

# Online Research @ Cardiff

This is an Open Access document downloaded from ORCA, Cardiff University's institutional repository: <https://orca.cardiff.ac.uk/id/eprint/106231/>

This is the author's version of a work that was submitted to / accepted for publication.

Citation for final published version:

Gange, A. C., Heegaard, E., Boddy, Lynne ORCID: <https://orcid.org/0000-0003-1845-6738>, Andrew, C., Kirk, P., Halvorsen, R., Kuyper, T. W., Bässler, C., Diez, J., Heilman-Clausen, J., Høiland, K., Büntgen, U. and Kauserud, H. 2018. Trait-dependent distributional shifts in fruiting of common British fungi. *Ecography* 41 (1) , pp. 51-61. 10.1111/ecog.03233 file

Publishers page: <http://dx.doi.org/10.1111/ecog.03233>  
<<http://dx.doi.org/10.1111/ecog.03233>>

Please note:

Changes made as a result of publishing processes such as copy-editing, formatting and page numbers may not be reflected in this version. For the definitive version of this publication, please refer to the published source. You are advised to consult the publisher's version if you wish to cite this paper.

This version is being made available in accordance with publisher policies.

See

<http://orca.cf.ac.uk/policies.html> for usage policies. Copyright and moral rights for publications made available in ORCA are retained by the copyright holders.



1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25

## Trait-dependent distributional shifts in fruiting of common British fungi

A. C. Gange<sup>1\*</sup>, E. Heegaard<sup>2\*</sup>, L. Boddy<sup>3</sup>, C. Andrew<sup>4</sup>, P. Kirk<sup>5</sup>, R. Halvorsen<sup>6</sup>, T. W. Kuyper<sup>7</sup>, C. Bäessler<sup>8</sup>, J. Diez<sup>9</sup>, J. Heilman-Clausen<sup>10</sup>, K. Høiland<sup>4</sup>, U. Büntgen<sup>11,12,13</sup> and H. Kauserud<sup>4</sup>

<sup>1</sup>*School of Biological Sciences, Royal Holloway, University of London, Egham, Surrey TW20 0EX UK*

<sup>2</sup>*Norwegian Institute of Bioeconomy Research, Fanaflaten 4, N-5244 Fana, Norway*  
*[ainer.heegaard@nibio.no](mailto:ainer.heegaard@nibio.no)*

<sup>3</sup>*Cardiff School of Biosciences, Biomedical Building, Museum Avenue, Cardiff CF10 3AX, UK*  
*[boddyl@Cardiff.ac.uk](mailto:boddyl@Cardiff.ac.uk)*

<sup>4</sup>*Section for Genetics and Evolutionary Biology (Evogene), Department of Biosciences, University of Oslo, P.O. Box 1066 Blindern, NO-0316 Oslo, Norway*  
*[c.j.andrew@ibv.uio.no](mailto:c.j.andrew@ibv.uio.no), [klaus.hoiland@ibv.uio.no](mailto:klaus.hoiland@ibv.uio.no), [havard.kauserud@bio.uio.no](mailto:havard.kauserud@bio.uio.no)*

<sup>5</sup>*Royal Botanical Gardens, Kew, Surrey TW9 3DS, UK*  
*[P.Kirk@kew.org](mailto:P.Kirk@kew.org)*

<sup>6</sup>*Geo-ecological Research Group, Natural History Museum, University of Oslo, P.O.Box 1172 Blindern, NO-0318 Oslo, Norway*  
*[rune.halvorsen@nhm.uio.no](mailto:rune.halvorsen@nhm.uio.no)*

<sup>7</sup>*Department of Soil Quality, Wageningen University & Research, P.O. Box 47, 6700AA Wageningen, The Netherlands*  
*[thom.kuyper@wur.nl](mailto:thom.kuyper@wur.nl)*

<sup>8</sup>*National Park Bavarian Forest, Freyunger Str.2, DE-94481 Grafenau, Germany*  
*[Claus.Baessler@npv-bw.bayern.de](mailto:Claus.Baessler@npv-bw.bayern.de)*

<sup>9</sup>*Botany and Plant Sciences Department, University of California, Riverside, 92521, USA*  
*[jeffrey.diez@ucr.edu](mailto:jeffrey.diez@ucr.edu)*

26 <sup>10</sup>*Centre for Macroecology, Evolution and Climate, Natural History Museum of Denmark,*  
27 *University of Copenhagen, DK-2100 Copenhagen, Denmark [jheilmann-clausen@snm.ku.dk](mailto:jheilmann-clausen@snm.ku.dk)*

28 <sup>11</sup>*Department of Geography, University of Cambridge, Downing Place, Cambridge, CB2*  
29 *3EN, UK [ulf.buentgen@geog.cam.ac.uk](mailto:ulf.buentgen@geog.cam.ac.uk)*

30 <sup>12</sup>*Swiss Federal Research Institute WSL, Zurcherstrasse 111, 8903 Birmensdorf, Switzerland*

31 <sup>13</sup>*Global Change Research Centre and Masaryk University Brno, Bělidla 986/4a, 61300*  
32 *Brno, Czech Republic*

### 33 **AUTHORSHIP**

34 EH, HK, and CA designed the study, CA and PMK collated the database and resolved  
35 taxonomy, EH and JD conducted statistical analyses. ACG and EH wrote the manuscript,  
36 with substantial contributions from all authors.

37 \*Joint first author

38 <sup>+</sup>Correspondence: E mail: [a.gange@rhul.ac.uk](mailto:a.gange@rhul.ac.uk) ORCID ID: [orcid.org/0000-0002-9918-1934](https://orcid.org/0000-0002-9918-1934)

39 Tel. +44(0)1784 443188

40 Fax +44(0)1784 414224

41

42 Running title: Fungal distribution changes

43 **Keywords** Climate change, distribution shift, ectomycorrhizal fungi, forest ecosystems,

44 saprotrophic fungi, fungal traits

45 Words in abstract: 298

**46 Abstract**

47 Despite the dramatic phenological responses of fungal fruiting to recent climate warming, it  
48 is unknown whether spatial distributions of fungi have changed and to what extent such  
49 changes are influenced by fungal traits, such as ectomycorrhizal (ECM) or saprotrophic  
50 lifestyles, spore characteristics, or fruit body size.

51 Our overall aim was to understand how climate and fungal traits determine whether and  
52 how species-specific fungal fruit body abundances have shifted across latitudes over time,  
53 using the UK national database of fruiting records. The data employed were recorded over 45  
54 years (1970 – 2014), and include 853,278 records of Agaricales, Boletales and Russulales,  
55 though we focus only on the most common species (with more than 3,000 records each). The  
56 georeferenced observations were analysed by a Bayesian inference as a Gaussian Additive  
57 Model with a specification following a joint species distribution model. We used an offset,  
58 random contributions and fixed effects to isolate different potential biases from the trait-  
59 specific interactions with latitude/climate and time. Our main aim was assessed by  
60 examination of the three-way-interaction of trait, predictor (latitude or climate) and time.

61 The results show a strong trait-specific shift in latitudinal abundance through time, as  
62 ECM species have become more abundant relative to saprotrophic species in the north. Along  
63 precipitation gradients, phenology was important, in that species with shorter fruiting seasons  
64 have declined markedly in abundance in oceanic regions, whereas species with longer  
65 seasons have become relatively more common overall. These changes in fruit body  
66 distributions are correlated with temperature and rainfall, which act directly on both  
67 saprotrophic and ECM fungi, and also indirectly on ECM fungi, through altered  
68 photosynthate allocation from their hosts. If these distributional changes reflect fungal  
69 activity, there will be important consequences for the responses of forest ecosystems to  
70 changing climate, through effects on primary production and nutrient cycling.

71 Mounting evidence shows that changes in global climate have large effects on the phenology,  
72 abundance and distribution of plant and animal species (Feehan et al. 2009). With plants,  
73 earlier leafing in spring and/or later leaf senescence in autumn prolongs the growing season  
74 (Menzel and Fabian 1999, Fitter and Fitter 2002), with subsequent effects on the productivity  
75 and functioning of ecosystems, such as forests (Richardson et al. 2010).

76 Recent studies have shown that fungi too are highly responsive to changing climates,  
77 measured by fruit body appearance (Kauserud et al. 2012, Boddy et al. 2014, Büntgen et al.  
78 2015). Shifts in the first and last dates of mushroom appearance have resulted in an extension  
79 of the autumnal fruiting season in the UK, and increased spring fruiting (Gange et al. 2007).  
80 These phenological changes reflect altered fungal activity, with consequences for forest  
81 ecosystem functioning, as fungi provide essential services such as decomposition, nutrient  
82 cycling and the formation of ectomycorrhizal (ECM) fungal mutualisms (Primicia et al.  
83 2016).

84 Another consequence of a warming climate is a change in the spatial distribution of  
85 organisms, along altitudinal (Wilson et al. 2005) or latitudinal gradients (Hickling et al. 2006,  
86 Chen et al. 2011). However, fungi are conspicuously absent from such analyses, with just two  
87 notable exceptions. Yan et al. (2017), using species distribution modelling, predict that the  
88 distribution range in Tibet of the economically valuable Chinese caterpillar fungus  
89 (*Ophiocordyceps sinensis*) will decrease with climate warming. Meanwhile, using a global  
90 dataset of crop pest and pathogen records, Bebbler et al. (2013) documented significant  
91 poleward shifts for many disease-causing fungi since 1960. Intriguingly, the northward shift  
92 by pathogens began in the late 1970s, mirroring increasing temperatures and the expansion of  
93 the overall UK fungal fruiting season (Gange et al. 2007). Given that we now know how  
94 fungal phenology responds to climate warming (Boddy et al. 2014), it is timely to assess if  
95 changes in the distribution of saprotrophic and ectomycorrhizal fungi have also occurred. To

96 predict community responses to climate change, we need a better understanding of how  
97 species' abundances change (Johnson et al. 2013), and studying fungal distributions is critical  
98 for understanding how these organisms influence ecosystem responses to climate change  
99 (Mohan et al. 2014).

100 Ectomycorrhizal and saprotrophic fungi co-occur in woodlands, but differ in their  
101 nutritional mode and other life history traits (Bässler et al. 2015). Changes in spatial  
102 distributions of ECM fungi could be constrained, if there is a level of specificity between  
103 fungus and host and/or if the distribution of the host is limiting (Vellinga et al. 2009).  
104 Saprotrophs may also be constrained by host distributions (Heilmann-Clausen et al. 2016).  
105 Meanwhile, there is evidence that some ECM species can associate with novel hosts,  
106 facilitating range expansion and invasion into new habitats (Wolfe and Pringle 2012). Range  
107 expansions may lead on to fungal species becoming invasive (Kausserud et al. 2007, Gladieux  
108 et al. 2015). Furthermore, interactions between saprotrophic and ECM fungi can contribute to  
109 the structuring of fungal communities (Leake et al. 2002), with important ecosystem-level  
110 consequences (Fernandez and Kennedy 2016). Thus, understanding if changes in fungal  
111 phenology lead to changes in abundance at range edges, and ultimately shifts in distributions,  
112 is an essential, but unresolved, part of determining the fungal role in climate effects at the  
113 ecosystem level.

114 A fundamental goal of community ecology is to understand the distribution and  
115 abundance of organisms in time and space. Against a backdrop of climate change, the amount  
116 of information required for such analyses at the community level can be colossal, given that  
117 species show individualistic responses to climate in ecological and evolutionary time  
118 (Stewart 2009, Buckley and Kingsolver 2012). There is evidence that a trait-based approach  
119 can be of use in understanding both distribution and range shifts (Angert et al. 2011), though  
120 this has yet to be applied to fungi. Such an approach is timely, given recent syntheses of trait-

121 based approaches in mycology (Crowther et al. 2014, Aguilar-Trigueros et al. 2015) and  
122 evidence of climate-driven reproductive trait selection in fungal communities (Andrew et al.  
123 2016). Ultimately, a trait-based approach should enable a better understanding of processes in  
124 fungal biogeography (Martiny et al. 2006, Crowther et al. 2014). Thus, a trait-based approach  
125 provides a realistic way of testing if and how climate affects fungal abundance at the edges of  
126 ranges. Several reproductive traits related to fruit body and spore characteristics are thought  
127 to be influenced by climate variability, and may ultimately affect distributions (Kausrud et  
128 al. 2010, Andrew et al. 2016). More water is required to produce larger fruit bodies and  
129 spores, but larger spores could also be required in drier environments for germination. Dark  
130 melanised spores have better protection against UV and may, together with thick-walled  
131 spores, survive and spread further than light spores. Several other traits affect dispersal,  
132 which again can be relevant for how quickly fungi respond to climate with shifts in  
133 distributions. Larger fruit bodies produce more spores and fruit bodies with longer stipes  
134 could spread spores more distantly. In theory, smaller spores spread farther than larger ones  
135 (Norros et al. 2014) and the exterior ornamentation may also influence the aerodynamics of  
136 spores and their dispersal ability (Halbwachs and Bässler 2015).

