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Supplementary material

Supplementary material Appendix 1.

Table A1. List of species included in the analyses.

Figure A1. Evaluation on MCMC convergence.

Table A2. Model fit statistics.

Table A3. Variance partitioning for a model with raw associations

Table A4. Consistency of associations between the data based on fruit-body observations and DNA metabarcoding.

Table A1. List of species included in the analyses (n = 37 for prevalence in the fruit-body data, and for prevalence and abundance in the DNA data; n = 16 for abundance in the fruit-body data, species with no abundance data available marked with NA), and their prevalences and mean abundances in the data based on fruit-body observations and DNA metabarcoding. Prevalence describes to the proportion of logs (n = 100) in which the species were recorded present. Abundance corresponds to hymenophore area (cm²) in the data based on fruit-body observations, and species-specific sequence counts in the data based on DNA metabarcoding. The species are listed in the order they appear in Figure 1.

Species	Data based on			
	Fruit-body observations		DNA metabarcoding	
	Prevalence	Mean Abundance	Prevalence	Mean Abundance
<i>Postia caesia</i>	0.26	4.1	0.02	0.02
<i>Coniophora arida</i>	0.10	NA	0.09	3.28
<i>Sistotrema coroniferum</i>	0.01	NA	0.13	4.39
<i>Gloiothele citrina</i>	0.11	966.7	0.10	4.22
<i>Stereum sanguinolentum</i>	0.05	8.5	0.11	19.92
<i>Sistotrema brinkmannii</i>	0.02	NA	0.17	4.8
<i>Paxillus involutus</i>	0.01	50.0	0.11	0.41
<i>Trichaptum abietinum</i>	0.54	1585.1	0.13	13.37
<i>Fomitopsis pinicola</i>	0.73	176.7	0.61	615.78
<i>Pycnoporellus fulgens</i>	0.05	139.7	0.10	4.0
<i>Athelia decipiens</i>	0.11	NA	0.24	3.27
<i>Coniophora olivacea</i>	0.14	NA	0.15	31.63
<i>Heterobasidion parviporum</i>	0.28	139.5	0.30	3.89
<i>Resinicium bicolor</i>	0.14	NA	0.15	76.9
<i>Amphinema byssoides</i>	0.30	NA	0.17	2.07
<i>Amyloporia sinuosa</i>	0.17	495.1	0.04	6.24
<i>Asterodon ferruginosus</i>	0.10	1476.8	0.01	0.14
<i>Alutaceodontia alutacea</i>	0.02	NA	0.15	49.51
<i>Leucogyrophana sororia</i>	0.01	NA	0.11	25.52
<i>Tomentellopsis echinospora</i>	0.15	NA	0.02	0.13
<i>Tubulicrinis borealis</i>	0.05	NA	0.34	48.95
<i>Athelopsis subinconspicua</i>	0.05	NA	0.23	8.09
<i>Basidioidendron caesiocinereum</i>	0.15	NA	0.32	33.75
<i>Botryobasidium intertextum</i>	0.08	NA	0.23	2.51
<i>Xylodon brevisetus</i>	0.17	NA	0.06	0.34
<i>Tylospora fibrillosa</i>	0.26	NA	0.02	0.03
<i>Piloderma bicolor</i>	0.07	30.0	0.17	5.22
<i>Hyphodontia pallidula</i>	0.16	NA	0.28	65.47
<i>Globulicium hiemale</i>	0.24	2500.0	0.09	0.65
<i>Butyrea luteoalba</i>	0.13	55.4	0.10	70.28
<i>Botryobasidium subcoronatum</i>	0.18	NA	0.32	3.09
<i>Phellinus viticola</i>	0.29	835.1	0.20	61.6

Species	Data based on			
	Fruit-body observation		DNA metabarcoding	
	<i>Prevalence</i>	<i>Mean Abundance</i>	<i>Prevalence</i>	<i>Mean Abundance</i>
<i>Phellopilus nigrolimitatus</i>	0.18	668.0	0.46	155.46
<i>Aphanobasidium pseudotsugae</i>	0.16	NA	0.29	53.36
<i>Xenasmatella vaga</i>	0.13	NA	0.04	9.99
<i>Piloderma byssinum</i>	0.18	NA	0.10	6.34
<i>Antrodia serialis</i>	0.41	332.9	0.58	295.31

