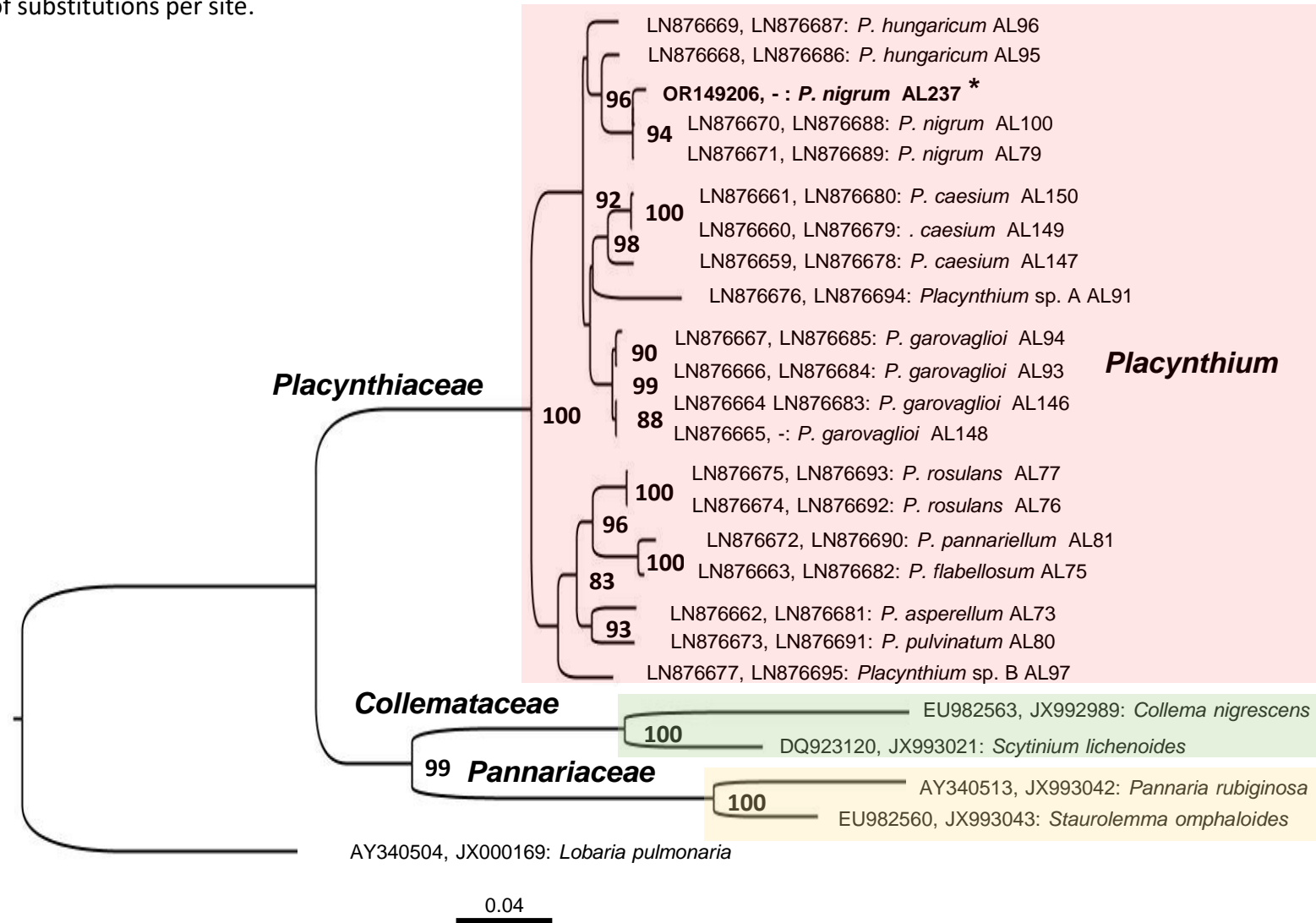
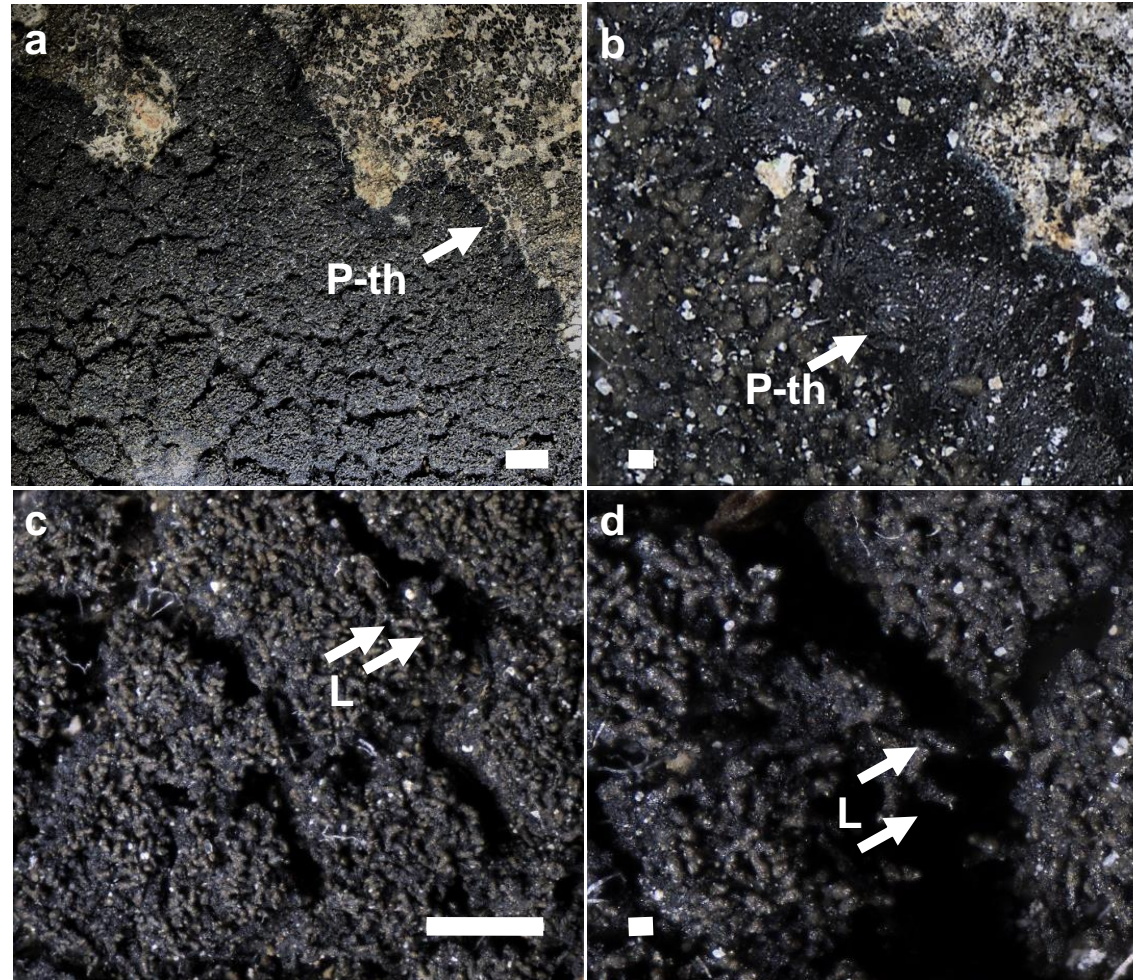