137 The scarcity of studies in fungal biogeography is due in part to the fungi being invisible  
138 within substrata for long periods of time and the difficulty in characterising the huge diversity  
139 of fungi within ecosystems. While such problems become tractable using molecular methods  
140 (Tedersoo et al. 2014), these techniques cannot readily document any historical changes in  
141 fungal distributions. However, as with plant pathogens, databases of fungal occurrence can  
142 provide excellent records of presence and can be used to document changes in time and space  
143 (Bebber et al. 2013, Schenk-Jäger et al. 2016). In this study, we used a unique database of  
144 fruit body records from the UK, termed the Fungal Records Database of the British Isles  
145 (FRDBI) (<http://www.fieldmycology.net/FRDBI/FRDBI.asp>). The snapshot of the database

146 was taken on 16 December 2015 and it then included 2,083,352 records of the fruiting of  
147 14,146 species from 1669 to the present day, collected by amateur naturalists (citizen  
148 scientists), professional mycologists and scientific organisations.

149 Here, we use this database to examine whether changes in the latitudinal abundance of  
150 fruit bodies of ECM and saprotrophic fungi have occurred over the last 45 years in the UK.  
151 We address two specific questions: (1) has the UK latitudinal gradient in fungal abundance  
152 changed over time in a trait-specific way? and (2) are temporal shifts in fungal abundance  
153 associated with climate change? Our overall hypothesis was that changes depend on fungal  
154 traits and differ between ECM and saprotrophic species (Halbwachs et al. 2015), given that  
155 characteristics such as nutritional mode and spore size are important in determining fungal  
156 responses to climate (Damialis et al. 2015, Andrew et al. 2016). Furthermore, we  
157 hypothesized that ECM species would show fewer changes in fruiting distributions compared  
158 to saprotrophic species, because any changes in ECM fruiting will be largely dependent on  
159 changes in their host trees (Primicia et al. 2016).

## 160 **Methods**

### 161 **Data characteristics**

162 The data set comprised a compilation of fungal fruit body occurrence recorded throughout  
163 mainland Britain. Most records provide a collecting date and location (latitude and  
164 longitude). Many records before 1970 are deficient in some aspect (missing date or location)  
165 and we therefore used data from 1970 to 2014, which make up 84% of the full data set. From  
166 this reduced set, we extracted fruiting records of the agaricoid and boletoid members of the  
167 Agaricales, Boletales and Russulales, comprising in total 853,278 records of 2,844 species.  
168 Using this information, we obtained species' prevalence and recording intensities within each  
169 of the 112 Watsonian vice-counties (VC) that map the UK, for every year (Fig. S1). We



170 chose to use VC instead of gridded representation as much of the older data are at this level  
171 and this enabled us to obtain estimates of recording intensities over time. This also guided our  
172 choice of using a first order conditional autoregressive procedure rather than trying a point  
173 pattern approach with spatial Gaussian fields defined (Blangiardo & Cameletti 2015). For  
174 analytical purposes and to reduce recording bias to a minimum, we selected common (with  
175 more than 3,000 records each) and widely distributed ECM and saprotrophic species that are  
176 easy to distinguish in the field (avoiding potential misidentification), with an ephemeral  
177 fleshy fruit body. Further, we eliminated species with long-lived fruit bodies or which are  
178 parasitic. The resulting data comprised 304,121 records of 61 (21 ECM, 40 saprotrophic)  
179 species.

180

### 181 **Fungal traits**

182 Information on seven traits was taken from Knudsen and Vesterholt (2012): functional group  
183 (ECM versus saprotrophic), cap size, stipe height, spore volume, spore colour, spore wall  
184 thickness, and spore wall ornamentation. In addition, average fruiting day and standard  
185 deviation of fruiting day (a measure of season length) of each species were calculated from  
186 the data. The traits and correlations between them are explained and listed by species in Table  
187 S1 and Figures S1.1-S1.5.

### 188 **Latitude and climate**

189 The individual statistical unit in our analyses is the abundance of a species in a VC each year.  
190 For each VC and year, we calculated each species' average geographical position, measured  
191 by latitude and longitude. Annual mean temperature and annual total precipitation data for  
192 each record were obtained from the UK Meteorological Office,

193 (<http://www.metoffice.gov.uk/climate>). These data were taken from the nine climate regions  
194 of the UK, as defined by the Meteorological Office. While we appreciate that higher  
195 resolution data may have provided more accurate representations of climate, such data were  
196 not available for the time period covered by this study. Combining the annual temperature  
197 and precipitation with the temperature difference between coldest and warmest month, we  
198 calculated a hygrothermic index (HT) reflecting the transition from continental (low values)  
199 to oceanic climate conditions (Lisewski and Ellis 2010):

$$200 \quad HT = \frac{P * T}{10 * (T_H - T_C)}$$

201 where P is annual precipitation (mm), T is annual mean temperature, and  $T_H$  and  $T_C$  are  
202 monthly mean temperature in the hottest and coldest months, respectively.

203

## 204 **Statistical analyses**

205 The overall goal of the statistical modelling was to quantify how species-specific abundances  
206 have changed over time across the latitudinal gradient, and to evaluate how species' traits and  
207 climate have influenced these changes. Our approach is an extension of the Community  
208 Assembly via Trait Selection (CATS) (Warton et al. 2015) following a multivariate  
209 regression specification (Jamil et al. 2013, ter Braak et al. 2017) and a joint species  
210 distribution model specification (Pollock et al. 2014, Ovaskainen et al. 2016). The key  
211 objectives were to obtain parametric estimates of how traits affected the latitudinal and  
212 climatic gradient in abundances over time, while also accounting for potential biases  
213 associated with multivariate presence-only data and uneven spatial and temporal sampling  
214 intensity.

215 To assess how abundance changes with time and latitude or climate, and whether changes  
 216 are associated with specific traits, we compiled the number of fruit body records ( $y_{ijk}$ ) for  
 217 each species  $i$ , in VC  $j$  (112 VCs), and year  $k$  (1970 to 2014). Because of the complex  
 218 structure of the data, we used hierarchical Bayesian models (Gelman et al. 2004), fitted using  
 219 the Integrated Nested Laplace Approximation, INLA (Table S3) (Rue et al. 2009). Because  
 220 the response data ( $y_{ijk}$ ) are discrete counts and over-dispersed relative to a Poisson  
 221 distribution, we assumed a negative binomial likelihood with a logarithmic link to a linear  
 222 predictor:

$$223 \quad y_{ijk} | \theta_{ijk}, \varphi_{ijk} \sim NB(\mu_{ijk}, n)$$

$$224 \quad \log(\mu_{ijk}) = \eta_{ijk}$$

225 Here  $\theta$  denotes all parameters describing the mean,  $\mu$ , and  $\varphi$  denotes the hyper-parameters  
 226 associated with parameter distributions. The parameter  $n$  denotes the negative binomial size,  
 227 which quantifies the degree of overdispersion.

228 Within the linear predictor ( $\eta_{ijk}$ ), we specify parametric relationships with predictors  
 229 (time, latitude, climate and traits) and several potential sources of bias common to datasets  
 230 such as this, including: (i) different likelihoods of species being collected because of recorder  
 231 bias; (ii) yearly differences in sampling intensities; (iii) spatial biases due to where observers  
 232 tend to search and (iv) the different sizes of VCs. These potential biases were incorporated  
 233 using an offset and by a number of random effects (described in detail below) as follows,  
 234 where  $i$  = species,  $j$  = VC, and  $k$  = year:

$$235 \quad \eta_{ijk} = \log(q_i E_{jk}) + t_k + v_j + u_j +$$

$$236 \quad \beta_0 + b_{0i} + (\beta_1 + b_{1i}) \cdot x_j + (\beta_2 + b_{2i}) \cdot time_k + (\beta_3 + b_{3i}) \cdot x_j \cdot time_k +$$

$$237 \quad \beta_4 trait_i + \beta_5 x_j \cdot trait_i + \beta_6 time_k \cdot trait_i + \beta_7 x_j \cdot time_k \cdot trait_i$$

238

239 We defined species' prevalence ( $q_i$ ) as the probability that a record selected at random  
240 from the full species pool belongs to species  $i$ . To account for variable sampling intensities  
241 both among years and between VCs, we included the sampling volume, defined as the  
242 number of records of all species for every year in each VC,  $E_{jk}$ , which is referred to as  
243 recording intensity per VC per year. This was combined with the species-specific prevalence  
244 in calculating the expected number of records per species per VC per year ( $q_i E_{jk}$ ). Using  
245  $\log(q_i E_{jk})$  as an offset brings the analysis into the realm of density, i.e., abundance relative to  
246 the expected number of records per species per VC per year. The logarithm was applied due  
247 to the log-link function between the linear predictor and the mean ( $\mu_{ijk}$ ).

248 Subsequently, because the records were structured by year, and needed to be grouped  
249 across a VC, we included an exchangeable random contribution for the year ( $t_k$ ). Note that  
250 year as a linear term was used as part of the fixed effect in this study. Furthermore, the VCs  
251 are spatially positioned discrete units, so we included an exchangeable random contribution  
252 of the VCs ( $v_j$ ) and neighbouring VCs ( $u_j$ ). This neighbourhood structure was modelled as a  
253 Conditional Autoregressive Process (CAR) using a first-order neighbouring graph (Besag  
254 1974), following the Besag-York-Mollie (BYM) model of spatial contribution (Blangiardo  
255 and Cameletti 2015).

256 To accommodate species-specific responses to the predictor variables ( $x_j$ ), we included  
257 species-specific random effects of intercept ( $b_{0i}$ ), the predictor variable ( $b_{1i}$ ), the time variable  
258 ( $b_{2i}$ ) and the interaction between the predictor variable and the time ( $b_{3i}$ ).

259 Finally, the  $\beta$ 's were the fixed effects answering the main aims of the study, including  
260 how abundances are related to the effects ( $\beta_1$  to  $\beta_3$ ) of time and predictors ( $x_j$  = latitude or  
261 climate) as well as their interactions, while  $\beta_4$  to  $\beta_7$  represent effects associated specifically

262 with the investigated traits. Herein,  $\beta_7$  is the trait-specific effect on how the gradient along the  
263 predictor changes with time, i.e., our main focus. In the study, each trait was analysed  
264 separately, and each of the predictor variables, i.e. latitude, temperature, precipitation and  
265 HT, was included separately, whereas time was always included. This produced 36 separate  
266 models, exploring all combinations of the four predictor variables with each of the nine trait  
267 variables.

268 In summary, the structure of the data necessitated a complex model specification with  
269 terms associated with biases and nuisance information ( $\log(qE)$ ,  $\beta_0$ ,  $\beta_1$ ,  $\beta_2$  and  $\beta_3$ ), with  
270 dependencies of the observations ( $t_k$ ,  $v_j$  and  $u_j$ ), with species-specific random contribution of  
271 terms ( $b_{0i}$ ,  $b_{1i}$ ,  $b_{2i}$  and  $b_{3i}$ ), and finally the fixed effects of traits ( $\beta_4$ ,  $\beta_5$ ,  $\beta_6$  and  $\beta_7$ ).

272 We used Gaussian weak priors for all fixed effects ( $\beta$ 's), and log-gamma priors for the  
273 hyper-parameters of negative binomial size ( $n$ ), the exchangeable VC contribution ( $v_j$ ), the  
274 spatial VC contribution ( $u_j$ ) and the temporal exchangeable contribution ( $t_k$ ). For the species-  
275 specific random contribution we were able to reduce a multivariate Wishart distribution prior  
276 to a set of univariate random contributions with individual priors of a log-gamma distribution.  
277 This reduction was possible when we used one predictor at a time and rescaled the predictor  
278 variables and the time vector to zero mean and unit variance prior to analysis. Factorial traits  
279 were analysed as a treatment contrast. All analyses were performed with the INLA package  
280 (Rue et al. 2009) in R v. 3.3.1 (R Core Team 2016).

281

## 282 **Results**

### 283 **Distribution of records within the dataset**

284 The number of records per VC of the 61 focal species showed a spatial differentiation but  
285 lacked an obvious latitudinal pattern (Fig. S1a). There was also a relatively even coverage in  
286 species richness per VC for these 61 species (Fig. S1b) and almost all species were present in  
287 every VC. Meanwhile, the average abundance per species per VC over time did not show an  
288 even pattern (Fig. S1c), with ‘hotspots’ of collection in some areas.

