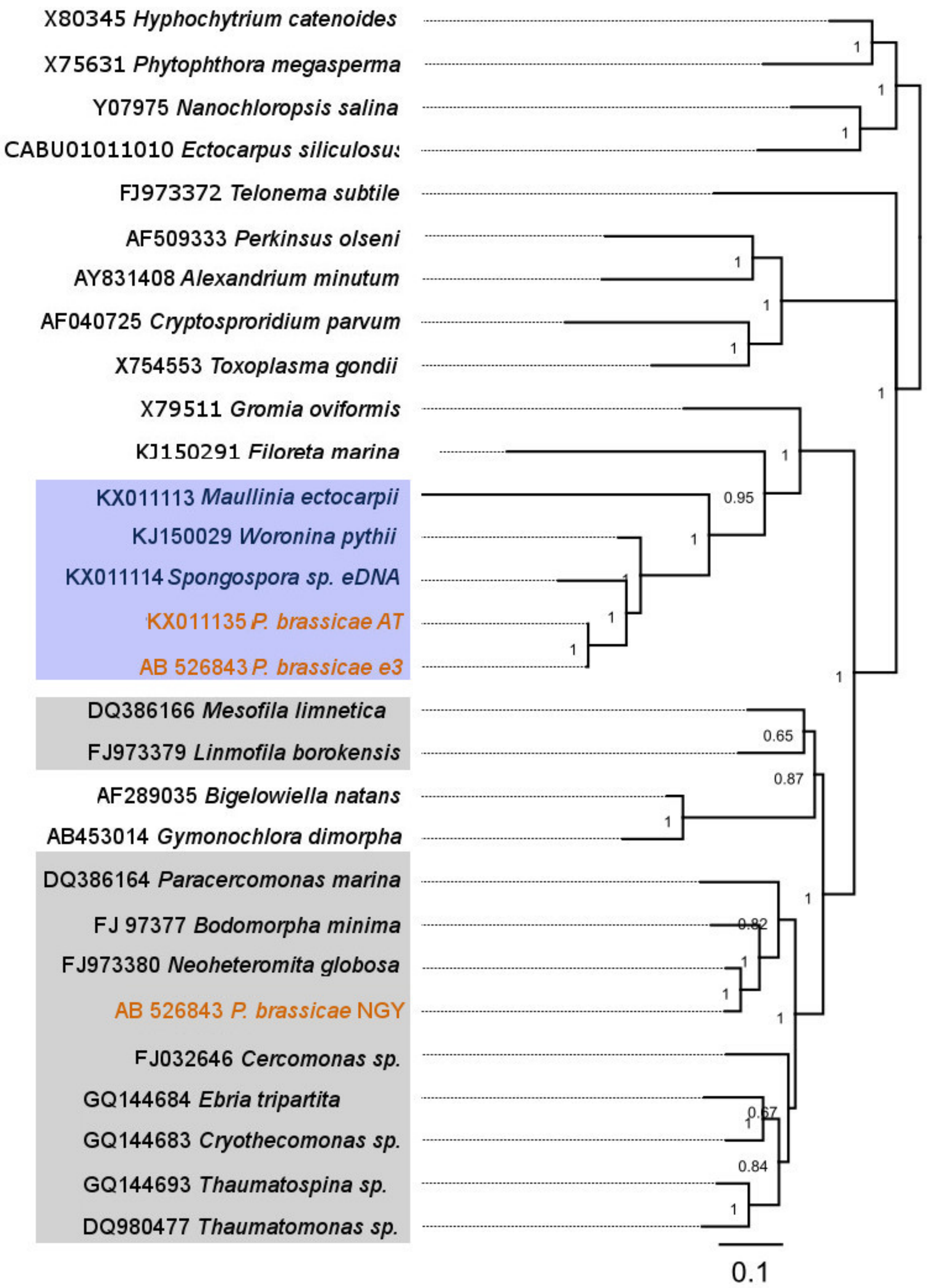
Supplementary Fig. S1: Schematic representation of the ribosomal cluster of *Plasmodiophora brassicae*, showing the position and respective length of the three coding regions (18S, 5.8S and 28S), the two internal transcribed spacers (ITS1 & ITS2), and the five introns. The fragment amplified and sequenced from isolate AT is represented (GenBank accession number KX011115); it is 7909 bp long and all regions are drawn to scale. The missing part at the 3' end of 28S (indicated with a dotted line) is expected to be ca. 230 bp long. Red arrows indicate the position of the only three differences we observed between the sequence of isolate AT and the genomic contig from isolate e3 (see the Results section for details).