S1. Fungal partner (mycobiont). The most likely phylogenetic tree from a RAxML analysis based on **1309** aligned characters of concatenated mtSSU rDNA and MCM7 from **25** specimens. Support values (ML) given when ML >80%. The families Pannariaceae, Collematataceae and Placynthiaceae are indicated by green, yellow, and red colour, respectively. *Placynthium nigrum* (AL237; Sweden, Öland) studied here is highlighted in bold. The scale bars indicate 0.04 of substitutions per site.



S2. The lichen *Placynthium nigrum* – picture of holotype S-F453718. P-th – mycobiont prothallus, L – lobe of the lichen. Scale bars 10 μm (2a, d), 100 μm (2b), 1000 μm (2c).



S3. Similarity matrices comparing the genetic divergence within the *Macrochaete* genus based on 16S rRNA and 16S–23S rRNA ITS (marked in bold) gene sequences respectively.

	1	2	3	4	5	6	7	8	9	10
1 <i>M. oelandica</i> AL469_cultured										
2 <i>M. oelandica</i> AL555_in_lichen	100/98.66									
3 KT336440_M._santannae_CCALA_1093_operon_1	97.08/76.79	97.08/77.17								
4 KU559619_M._lichenoides_SAG_32.92_operon_1	99.54/81.13	99.54/81.25	97.17/75.07							
5 KU559618_M._lichenoides_SAG_32.92_operon_2	99.54/83.83	99.54/83.97	97.17/75.61	100/85.68						
6 KT336439_M._psychrophila_CCALA_32	96.25/77.32	96.25/77.96	95.16/73.44	96.25/83.99	96.25/80.21					
7 KU559617_M._psychrophila_ANT_SPH_13/96	96.34/79.45	96.34/79.83	95.25/75.60	96.34/79.90	96.34/83.99	99.91/82.28				
8 KR350577_M._psychrophila_CCALA_1092_operon_1	96.62/80.43	96.62/81.10	94.97/74.74	96.62/81.73	96.62/79.39	99.45/87.66	99.54/81.20			
9 KR350580_M._psychrophila_NU16B/09_operon_1	96.71/79.84	96.71/80.49	95.06/75.72	96.71/80.90	96.71/77.81	99.54/86.72	99.63/81.66	99.91/98.79		
10 KR350574_M._psychrophila_TS40B/09_operon_1	96.71/80.22	96.71/81.18	95.06/75.66	96.71/81.79	96.71/78.01	99.54/88.08	99.63/83.46	99.91/95.96	100/96.58	