### 289 **Latitudinal changes in abundance**

290 To set the scene for assessing the trait-specific effects we illustrate the relative trend of the  
291 focal species as a group relative to the less frequent species, i.e. those included in the full  
292 species pool. This information may be interpreted as bias and therefore we needed to isolate it  
293 from the information carried by the interactions involving the traits. In this we found a clear  
294 negative main effect of time ( $p < 0.001$ ), showing that recordings of the most common  
295 species have declined in average abundance over time (Fig. 1, Table S2), and this decline was  
296 consistent across all trait groups (Table S2). However, there was also a significant positive  
297 latitude:time interaction term (probability of being positive = 0.953), indicating that the  
298 decline in abundance of common species was less at higher latitudes (Fig. 1, Table S2).

299 The three-way interaction term between latitude, time, and nutritional mode was highly  
300 significant (probability of coefficient being positive  $< 0.001$ , Fig. 1, Table S2, S3), indicating  
301 that changes in abundance over time differ between ECM and saprotrophic species. As a  
302 result of this significant interaction, the modelled abundances over time and across latitudes  
303 were remarkably different for ECM (Fig. 2a) and saprotrophic species (Fig. 2b). Abundance  
304 of ECM species was relatively low in the north, but the trend has been toward increasing  
305 abundances in this area. However, in the southern region there was a marked decline in  
306 average abundance relative to the saprotrophic species over time (Fig. 2a). Meanwhile, the  
307 saprotrophic species had a more even latitudinal abundance in the early period of records than

308 ECM species, but have declined in abundance in both the north and south, with the decline in  
309 the north more pronounced (Fig. 2b). This pattern indicates that today it is more common to  
310 record ECM species in northern parts of the UK, whereas in the south the higher average  
311 abundance of ECM records seen in the past has declined to a level similar to or lower than  
312 that of the saprotrophic species.

313 The probabilities associated with coefficients being positive are depicted in Fig. 3 and  
314 95% credibility intervals are presented in Table S2. Three of the three-way interaction terms  
315 (Latitude:Time:Trait) are noteworthy here. Firstly, cap area showed a significant positive  
316 coefficient (Fig. 4a). The abundance of species with small caps was relatively evenly  
317 distributed from south to north at the start of the study period. The lack of a latitudinal trend  
318 persisted through time, but the abundance of small-capped fungi decreased over time. Species  
319 with larger caps, on the other hand, were previously more common in the south of the country  
320 than in the north. During the study period, this latitudinal abundance gradient shifted  
321 direction due to a strong decline in the south and a weak increase in the north (Fig. 4b).

322 Both spore-wall smoothness and length of the fruiting season (the standard deviation of  
323 fruiting day) have shown significant and similar latitudinal trends over time to that of  
324 functional group (Fig. 3). Fungal species with smooth spores are on average more frequently  
325 recorded today than previously, relative to species with ornamented spores (Table S2, Fig.  
326 4c,d). There has been a strong change among the species with ornamented spores in the  
327 south, where they have shown a considerable drop in average abundance (Fig. 4c), compared  
328 with a weak increase in the north. Species with smooth spores have declined in relative  
329 abundance in both south and north, but the decline was more pronounced in the north (Fig  
330 4d). Fruiting season width is another important parameter, and species with short seasons,  
331 (standard deviation of fruiting about 1 month), have become less abundant in the south, while  
332 maintaining their abundance in the north (Fig. 4e). However, species with long fruiting

333 seasons, (standard deviation of about 2 months), have tended to become less abundant  
334 regardless of latitude, but with stronger declines in the north than in the south (Fig. 4f).

335 Finally, there was a weak tendency for species with thick-walled spores to be more  
336 abundant in the northern regions ('Env:trait' for 'spore wall' in Fig 3). However, this pattern  
337 did not change with time, as the three-way interaction (Latitude:Time:Trait) was not  
338 significant (Fig 3, Table S2).

### 339 **Climatic gradients**

340 Across the UK, temperatures decrease towards the north (Fig. S2a), and precipitation  
341 increases toward the west (Fig. S2b), while the hygrothermic index shows a southeast –  
342 northwest gradient (Fig. S2c). These three climate variables each showed different, complex  
343 relationships with fungal fruiting via both direct effects and through interactions with traits  
344 and time (Fig. 3).

345 We found a high probability ( $p = 0.982$ ) that the three-way interaction of  
346 temperature:time:nutritional mode was positive, indicating that the influence of temperature  
347 over time differs between ECM and saprotrophs (Fig.3,Table S2). However, neither rainfall  
348 nor the hygrothermic index showed a change across latitudes over time. None of the three-  
349 way interactions involving rainfall were significant, suggesting that changes in abundance  
350 across latitude over time are not related to average annual precipitation alone.

351 Cap area, fruiting time and length of fruiting season all showed significant three-way  
352 interactions with the hygrothermic index (Fig 3, Table S2), with negative coefficients for cap  
353 area and average fruiting time and a positive coefficient for fruiting season. Overall, we  
354 found a high probability that later fruiting species occurred more frequently in more oceanic  
355 areas (probability of coefficient being positive = 0.989, Table S2). The trend for species with



356 larger caps was similar, but weaker (probability of being positive = 0.786). However, over  
357 time, there has been a relative increase in abundance of later fruiterers in more continental  
358 areas, relative to oceanic areas. This trend was less pronounced in the earlier fruiting species.  
359 Thus, over time, the relative difference between early and late fruiting species has reduced,  
360 leading to a high probability ( $p = 0.998$ ) that the coefficient of the three way interaction was  
361 negative (Fig. 3, Table S2). For fruiting season length, we found a high certainty ( $p = 1.000$ )  
362 that the coefficient for the time:fruiting width was positive, i.e. that the temporal change in  
363 relative abundance depends on fruiting-season length. The species with broader fruiting  
364 seasons have become relatively more common compared with those of shorter fruiting-season  
365 length. The significant three-way interaction ( $p = 0.996$ , Table S2) suggests that this  
366 favouring of species with broader seasons has been particularly strong in regions with a high  
367 hygrothermic index (oceanic areas). However, there has been a dramatic decline in the  
368 relative abundance of the short seasoned species in the oceanic parts of UK.

369

## 370 **Discussion**

371 Over the last 45 y, there has been a significant change in the distribution of fungal fruiting in  
372 the UK and this change is clearly trait-specific, upholding our original hypothesis. Among the  
373 most frequently recorded fungal species, ECM fungi now fruit more prolifically in the north  
374 of the country than in the past, but less so in the south, while saprotrophic fungi fruit less  
375 commonly now in both areas. Changes in fungal fruiting over time are strongly related to  
376 climate (seen in the hygrothermic index), suggesting that both temperature and rainfall are  
377 responsible for these distributional changes in fungal fruiting, but in association with  
378 different sets of traits.

379 Our most important finding is that the abundance of ECM fungal fruiting has increased in  
380 more northerly latitudes and declined markedly in the south. This finding contradicts our  
381 hypothesis that ECM fungi might show few changes over time. Autumnal mean daily  
382 temperature and rainfall in the UK have increased over our study period, but more so in the  
383 north (Anonymous 2009). Such climatic changes may result in direct effects on the ECM  
384 fungi and also in indirect effects through enhanced growth and later leaf fall of their tree  
385 hosts (Gill et al. 2015). Delayed leaf senescence in autumn has been reported across Europe  
386 (Kolarova et al. 2014), and it is perhaps no coincidence that the most prevalent host for ECM  
387 fungi in the UK, *Quercus robur*, has shown the greatest growing-season elongation (of 18  
388 common tree species) of 31 days, between 1976-2010 (Kolarova et al. 2014). As the carbon  
389 supply from the host may have a strong influence on ECM fungal fruiting (Egli et al. 2010,  
390 Buntgen et al. 2012b), we conclude that temperature-driven increases in resource allocation  
391 from host trees to ECM associates, coupled with enhanced autumnal soil moisture  
392 availability, are the most likely causes of increased fruiting of ECM fungi towards the north,  
393 corroborating results from Primicia et al (2016). The decline in ECM fungal fruiting in the  
394 south may be due more to rainfall than temperature. In the UK, over the time period covered  
395 by our study, rainfall in southern England in summer has decreased by 13%, while in the  
396 north of the UK, the decrease is only 2% (Anon. 2009). It is known that both ECM and  
397 saprotrophic fungal fruiting are related to prevailing weather conditions between April and  
398 August (Buntgen et al. 2013). Thus, ECM fungal fruiting may have decreased in the south  
399 because of insufficient rainfall prior to fruiting. This ecological response may be comparable  
400 to the drought-induced declines of edible mycorrhizal fungal harvests in the Mediterranean  
401 area (Buntgen et al. 2012a, 2015).

402 Meanwhile, saprotrophic species have shown a decline in fruiting in both the north and  
403 south, with the trend being strongest in the north. Like ECM, saprotrophic fungal fruiting is

404 also thought to be influenced by temperature and moisture effects on the process of  
405 decomposition (Rousk and Bååth 2011, Buntgen et al. 2013). Moore et al. (2008) suggest that  
406 appearance of saprotrophic fruit bodies in autumn is related to rainfall in summer. Over the  
407 study period, there has been a weak trend for fewer days of rain during the summer, a trend  
408 which is stronger in the north of the country. However, in our study the precipitation is not  
409 strongly associated with nutritional mode, i.e. the response seen among saprotrophic species  
410 is mirrored by ECM species. Thus, the latitudinal trends in changes of abundance are likely to  
411 be more driven by temperature.

412 Resource availability, temperature and rainfall are just three of the factors that influence  
413 the start and end of a fungal fruiting season and it is certain that these factors are inter-  
414 dependent. The Hygrothermic Index (combining temperature and rainfall) was a major factor  
415 related to the fruiting time and width of the fruiting season. We found that species with  
416 broader seasons have become more frequently recorded, and that this effect was stronger in  
417 more oceanic parts of the country. Meanwhile a strong decline in short-season species has  
418 occurred in the more oceanic areas. Although the fruiting season of saprotrophs in the UK is  
419 generally longer than that of ECM fungi (Kausrud et al. 2012), the patterns seen with  
420 fruiting season length did not correspond with those seen in the nutritional modes. This  
421 suggests that there is an additional climatic force acting on the fruiting season length, in  
422 saprotrophic and ECM species alike. It is likely that resource availability and a sudden drop  
423 in temperature (e.g. frost) are likely to play significant roles in determining the end of a  
424 fruiting season (Gange et al. 2013). Autumnal frost frequency has declined over the study  
425 period, but whether the timing of frosts in different parts of the country has changed is less  
426 clear (Anonymous 2009). Whether short- and broad-season species are differentially  
427 susceptible to frost is also unknown, but possible (Ohenoja 1989).

428 In addition to nutritional mode, other traits were important for predicting changes in  
429 latitudinal abundance. Cap area was a particularly important trait, as species with larger caps  
430 have become more common in the north, while those with smaller caps have declined in  
431 abundance generally. ECM fungi produce larger caps than saprotrophic fungi (Bässler et al.  
432 2015), a phenomenon thought to be driven by the receipt of carbon from the host. The change  
433 in ECM fungal fruiting in northern areas mirrors the changes in cap area and is further  
434 evidence for enhanced resource allocation from hosts leading to increased fruit body  
435 production. However, there is also an oceanic element, not correlated with nutritional mode,  
436 as smaller cap sizes seem to be positively influenced by oceanic climate relative to species  
437 with larger cap sizes. Although, large fruit bodies need large amounts of water to expand, so  
438 also do many small fruit bodies, and the greater reduction in rainfall seen in the south may be  
439 part of the explanation of why we observed a combination of a clear nutritional mode/cap-  
440 size differentiation northwards, but also a simultaneous association with a continental  
441 gradient and cap-sizes.

442 A similar trend was seen with spore surface traits. Species with ornamented spores have  
443 become more abundant in the north, while smooth-walled species have become less abundant  
444 overall. ECM species often have more ornamented spore walls than saprotrophic species  
445 (Halbwachs et al. 2015) and so these changes correlate with those for nutritional mode.  
446 However, spore colour and wall thickness traits showed little change over time.

447 It is not just temperature and rainfall that have changed over our study period. Important  
448 changes in atmospheric CO<sub>2</sub> levels and nitrogen deposition have occurred simultaneously and  
449 may all affect fruit body production of forest fungal species. Elevated CO<sub>2</sub> can lead to  
450 increased fruit body production of ECM species, through enhanced carbon supply via their  
451 hosts (Andrew and Lilleskov 2009, Godbold et al. 2015). Elevated CO<sub>2</sub> also results in altered  
452 leaf litter quality that slows decomposition (Cotrufo et al. 1994), though whether this results

453 in reduced fruit body production of saprotrophic species is far less clear (Büntgen et al.  
454 2013). High rates of N deposition reduce ECM fruit body production (Peter et al. 2001), and  
455 deposition rates have been higher in the south of the country over the study period (Fowler et  
456 al. 2004). Neither CO<sub>2</sub> nor N can fully explain the increase in ECM fruiting, but both may  
457 play a role in a complex array of atmospheric factors, all of which interact (Büntgen et al.  
458 2013).