Supplementary Fig. S2: Diagrammatic representation of the LSU gene (not to scale) showing the distribution of the probes along the LSU gene. Arrow marks the point where the two sequences start to differ, a box highlights the region used for intraspecific diversity analyses (see Fig. 2).



Supplementary Fig. S3: Bayesian tree with distances belonging to Fig. 1A with posterior probabilities. Only the 5' of the LSU gene was used to generate this tree. All *P. brassicae* sequences form one, consistent and well supported clade together with the other phytomyxid sequences. Dotted lines are for visual support only.



Supplementary Fig. S4: Bayesian tree with distances belonging to Fig. 1B with posterior probabilities. Only the 3’ of the LSU gene was used to generate this tree. *P. brassicae* sequences generated in this study form one, consistent and well supported clade together with the other phytomyxid sequences. The sequence P. brassicae NGY, however, groups within Cercozoa with high support values and is very similar to the Neoheteromitha globosa sequence. Dotted lines are for visual support only.

Supplementary Tabe S1. Description of the PCR primers used in this study.

name	**sequence**	**orientation**	**specificity**	**position ***
sA1n	5'-TACCTGGTTGATCCTGCCAGT-3'	forward	universal (eukaryotes)	1-21
sA6-phy	5'-GATGGCTCATTAHAWCAGTYTGAA-3'	forward	Phytomyxea	93-116
V7f-Phag	5'-GACCTCAGCYTRYTGGTTGTT-3'	forward	Phagomyxida	2133-2153
V7f-Plas	5'-GACCTCAGCCTGCTTTTGTAG-3'	forward	Plasmodiophorida	2133-2153
C9f-Phag	5'-CTTGYAAYTMGCCGCACCAAC-3'	forward	Phagomyxida	2367-2387
C9f-Plas	5'-CTTGSAAYTAGAGGCACCAAC-3'	forward	Plasmodiophorida	2367-2387
C9r-Phyt	5'-GGAATTCCTCGTTGGTGCGGSBART-3'	forward	most Phytomyxea	2373-2397
V9r-Mau	5'-GTCAAGATTCAGAATAGTTCATC-3'	forward	*Maullinia*	2532-2554
sB2phy	5'-CCTTGTTACGACTTCTYCTTCYTC-3'	reverse	Phytomyxea and many other eukaryotes	2560-2583
sB1n	5'-GATCCHTCYGCAGGTTCACCTACG-3'	reverse	universal (eukaryotes)	3067-3090
D14f-phy1	5'-GATTAGAGGCSTTTGGSGCAA-3'	forward	Phytomyxea	4744-4764
D14f-phy2	5'-GCAAAATGCWCYGAACCTATTCTC-3'	forward	Phytomyxea	4761-4784
21R	5'-GACGAGGCATTTGGCTACCTT-3'	reverse	universal (eukaryotes)	6529-6549
22R	5'-CCATTCATGCRCGTCACWART-3'	reverse	universal (eukaryotes)	6555-6575
nH2r	5'-GAHHBARCKGTTCCTCTCGTACT-3'	reverse	universal (eukaryotes)	7796-7818
nH4r	5'-GGNTTCBRDYTTAGAGGCGTTCA-3'	reverse	universal (eukaryotes)	7886-7908

* based on the sequence of *Plasmodiophora brassicae* isolate AT, GenBank accession number KX011115.