

Table 1: List of matrices used in the analyses, with the biont and the taxonomic breadth of the taxa it contains, the loci, number of taxa, number of character included, total number of sites, number of variable characters and of parsimony-informative characters. The numbers inside parentheses represent the proportion of the total.

Matrix No.	Biont	Taxonomic breadth	Loci	No. taxa	No. char. incl. / Total No. of sites	No. variable char.	No. parsimony-inf. char.
1	Mycobiont	Genus <i>Peltigera</i> (+outgroup)	Concatenated : 4	105	3135/3736 (0.84)	975 (0.31)	776 (0.25)
			LSU	84 (0.8)	1218/1392 (0.875)	244 (0.2)	163 (0.13)
			<i>RPB1</i>	98 (0.93)	638/716 (0.89)	276 (0.43)	235 (0.35)
			<i>EFT2.1</i>	78 (0.74)	784/942 (0.83)	261 (0.33)	216 (0.28)
			β -tubulin	80 (0.76)	495/686 (0.72)	194 (0.39)	162 (0.33)
2	Mycobiont	Section <i>Polydactylon</i>	Concatenated: 5	119	3803/4621 (0.82)	566 (0.15)	410 (0.11)
			ITS	119 (1)	505/907 (0.56)	150 (0.3)	123 (0.24)
			LSU	118 (0.99)	1252/1374 (0.94)	78 (0.06)	61 (0.05)
			<i>RPB1</i>	109 (0.92)	676/716 (0.94)	87 (0.13)	61 (0.09)
			<i>EFT2.1</i>	84 (0.71)	818/942 (0.87)	120 (0.15)	81 (0.1)
3	Cyanobiont	Genus <i>Nostoc</i> (+outgroup)	β -tubulin	104 (0.87)	552/682 (0.81)	131 (0.24)	84 (0.15)
			<i>rbcLX</i>	417	636/1162 (0.55)	319 (0.5)	277 (0.44)
			ITS	206	861/907 (0.95)	313 (0.36)	280 (0.33)
			Section <i>Polydactylon</i>				
			Genus <i>Nostoc</i>	209	636/1162 (0.55)	237 (0.37)	176 (0.28)
6	Mycobiont	Section <i>Polydactylon</i>	Concatenated: 6	119	3907/4769 (0.82)	690 (0.18)	526 (0.13)
			ITS	119 (1)	475/907 (0.52)	135 (0.28)	108 (0.23)
			LSU	84 (0.8)	1231/1374 (0.9)	69 (0.06)	53 (0.04)
			<i>RPB1</i>	98 (0.93)	676/716 (0.94)	89 (0.13)	61 (0.09)
			<i>EFT2.1</i>	78 (0.74)	817/942 (0.87)	120 (0.15)	81 (0.1)
7	Mycobiont	Section <i>Polydactylon</i>	β -tubulin	80 (0.76)	560/682 (0.82)	129 (0.23)	82 (0.15)
			PICS-ORD	119 (1)	148	148 (1)	141 (0.95)
			char.				
			ITS	173	563/907 (0.62)	233 (0.41)	195 (0.35)
			Section <i>Polydactylon</i>				