459 In any analysis of this type, the biases within such datasets must be considered. Large  
460 datasets assembled by a mixture of citizen scientists and professionals can be influenced  
461 heavily by the distribution and knowledge of recorders, the geographical structure of the  
462 landscape and spatial patterns of land use (Ward 2014, Mair and Ruete 2016). However,  
463 appropriate data management and statistical methods can still yield robust analyses of  
464 changes in fungal phenology and distributions (Boddy et al. 2014, Davis et al. 2015, Taheri et  
465 al. 2016). There are several arguments for our claim that the trends found here are not caused  
466 by inherent biases in the data. Firstly, we restricted our analysis to the last 45 years, when  
467 recording has been much more organised and coordinated, resulting in a relatively even  
468 distribution of records (see Supporting Information). Secondly, because rare species can be  
469 over-represented due to collector bias (Halme et al. 2012), we analysed only a subset of  
470 common species, each with a large number of records evenly distributed across the country.  
471 Thirdly, our models explicitly account for and identify the influences of species' prevalence,  
472 sampling effort, data structure and temporal changes in recording. The latter includes changes  
473 in human population sizes, number of recorders and differences in recording intensity and  
474 recorder specialisation. Moreover, if there was recorder bias, then ECM and saprotrophic  
475 species would show similar trends, as they fruit in the same locations, but they do not.  
476 Furthermore, we identified two broad-scale distinct biological phenomena: temperature-  
477 related changes in distributions of nutritional modes and precipitation-related changes in

478 fruiting period, which in combination make changes in recorder specialisation unlikely. As  
479 these are trait-related, it also makes bias from climatic structure unlikely (Chapman 2010).  
480 Finally, changes in forestry practices over the last 45 years could introduce further biases.  
481 However, in this study very few fungal species are associated with actively managed  
482 coniferous plantations, with most records from less managed pine forests, and there has been  
483 relatively little change in the latitudinal distribution of broad-leaved woodlands across the  
484 UK over our study period (Quine et al. 2011).

485 In summary, it is clear that distributions of fungal fruiting have changed across the UK  
486 over the last 45 years, driven by two distinct trait specific processes acting on different  
487 climatic gradients. These changes may reflect altered resource acquisition patterns of both  
488 ECM and saprotrophic species (Bässler et al. 2016). Changes in fruiting presumably reflect  
489 changes in fungal activity, and such changes may affect ecosystem processes such as  
490 decomposition and nutrient cycling, which will have implications for the functioning and  
491 productivity of both broad-leaved forests and managed coniferous plantations (Fernandez and  
492 Kennedy 2016). Our study specifically focused on the most common species in the UK which  
493 show a decline in recording intensity relative to the less frequent species, but we do not  
494 believe that this will affect the generality of our results in the wider British mycobiota. This is  
495 because the species-specific traits show a stronger pattern than the identity of the species. For  
496 example, if a rare species has the same trait as one of the investigated common species, we  
497 can anticipate that its response will be similar to that common species, but different to an  
498 equally common one, with a different trait. Furthermore, we isolate/identify this type of bias  
499 by the main-effect of time in our models. Thus we suggest that the temperature and  
500 precipitation influences on fruiting processes are similar for the less frequent species, but this  
501 must be shown by future rigorous analyses. In addition, our results show that the exploration  
502 of historical databases to document changes in fungal fruiting abundance is a valuable

503 approach for indicating how fungal communities may change in ecosystems such as forests,  
504 particularly in response to environmental change.

505

506 *Acknowledgements* — We acknowledge the Research Council of Norway for financial  
507 support to the ClimFun project (grant 225043) and all persons responsible for data collection  
508 and management.

509

## 510 **References**

- 511 Aguilar-Trigueros, C. A. et al. 2015. Branching out: Towards a trait-based understanding of  
512 fungal ecology. — *Fungal Biol. Rev.* 29: 34-41.
- 513 Andrew, C. et al. 2016. Climate impacts on fungal community and trait dynamics. — *Fungal*  
514 *Ecol.* 22: 17-25.
- 515 Andrew, C. and Lilleskov, E. A. 2009. Productivity and community structure of  
516 ectomycorrhizal fungal sporocarps under increased atmospheric CO<sub>2</sub> and O<sub>3</sub>. — *Ecol.*  
517 *Lett.* 12: 813-822.
- 518 Angert, A. L. et al. 2011. Do species' traits predict recent shifts at expanding range edges? —  
519 *Ecol. Lett.* 14: 677-689.
- 520 Anonymous. 2009. The climate of the United Kingdom and recent trends. — DEFRA, UK.
- 521 Bäessler, C. et al. 2016. Mean reproductive traits of fungal assemblages are correlated with  
522 resource availability. — *Ecol. Evol.* 6: 582-592.
- 523 Bäessler, C. et al. 2015. Ectomycorrhizal fungi have larger fruit bodies than saprotrophic  
524 fungi. — *Fungal Ecol.* 17: 205-212.

- 525 Bebber, D. P. et al. 2013. Crop pests and pathogens move polewards in a warming world. —  
526 Nat. Clim. Change 3: 985-988.
- 527 Besag, J. 1974. Spatial interaction and statistical analysis of lattice systems. — J. Roy. Stat.  
528 Soc B - Method. 36: 192-236.
- 529 Blangiardo, M. and Cameletti, M. (eds) 2015. Spatial and spatio-temporal Bayesian models  
530 with R - INLA. — John Wiley & Sons.
- 531 Boddy, L. et al. 2014. Climate variation effects on fungal fruiting. — Fungal Ecol. 10: 20-33.
- 532 Buckley, L. B. and Kingsolver, J. G. 2012. Functional and phylogenetic approaches to  
533 forecasting species' responses to climate change. — Ann. Rev. Ecol. Evol. Syst. 43: 205-  
534 226.
- 535 Büntgen, U. et al. 2012. Drought-induced decline in Mediterranean truffle harvest. — Nat.  
536 Clim. Change 2: 827-829.
- 537 Büntgen, U. et al. 2015. Drought-induced changes in the phenology, productivity and  
538 diversity of Spanish fungi. — Fungal Ecol. 16: 6-18.
- 539 Büntgen, U. et al. 2012. Linking climate variability to mushroom productivity and  
540 phenology. — Front. Ecol. Env. 10: 14-19.
- 541 Büntgen, U. et al. 2013. Unraveling environmental drivers of a recent increase in Swiss fungi  
542 fruiting. — Glob. Change Biol. 19: 2785-2794.
- 543 Chapman, D. S. 2010. Weak climatic associations among British plant distributions. — Glob.  
544 Ecol. Biogeog. 19: 831-841.
- 545 Chen, I. C. et al. 2011. Rapid range shifts of species associated with high levels of climate  
546 warming. — Science 333: 1024-1026.
- 547 Cotrufo, M. F. et al. 1994. Decomposition of tree leaf litters grown under elevated CO<sub>2</sub> -  
548 effect of litter quality. — Plant Soil 163: 121-130.



- 549 Crowther, T. W. et al. 2014. Untangling the fungal niche: the trait-based approach. — *Front.*  
550 *Microbiol.* 5: 579, DOI: 510.3389/fmicb.2014.00579.
- 551 Damialis, A. et al. 2015. Fungi in a changing world: growth rates will be elevated, but spore  
552 production may decrease in future climates. — *Int. J. Biometeorol.* 59: 1157-1167.
- 553 Davis, C. C. et al. 2015. Herbarium records are reliable sources of phenological change  
554 driven by climate and provide novel insights into species' phenological cueing  
555 mechanisms. — *Am. J. Bot.* 102: 1599-1609.
- 556 Egli, S. et al. 2010. Is forest mushroom productivity driven by tree growth? Results from a  
557 thinning experiment. — *Ann For. Sci.* 67: 509, DOI: 510.1051/forest/2010011
- 558 Feehan, J. et al. 2009. Climate change in Europe. 1. Impact on terrestrial ecosystems and  
559 biodiversity. A review. — *Agron. Sustain. Dev.* 29: 409-421.
- 560 Fernandez, C. W. and Kennedy, P. G. 2016. Revisiting the 'Gadgil effect': do interguild  
561 fungal interactions control carbon cycling in forest soils? — *New Phytol.* 209: 1382-1394.
- 562 Fitter, A. H. and Fitter, R. S. R. 2002. Rapid changes in flowering time in British plants. —  
563 *Science* 296: 1689-1691.
- 564 Fowler, D. et al. 2004. A chronology of nitrogen deposition in the UK between 1900 and  
565 2000. — *Water Air Soil Pollut: Focus* 4: DOI: 10.1007/s11267-11004-13009-11261.
- 566 Gange, A. C. et al. 2007. Rapid and recent changes in fungal fruiting patterns. — *Science*  
567 316: 71-71.
- 568 Gange, A. C. et al. 2013. Mushroom phenological changes: a role for resource availability?  
569 — *Proc. Nat. Acad. Sci. USA.* 110: E333-E334.
- 570 Gelman, A. et al. (eds) 2004. Bayesian data analysis. — Chapman & Hall.
- 571 Gill, A. L. et al. 2015. Changes in autumn senescence in northern hemisphere deciduous  
572 trees: a meta-analysis of autumn phenology studies. — *Ann. Bot.* 116: 875-888.

- 573 Gladieux, P. et al. 2015. The population biology of fungal invasions. — *Mol. Ecol.* 24: 1969-  
574 1986.
- 575 Godbold, D. L. et al. 2015. Elevated atmospheric CO<sub>2</sub> affects ectomycorrhizal species  
576 abundance and increases sporocarp production under field conditions. — *Forests* 6: 1256-  
577 1273.
- 578 Halbwegs, H. and Bässler, C. 2015. Gone with the wind - a review on basidiospores of  
579 lamellate agarics. — *Mycosphere* 6: 78-112.
- 580 Halbwegs, H. et al. 2015. Spore wall traits of ectomycorrhizal and saprotrophic agarics may  
581 mirror their distinct lifestyles. — *Fungal Ecol.* 17: 197-204.
- 582 Halme, P. et al. 2012. Monitoring fungal biodiversity - towards an integrated approach. —  
583 *Fungal Ecol.* 5: 750-758.
- 584 Heilmann-Clausen, J. et al. 2016. Citizen science data reveal ecological, historical and  
585 evolutionary factors shaping interactions between woody hosts and wood-inhabiting  
586 fungi. — *New Phytol.* 212: 1072-1082.
- 587 Hickling, R. et al. 2006. The distributions of a wide range of taxonomic groups are expanding  
588 polewards. — *Glob. Change Biol.* 12: 450-455.
- 589 Jamil, T. et al. 2013. Selecting traits that explain species-environment relationships: a  
590 generalized linear mixed model approach. — *J. Veg. Sci.* 24: 988-1000.
- 591 Johnson, N. C. et al. 2013. Predicting community and ecosystem outcomes of mycorrhizal  
592 responses to global change. — *Ecol. Lett.* 16: 140-153.
- 593 Kauserud, H. et al. 2012. Warming-induced shift in European mushroom fruiting phenology.  
594 — *Proc. Nat. Acad. Sci. USA.* 109: 14488-14493.
- 595 Kauserud, H. et al. 2010. Climate change and spring-fruited fungi. — *Proc. Roy. Soc. B.*  
596 277: 1169-1177.

- 597 Kauserud, H. et al. 2007. Asian origin and rapid global spread of the destructive dry rot  
598 fungus *Serpula lacrymans*. — *Mol. Ecol.* 16: 3350-3360.
- 599 Knudsen, H. and Vesterholt, J. (eds) 2012. *Funga Nordica*, 2nd ed. — Nordsvamp.
- 600 Kolarova, E. et al. 2014. Long-term temporal changes in central European tree phenology  
601 (1946-2010) confirm the recent extension of growing seasons. — *Int. J. Biometeorol.* 58:  
602 1739-1748.
- 603 Leake, J. R. et al. 2002. Interactions between ecto-mycorrhizal and saprotrophic fungi. — In:  
604 van der Heijden, M. G. A. and Sanders, I. R. (eds), *Ecological studies: Mycorrhizal*  
605 *ecology*. Springer. pp. 345-372.
- 606 Lisewski, V. and Ellis, C. J. 2010. Epiphyte sensitivity to a cross-scale interaction between  
607 habitat quality and macroclimate: an opportunity for range-edge conservation. —  
608 *Biodivers. Cons.* 19: 3935-3949.
- 609 Mair, L. and Ruete, A. 2016. Explaining spatial variation in the recording effort of citizen  
610 science data across multiple taxa. — *PLoS One* 11: e0147796, DOI:  
611 10.1371/journal.pone.0147796
- 612 Martiny, J. B. H. et al. 2006. Microbial biogeography: putting microorganisms on the map.  
613 — *Nat. Rev. Microbiol.* 4: 102-112.
- 614 Menzel, A. and Fabian, P. 1999. Growing season extended in Europe. — *Nature* 397: 659-  
615 659.
- 616 Mohan, J. E. et al. 2014. Mycorrhizal fungi mediation of terrestrial ecosystem responses to  
617 global change: mini-review. — *Fungal Ecol.* 10: 3-19.
- 618 Moore, D. et al. 2008. Fruit bodies: Their production and development in relation to  
619 environment. — In: Boddy, L. et al. (eds), *Ecology of saprotrophic basidiomycetes*.  
620 Elsevier, pp. 79-103.