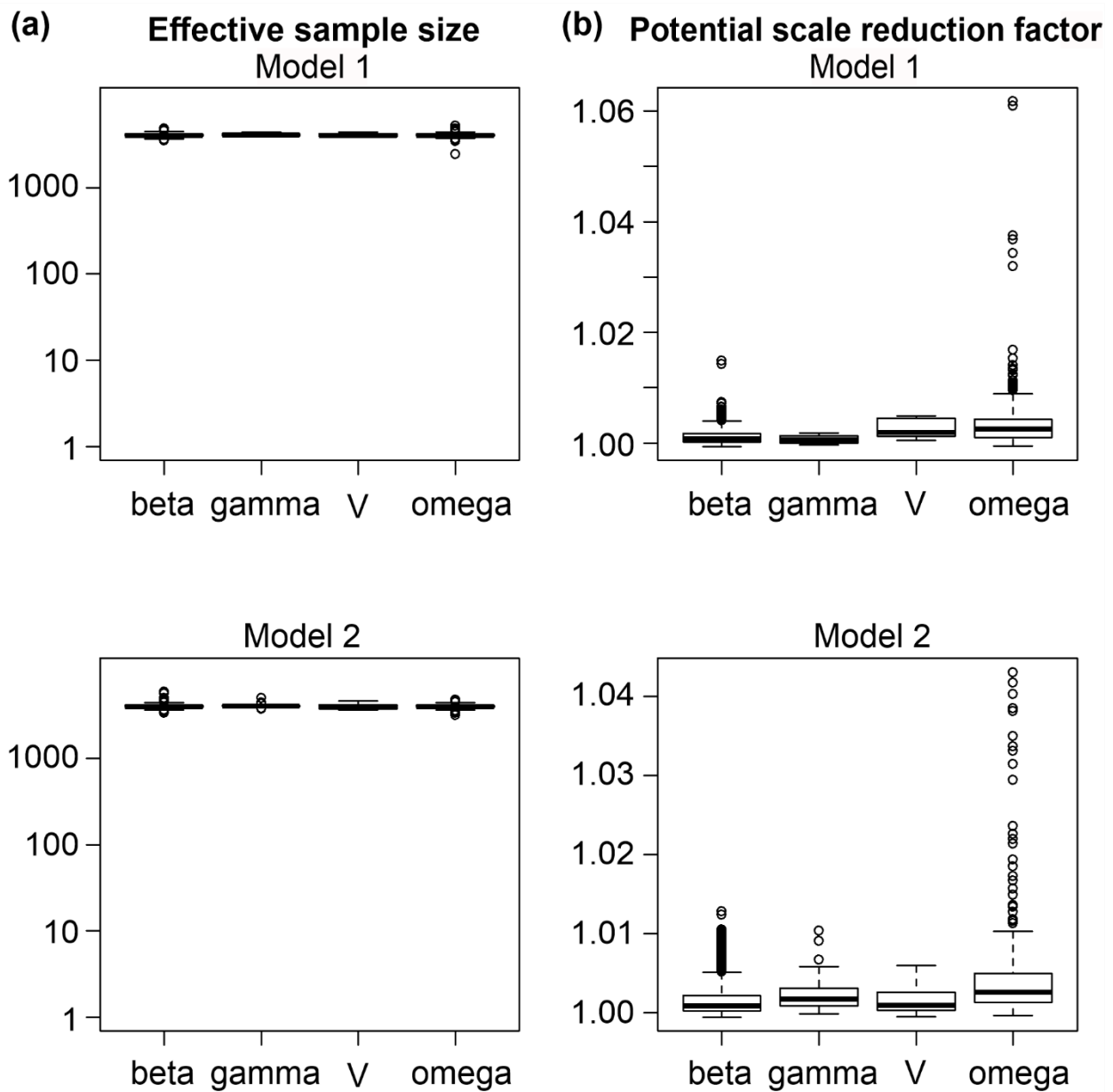


Figure A1. (a) The effective sample sizes and (b) the potential scale reduction factors for model variants

Model 1 (raw associations) and Model 2 (residual associations) resulting from the MCMC sampling.

Table A2. The model fit for the model variant with raw associations measured by the AUC statistics in the occurrence data and by R^2 in the abundance data.

Model fit statistics	Data type	Model fit %
AUC	Fruit-body occurrence	76
	Mycelial occurrence	79
R^2	Fruit-body abundance	7
	Mycelial abundance	11

Table A3. The proportion of variance explained by explanatory variables included in the model variant with raw associations. The results are inferred at the log level and averaged over all species and data types.

Explanatory variable	Proportion of variance explained %
Sequencing depth	37
Random effects	63

Table A4. The proportion of species pairs showing consistent (both positive (+/+), both negative (-/-), or both neutral (0/0)), contradictory (one positive and the other one negative (+/-)), and not consistent nor contradictory associations (one positive or negative and the other one neutral (+/0, -/0)) between the data based on fruit-body observations and DNA metabarcoding. The table shows the proportions of different association combinations separately for different data (occurrence/abundance) and association (raw/residual) types.

		Association in data based on DNA metabarcoding			Data and association type
		+	-	0	
Association in data based on fruit-body observations	+	0.177	0.003	0.137	occurrence raw
	-	0.009	0.072	0.029	
	0	0.161	0.138	0.275	
	+	0.114	0	0.066	occurrence residual
	-	0	0.081	0.042	
	0	0.150	0.126	0.420	
	+	0	0	0	abundance raw
	-	0	0	0	
	0	0	0.008	0.992	
	+	0	0	0	abundance residual
	-	0	0	0	
	0	0	0.008	0.992	