- 621 Norros, V. et al. 2014. Do small spores disperse further than large spores? — *Ecology* 95:  
622 1612-1621.
- 623 Ohenoja, E. 1989. Effect of winter conditions on mushroom production. . — *Mem. Soc.*  
624 *Fauna Flora Fenn.* 65: 77-80.
- 625 Ovaskainen, O. et al. 2016. Uncovering hidden spatial structure in species communities with  
626 spatially explicit joint species distribution models. — *Methods Ecol Evol* 7: 428-436.
- 627 Peter, M. et al. 2001. Nitrogen addition in a Norway spruce stand altered macromycete  
628 sporocarp production and below-ground ectomycorrhizal species composition. — *New*  
629 *Phytol.* 149: 311-325.
- 630 Pollock, L. J. et al. 2014. Understanding co-occurrence by modelling species simultaneously  
631 with a Joint Species Distribution Model (JSDM). — *Methods Ecol. Evol.* 5: 397-406.
- 632 Primicia, I. et al. 2016. Linkages between climate, seasonal wood formation and mycorrhizal  
633 mushroom yields. — *Agric. For. Meteorol.* 228: 339-348.
- 634 Quine, C. et al. (eds) 2011. *Woodlands*. — NEP-WCMC.
- 635 R Core Team 2016. *R: A language and environment for statistical computing*. — R  
636 Foundation for Statistical Computing.
- 637 Richardson, A. D. et al. 2010. Influence of spring and autumn phenological transitions on  
638 forest ecosystem productivity. — *Phil. Trans. R. Soc. B-Biol. Sci.* 365: 3227-3246.
- 639 Rousk, J. and Bååth, E. 2011. Growth of saprotrophic fungi and bacteria in soil. — *FEMS*  
640 *Microbiol. Ecol.* 78: 17-30.
- 641 Rue, H. et al. 2009. Approximate Bayesian inference for latent Gaussian models by using  
642 integrated nested Laplace approximations. — *J. Roy. Stat. Soc B - Stats Method.* 71: 319-  
643 392.

- 644 Schenk-Jäger, K. M. et al. 2016. Introducing mushroom fruiting patterns from the Swiss  
645 National Poisons Information Centre. — PLoS One 11: e0162314 DOI:  
646 10.1371/journal.pone.0162314
- 647 Stewart, J. R. 2009. The evolutionary consequence of the individualistic response to climate  
648 change. — J. Evol. Biol. 22: 2363-2375.
- 649 Taheri, S. et al. 2016. Did British breeding birds move north in the late 20th century? — Clim  
650 Ch. Resp. 3:5: DOI 10.1186/s40665-40016-40020-40665.
- 651 Tedersoo, L. et al. 2014. Global diversity and geography of soil fungi. — Science 346: 1078-  
652 DOI: 10.1126/science.1256688.
- 653 Ter Braak, C. J. F. et al. 2017. A critical issue in model-based inference for studying trait-  
654 based community assembly and a solution. — PeerJ 5: e2885  
655 <https://doi.org/2810.7717/peerj.2885>.
- 656 Vellinga, E. C. et al. 2009. Global patterns of ectomycorrhizal introductions. — New Phytol.  
657 181: 960-973.
- 658 Ward, D. F. 2014. Understanding sampling and taxonomic biases recorded by citizen  
659 scientists. — J. Insect Cons. 18: 753-756.
- 660 Warton, D. I. et al. 2015. CATS regression - a model-based approach to studying trait-based  
661 community assembly. — Methods Ecol. Evol. 6: 389-398.
- 662 Wilson, R. J. et al. 2005. Changes to the elevational limits and extent of species ranges  
663 associated with climate change. — Ecol. Lett. 8: 1138-1146.
- 664 Wolfe, B. E. and Pringle, A. 2012. Geographically structured host specificity is caused by the  
665 range expansions and host shifts of a symbiotic fungus. — ISME J. 6: 745-755.
- 666 Yan, Y. et al. 2017. Range shifts in response to climate change of *Ophiocordyceps sinensis*, a  
667 fungus endemic to the Tibetan Plateau. — Biol. Cons. 206: 143-150.
- 668

669

670

671 **Figure legends**

672 Figure 1. The posterior distribution of the coefficients for the model including the functional  
 673 groups, i.e. ECM vs saprotrophic. The darkness of the individual horizontal bars reflect the  
 674 probabilities (dark = high). The centre point of the horizontal bars is the expected value, and  
 675 the darkest bars are those with a significant effect, i.e. the 95% credibility interval excludes 0  
 676 (for no effect). The scale of the coefficients relates to a standard deviation change of the  
 677 predictor variables. Each number in brackets corresponds to those in Table S2.

678 Figure 2. Diagrammatic representation of the modelled abundances over time and across  
 679 latitude (northing) for hypothetical fungal species, each with a median prevalence of  $p=0.005$ ,  
 680 and for a mean of 1000 records per grid cell. (a) Expectation for the functional group ECM  
 681 (b) Expectation for the functional group saprotroph. Degree of shading represents abundance,  
 682 with dark colour indicating high abundance and vice versa.

683 Figure 3. A colour chart depicting interaction effects of the different traits with and climate  
 684 and latitude. Each trait is listed in the left of the figure. 'Env' in each legend corresponds to  
 685 the particular variable: Latitude, Temperature, Rainfall or Hygrothermic Index (HT). Red  
 686 colours indicate a positive expected effect, whereas blue colours indicate negative effects.  
 687 The intensity of the colours correspond to the probability of being either negative or positive.  
 688 The stars relate to the credibility interval of the effects \*  $p = 0.9$ , \*\*  $p = 0.95$ , and \*\*\*  $p =$   
 689  $0.99$ . See also Table S2 for the actual 95% credibility intervals associated with these effects;  
 690 those depicted here are the coefficients labelled 3, 5, 6 and 7 of latitude, temperature, rainfall  
 691 and Hygrothermic Index (HT) from Table S2. These are the coefficients that specifically  
 692 address trait-dependent distributional shifts among fruiting records in UK.

693 Figure 4. Diagrammatic representation of the modelled abundances over time and across  
694 latitude (northing) for hypothetical fungal species, each with a median prevalence of  $p=0.005$ ,  
695 and for a mean of 1000 records per grid cell. Expectation for species with: (a) small caps, (b)  
696 large caps, (c) ornamented spores, (d) smooth spores, (e) species with short and (f) species  
697 with long fruiting seasons. Darker shading indicates higher abundance.

698

### 699 **Supplementary Information**

700 Table S1. List of species used in the analysis, with data for their different traits and summary  
701 statistics for the relationship between the traits (Figures S1.1-1.5).

702 Table S2. Table of 95 % credibility intervals for different terms in the fitted models.

703 Table S3. A brief outline of the INLA analysis and output for the trait nutritional mode.

704 Figure S1. Distribution of records in the dataset across Vice Counties. a) Log number of  
705 records; b) Number of species; c) Average abundance per species per year. The left hand  
706 vertical axis on (a) and (c) depicts latitude.

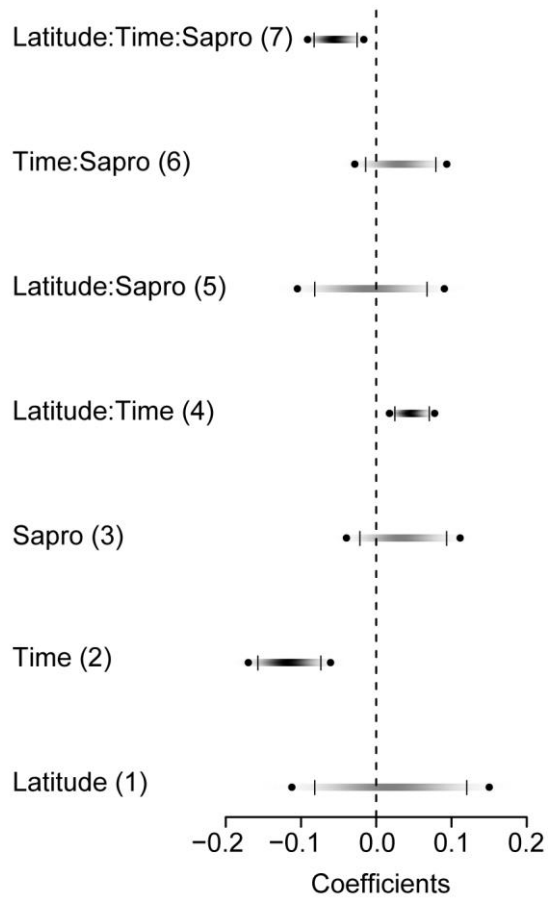
707 Figure S2. Climatic data across Vice Counties. a) Mean annual temperature ( $^{\circ}\text{C}$ ), b) Mean  
708 annual precipitation (mm), c) Hygrothermic Index, higher values represent oceanic climate,  
709 lower value a more continental climate. The left hand vertical axis on (a) and (c) depicts  
710 latitude.

711

712

713

714 Figure 1



715

716

717

718

719

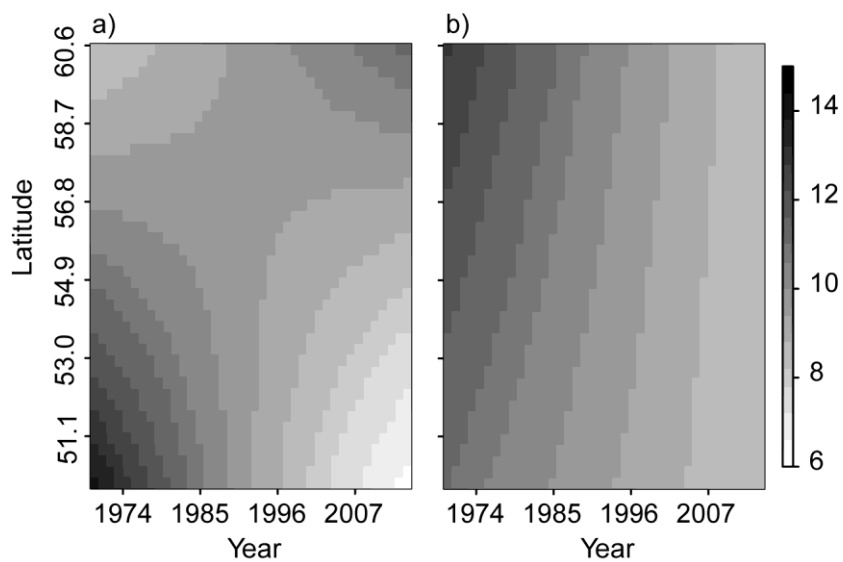
720

721

722

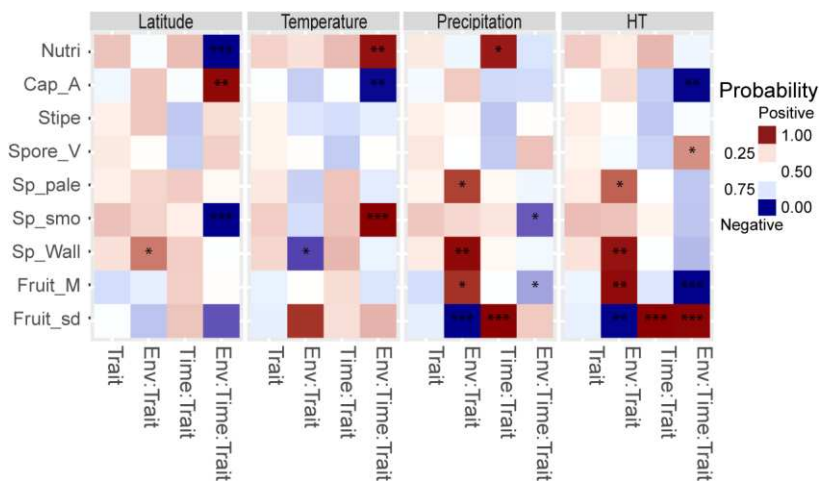


723 Figure 2



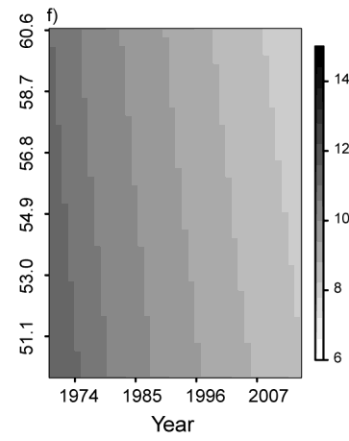
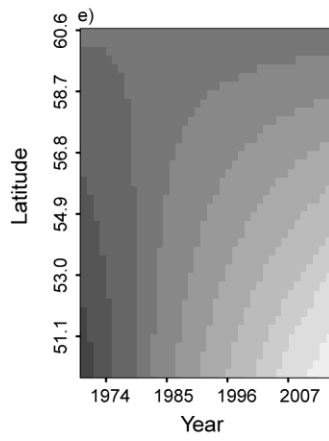
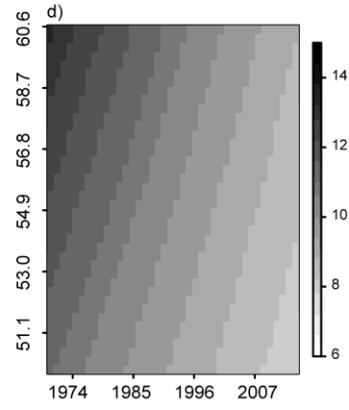
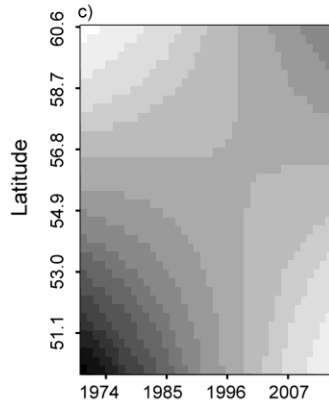
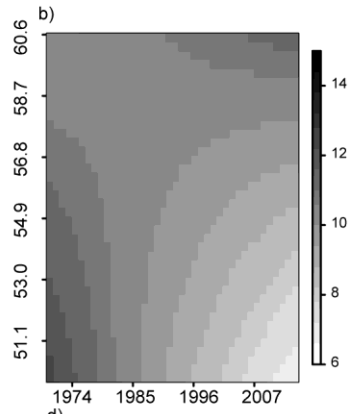
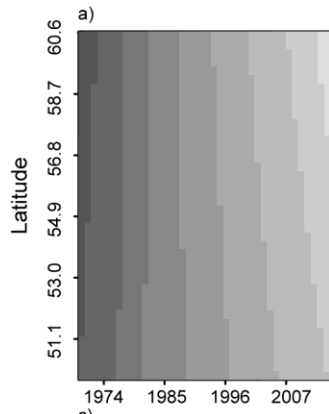
724

725 Figure 3



726

727 Figure 4



728

729

Species	Nutri. Mode	Stipe mean	Stipe max	Cap area	Spore vol.	log(Vol)	Spore colour	Spore wall	Spore smooth	Fruiting mean	Fruiting SD
<i>Cantharellus cibarius</i>	ECM	80	120	3318.31	37.70	3.63	pale	thin	TRUE	280.01	23.61
<i>Cantharellus fulva</i>	ECM	125	180	2375.83	63.36	4.15	pale	thin	TRUE	254.17	32.29
<i>Cantharellus muscaria</i>	ECM	165	250	13273.23	30.63	3.42	pale	thin	TRUE	281.68	25.28
<i>Cantharellus rubescens</i>	ECM	105	150	7853.98	28.93	3.36	pale	thin	TRUE	258.37	38.18
<i>Cantharellus titubans</i>	Sap	62.5	100	706.86	46.50	3.84	dark	thick	TRUE	241.89	63.37
<i>Cantharellus edulis</i>	ECM	95	150	12271.85	42.61	3.75	dark	thick	TRUE	267.75	28.19
<i>Cantharellus trophillum rachodes</i>	Sap	115	200	11309.73	37.99	3.64	pale	thick	TRUE	281.20	41.62
<i>Cantharellus cybe fragrans</i>	Sap	42.5	60	433.74	17.25	2.85	pale	thin	TRUE	262.82	91.22
<i>Cantharellus cybe nebularis</i>	Sap	75	90	7088.22	14.24	2.66	pale	thin	TRUE	299.12	33.50
<i>Cantharellus tricolor micaceus</i>	Sap	70	100	213.82	24.05	3.18	dark	thick	TRUE	245.39	79.81
<i>Cantharellus tricolor atramentaria</i>	Sap	110	170	1963.50	27.36	3.31	dark	thick	TRUE	256.88	69.13
<i>Cantharellus tricolor comatus</i>	Sap	175	300	1590.43	43.66	3.78	dark	thick	TRUE	276.59	39.25
<i>Cantharellus trophillum pratensis</i>	Sap	90	150	4417.86	14.14	2.65	pale	thin	TRUE	289.90	33.50
<i>Cantharellus trophillum virgineus</i>	Sap	40	60	1256.64	19.27	2.96	pale	thin	TRUE	297.02	28.38
<i>Cantharellus trophillum mulina velutipes</i>	Sap	45	80	881.41	14.20	2.65	pale	thin	TRUE	183.90	138.30
<i>Cantharellus trophillum phorus psittacinus</i>	Sap	40	60	829.58	23.76	3.17	pale	thin	TRUE	287.13	37.77
<i>Cantharellus trophillum anopilus penetrans</i>	Sap	50	80	1963.50	19.90	2.99	dark	thick	FALSE	283.06	47.13
<i>Cantharellus trophillum anopus confluens</i>	Sap	85	120	593.96	13.29	2.59	pale	thin	TRUE	264.75	35.93
<i>Cantharellus trophillum anopus dryophilus</i>	Sap	75	120	962.11	9.36	2.24	pale	thin	TRUE	259.82	44.11
<i>Cantharellus trophillum anopus peronatus</i>	Sap	52.5	75	1418.63	16.49	2.80	pale	thin	TRUE	269.56	37.12
<i>Cantharellus trophillum meloma crustuliniforme</i>	ECM	47.5	70	2827.43	33.12	3.50	dark	thick	FALSE	283.32	26.41
<i>Cantharellus trophillum cybe chlorophana</i>	Sap	50	80	1590.43	19.90	2.99	pale	thin	TRUE	285.74	34.23
<i>Cantharellus trophillum cybe conica</i>	Sap	67.5	120	2164.75	27.85	3.33	pale	thin	TRUE	273.66	34.30
<i>Cantharellus trophillum sporopsis aurantiaca</i>	Sap	25	40	2375.83	10.54	2.35	pale	thin	TRUE	278.79	35.41
<i>Cantharellus trophillum menopellis radicata</i>	Sap	150	250	3578.47	87.31	4.47	pale	thin	TRUE	267.58	36.90
<i>Cantharellus trophillum holoma fasciculare</i>	Sap	55	80	962.11	15.58	2.75	dark	thick	TRUE	257.53	66.89
<i>Cantharellus trophillum aria badia</i>	ECM	80	120	7853.98	31.81	3.46	dark	thick	FALSE	273.89	31.13
<i>Cantharellus trophillum cybe geophylla</i>	ECM	32.5	50	397.61	25.92	3.25	dark	thick	TRUE	277.11	31.24

<i>aria amethystina</i>	ECM	55	80	490.87	41.23	3.72	pale	thick	FALSE	280.74	28.00
<i>aria laccata</i>	ECM	45	70	490.87	41.04	3.71	pale	thick	FALSE	273.07	40.31
<i>arius quietus</i>	ECM	50	70	2164.75	25.36	3.23	pale	thin	FALSE	276.52	27.57
<i>arius subdulcis</i>	ECM	45	65	1104.47	28.08	3.33	pale	thin	FALSE	277.73	33.63
<i>arius tabidus</i>	ECM	50	80	490.87	22.78	3.13	pale	thin	FALSE	273.42	30.84
<i>arius turpis</i>	ECM	42.5	65	5674.50	23.33	3.15	pale	thin	FALSE	280.36	24.30
<i>inum scabrum</i>	ECM	135	200	7853.98	48.96	3.89	pale	thick	TRUE	268.51	28.24
<i>ota cristata</i>	Sap	42.5	70	1590.43	11.00	2.40	pale	thick	TRUE	273.87	36.60
<i>sta nuda</i>	Sap	70	90	7853.98	17.08	2.84	pale	thin	FALSE	291.93	62.64
<i>opperdon perlatum</i>	Sap	52.5	75	1772.05	8.25	2.11	dark	thick	TRUE	270.47	58.34
<i>opperdon pyriforme</i>	Sap	32.5	45	706.86	7.07	1.96	dark	thick	TRUE	256.75	77.26
<i>asmiellus ramealis</i>	Sap	12.5	20	122.72	16.95	2.83	pale	thin	TRUE	271.63	46.16
<i>asmius oreades</i>	Sap	60	80	706.86	24.87	3.21	pale	thin	TRUE	243.50	55.87
<i>ena galericulata</i>	Sap	115	200	593.96	42.61	3.75	pale	thin	TRUE	278.50	56.65
<i>ena galopus</i>	Sap	65	80	176.71	34.56	3.54	pale	thin	TRUE	282.28	37.73
<i>ena inclinata</i>	Sap	70	110	397.61	30.63	3.42	pale	thin	TRUE	289.64	45.50
<i>ena pura</i>	Sap	65	100	706.86	11.91	2.48	pale	thin	TRUE	282.13	36.46
<i>ena vitilis</i>	Sap	70	90	122.72	31.91	3.46	pale	thin	TRUE	283.82	49.31
<i>lepista flaccida</i>	Sap	35	50	3318.31	8.84	2.18	pale	thin	FALSE	287.95	57.91
<i>sola plicatilis</i>	Sap	75	120	38.48	56.12	4.03	dark	thick	TRUE	250.22	58.65
<i>llus involutus</i>	ECM	70	100	7088.22	27.10	3.30	dark	thin	TRUE	272.77	31.21
<i>eus cervinus</i>	Sap	70	100	5674.50	20.88	3.04	pale	thick	TRUE	257.31	53.12
<i>hyrella candolleana</i>	Sap	70	100	2827.43	20.52	3.02	dark	thick	TRUE	233.06	56.93
<i>hyrella piluliformis</i>	Sap	65	90	1963.50	10.08	2.31	dark	thick	TRUE	275.71	55.65
<i>docollybia butyracea</i>	Sap	65	90	2375.83	13.74	2.62	pale	thin	TRUE	290.19	51.94
<i>docollybia maculata</i>	Sap	100	150	3848.45	15.71	2.75	pale	thin	TRUE	276.68	27.13
<i>gula atropurpurea</i>	ECM	45	60	3848.45	26.38	3.27	pale	thin	FALSE	272.06	30.67
<i>gula cyanoxantha</i>	ECM	75	100	7853.98	28.27	3.34	pale	thin	FALSE	259.20	36.03
<i>gula nigricans</i>	ECM	50	70	13273.23	24.67	3.21	pale	thin	FALSE	270.08	34.82
<i>gula ochroleuca</i>	ECM	50	70	5674.50	35.34	3.57	pale	thin	FALSE	276.64	30.49
<i>holomopsis rutilans</i>	Sap	80	120	5674.50	18.56	2.92	pale	thin	TRUE	274.84	30.80

<i>aria furfuracea</i>	Sap	27.5	40	363.05	22.68	3.12	dark	thick	TRUE	219.73	119.12
<i>ocomellus chrysenteron</i>	ECM	65	100	4417.86	36.00	3.58	dark	thick	FALSE	262.08	35.03

Table S1. The 61 species used in the analysis, with information on their Nutritional mode (Nutri mode) (Ectomycorrhizal (ECM) or saprotrophic (Sap), mean and maximum stipe height (in mm), cap area (in mm<sup>2</sup>), spore volume ( $\mu^3$ ), spore colour, spore wall thickness, spore smoothness, mean fruiting day and standard deviation of fruiting day.

## Relationships between traits

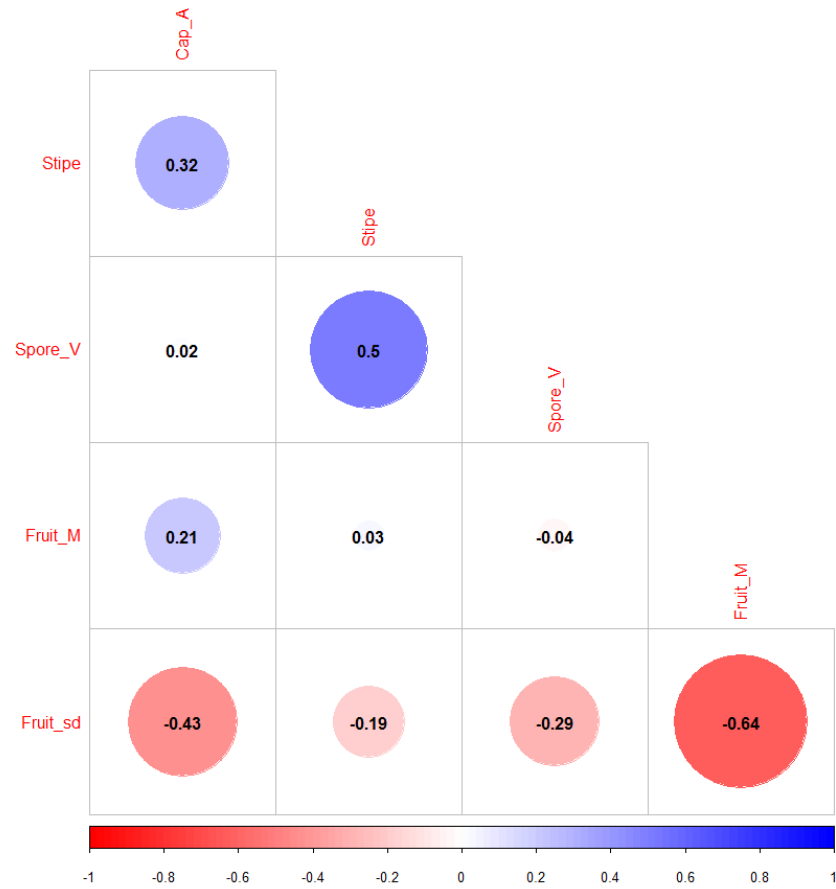


Figure S1.1 The correlation values between the continuous traits.

Chi-square tests of categorical traits, only significant listed:

Nutritional mode vs spore\_smooth:

	Spore_smooth	
Nutri_Mode	FALSE	TRUE
ECM	13	8
Sap	3	37

Pearson's Chi-squared test with Yates' continuity correction

```
data: table(Nutri_Mode, Spore_smooth)
X-squared = 18.347, df = 1, p-value = 1.841e-05
```

Spore wall vs spore colour

	Spore_wall	
Spore_colour	thick	thin
dark	17	1
pale	6	37

Pearson's Chi-squared test with Yates' continuity correction

```
data: table(Spore_colour, Spore_wall)
X-squared = 31.656, df = 1, p-value = 1.841e-08
```

Boxplot of continuous traits against categorical traits:

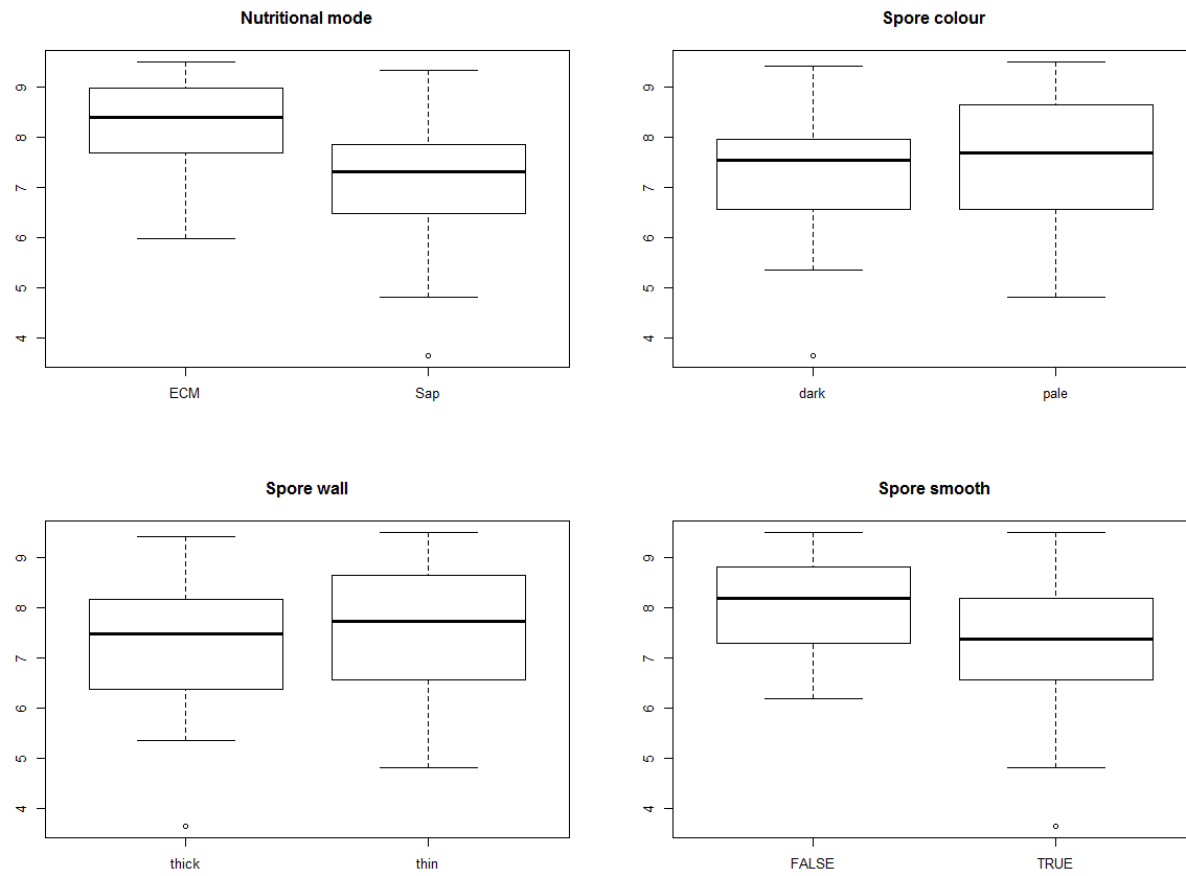


Figure S1.2. Continuous variable is Cap area.



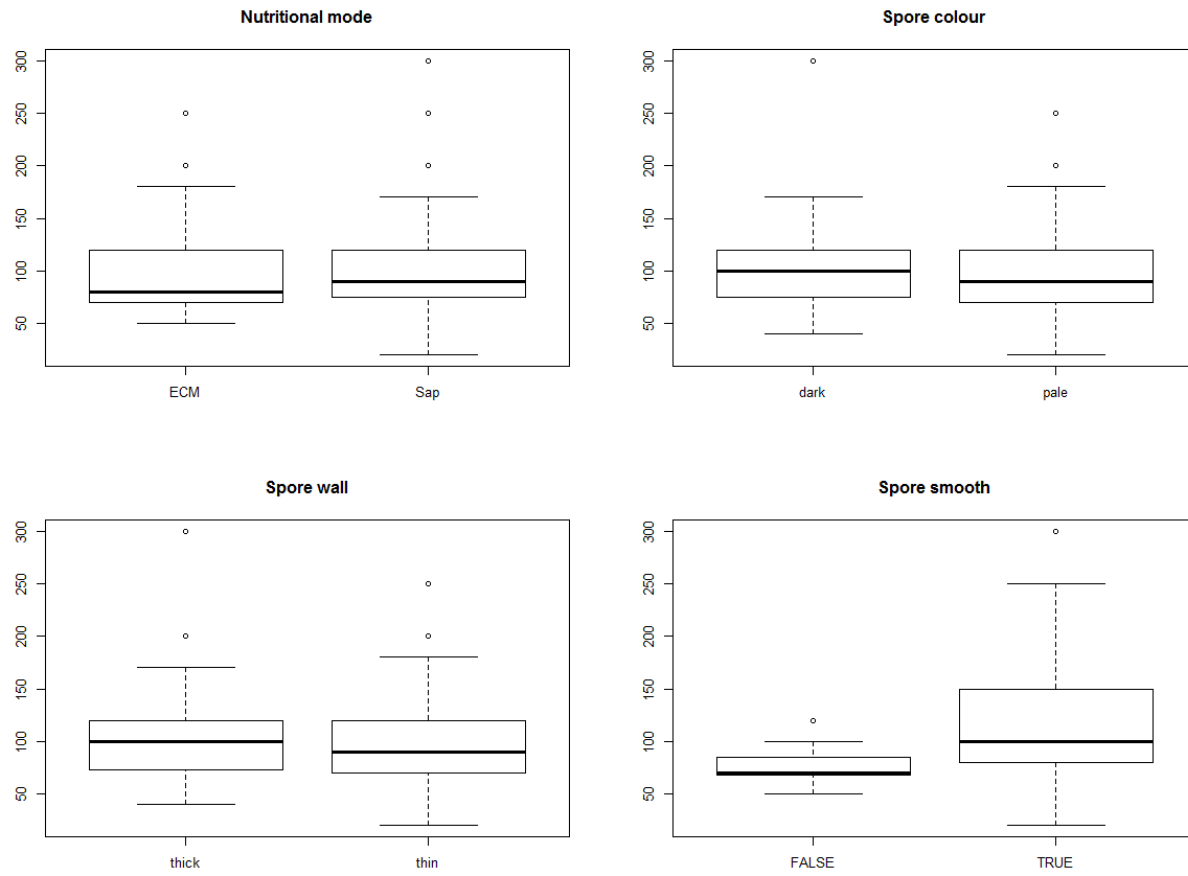


Figure S1.3. Continuous variable is Stipe height.

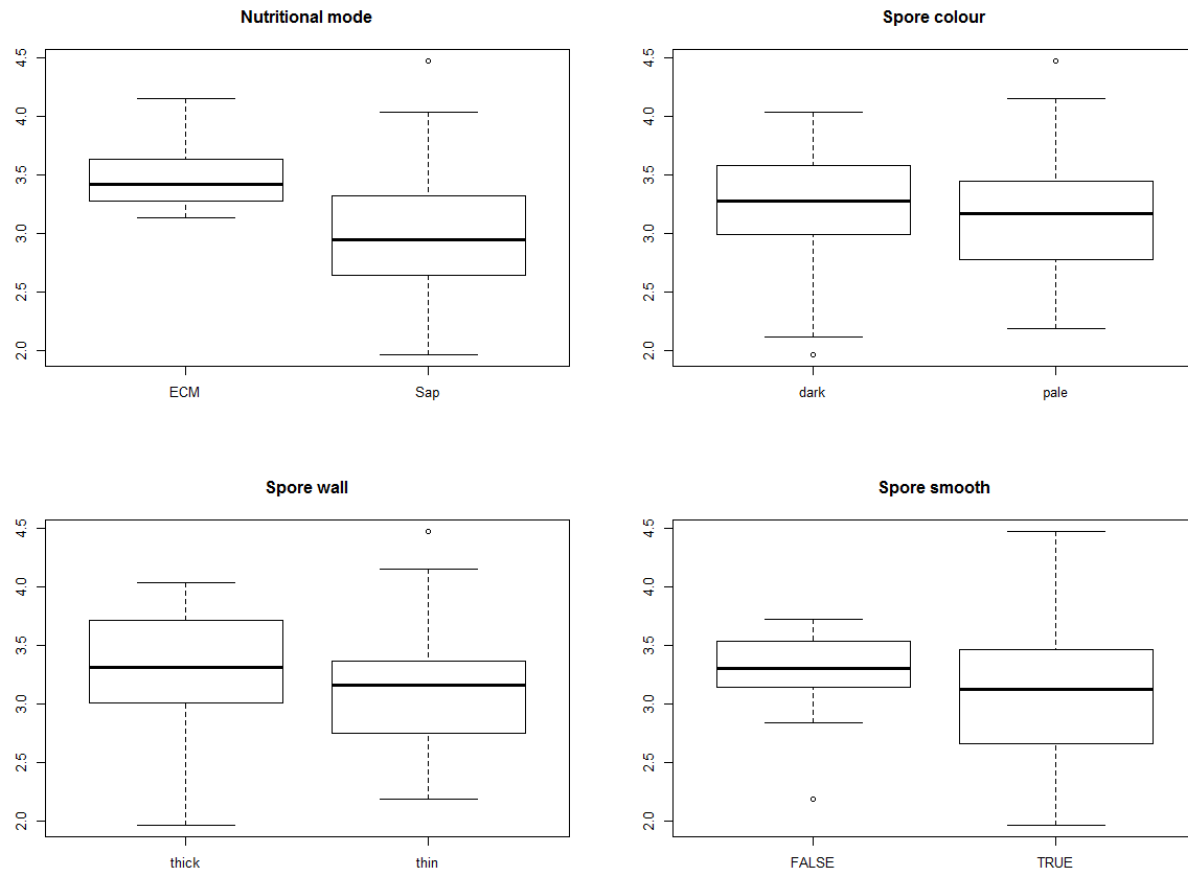


Figure S1.4. Continuous variable is Spore volume

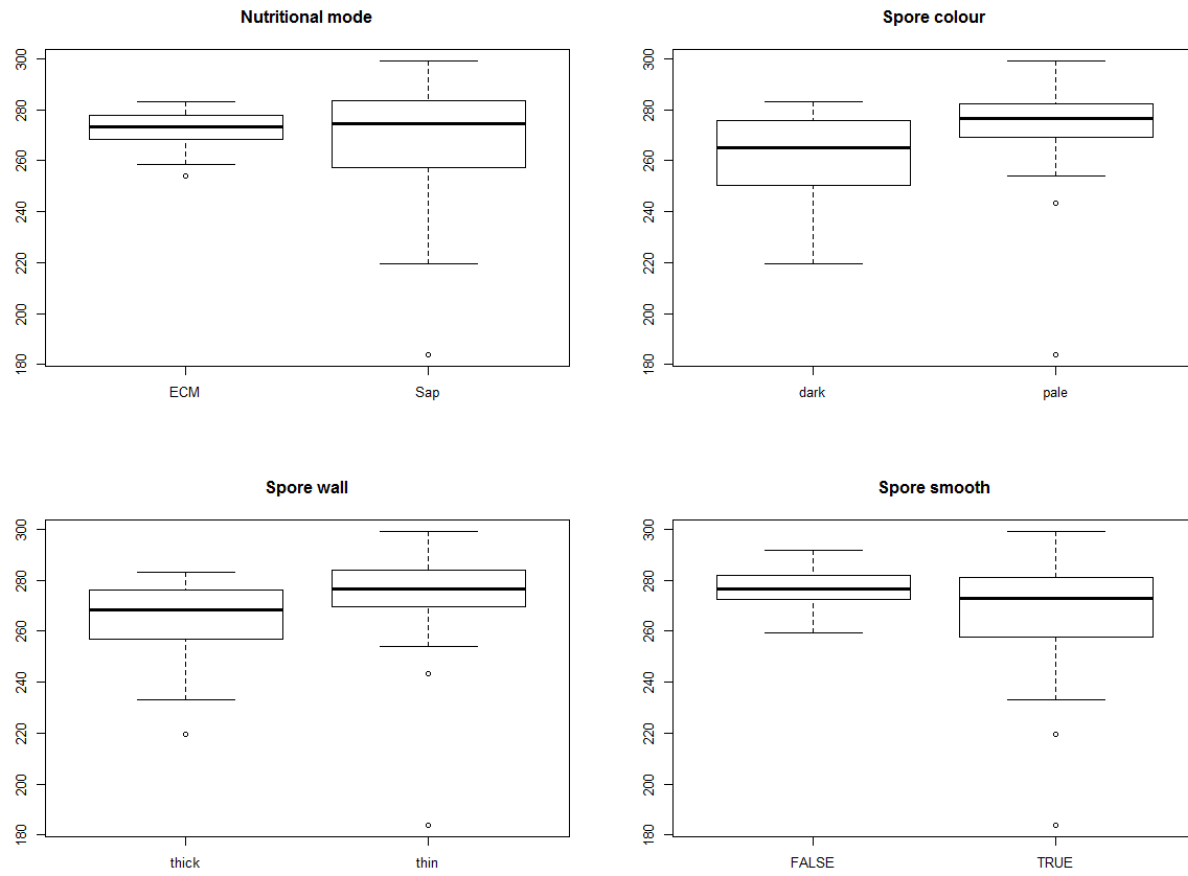


Fig. S1.5. Continuous variable is mean Fruiting day.

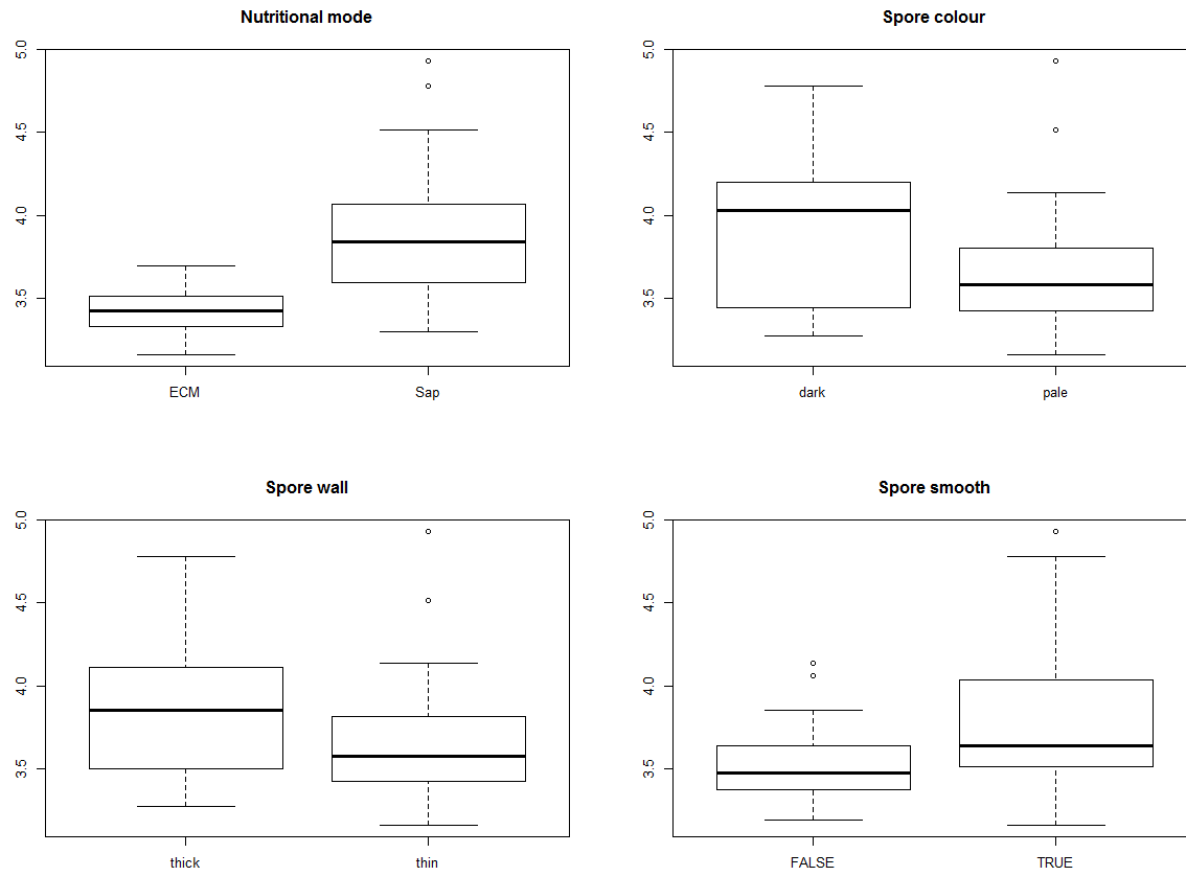


Figure S1.5. Continuous variable is standard deviation fruiting day.

	No traits		Nutri		Caparea		Stipe		Spore_V		Sp_pale		Sp_smo		Sp_Wall		Fruit_M		Fruit_sd	
	Low	High	Low	High	Low	High	Low	High	Low	High	Low	High	Low	High	Low	High	Low	High	Low	High
Intercept	0.543	0.705	0.511	0.691	0.542	0.706	0.542	0.706	0.542	0.706	0.522	0.707	0.499	0.688	0.523	0.700	0.542	0.706	0.543	0.706
Latitude (1)	-0.073	0.104	-0.082	0.120	-0.073	0.104	-0.073	0.103	-0.074	0.103	-0.115	0.093	-0.120	0.093	-0.124	0.074	-0.073	0.104	-0.073	0.103
Time (2)	-0.123	-0.065	-0.157	-0.074	-0.123	-0.065	-0.123	-0.065	-0.122	-0.065	-0.157	-0.067	-0.151	-0.056	-0.150	-0.068	-0.123	-0.065	-0.123	-0.065
Lati:Time (4)	-0.002	0.029	0.025	0.071	-0.002	0.028	-0.002	0.029	-0.002	0.029	-0.019	0.038	0.031	0.085	-0.011	0.039	-0.002	0.029	-0.002	0.028
Trait (3)			-0.022	0.094	-0.032	0.023	-0.022	0.034	-0.020	0.036	-0.047	0.075	-0.022	0.105	-0.037	0.077	-0.038	0.015	-0.029	0.026
Latitude:Trait (5)			-0.082	0.067	-0.014	0.056	-0.014	0.056	-0.034	0.038	-0.041	0.114	-0.042	0.120	-0.008	0.136	-0.044	0.025	-0.059	0.011
Time:Trait (6)			-0.014	0.079	-0.024	0.020	-0.036	0.008	-0.035	0.009	-0.023	0.075	-0.038	0.064	-0.022	0.070	-0.010	0.033	-0.009	0.035
Lati:Time:Trait (7)			-0.082	-0.025	0.003	0.032	-0.009	0.021	-0.007	0.023	-0.029	0.039	-0.092	-0.029	-0.032	0.031	-0.015	0.016	-0.029	0.001
Intercept	0.564	0.714	0.536	0.703	0.564	0.713	0.566	0.712	0.564	0.713	0.539	0.711	0.528	0.701	0.540	0.705	0.564	0.713	0.564	0.713
Temp	-0.074	0.020	-0.103	0.021	-0.075	0.021	-0.075	0.021	-0.075	0.021	-0.068	0.062	-0.073	0.062	-0.053	0.067	-0.075	0.021	-0.074	0.020
Time	-0.122	-0.059	-0.160	-0.069	-0.122	-0.059	-0.123	-0.059	-0.122	-0.059	-0.162	-0.065	-0.167	-0.065	-0.158	-0.070	-0.122	-0.059	-0.122	-0.059
Temp:Time	-0.015	0.016	-0.045	0.004	-0.015	0.016	-0.015	0.016	-0.015	0.016	-0.021	0.035	-0.062	-0.007	-0.020	0.030	-0.015	0.016	-0.015	0.016
Trait			-0.029	0.087	-0.029	0.026	-0.022	0.033	-0.023	0.034	-0.043	0.081	-0.030	0.096	-0.032	0.083	-0.034	0.020	-0.035	0.021
Temp:Trait			-0.039	0.082	-0.045	0.012	-0.039	0.018	-0.027	0.030	-0.097	0.028	-0.093	0.036	-0.113	0.003	-0.027	0.028	-0.001	0.054
Time:Trait			-0.014	0.087	-0.024	0.023	-0.034	0.014	-0.039	0.009	-0.020	0.084	-0.020	0.088	-0.011	0.086	-0.014	0.032	-0.015	0.033
Temp:Time:Trait			0.002	0.062	-0.030	-0.002	-0.019	0.011	-0.015	0.015	-0.042	0.023	0.016	0.079	-0.038	0.024	-0.020	0.009	-0.002	0.027
Intercept	0.514	0.649	0.496	0.648	0.515	0.649	0.514	0.649	0.515	0.649	0.497	0.652	0.479	0.636	0.498	0.648	0.514	0.649	0.514	0.649
Rain	-0.018	0.081	-0.035	0.122	-0.017	0.081	-0.018	0.081	-0.018	0.082	-0.114	0.050	-0.088	0.089	-0.107	0.040	-0.017	0.080	-0.016	0.078
Time	-0.129	-0.073	-0.169	-0.090	-0.129	-0.073	-0.129	-0.073	-0.129	-0.073	-0.149	-0.063	-0.158	-0.068	-0.145	-0.066	-0.129	-0.073	-0.128	-0.074
Rain:Time	-0.026	0.000	-0.027	0.013	-0.026	0.000	-0.026	0.000	-0.026	0.000	-0.032	0.014	-0.018	0.028	-0.031	0.010	-0.026	0.000	-0.025	0.001
Trait			-0.037	0.068	-0.029	0.021	-0.020	0.030	-0.017	0.034	-0.044	0.066	-0.024	0.089	-0.038	0.067	-0.035	0.013	-0.031	0.018
Rain:Trait			-0.111	0.075	-0.019	0.067	-0.040	0.048	-0.046	0.043	-0.004	0.184	-0.057	0.142	0.016	0.192	-0.001	0.081	-0.106	-0.025
Time:Trait			0.000	0.086	-0.031	0.011	-0.034	0.007	-0.034	0.008	-0.039	0.053	-0.032	0.063	-0.037	0.050	-0.021	0.020	0.009	0.049
Rain:Time:Trait			-0.034	0.016	-0.017	0.007	-0.011	0.013	-0.004	0.020	-0.032	0.022	-0.051	0.002	-0.029	0.021	-0.023	0.002	-0.005	0.019
Intercept	0.568	0.705	0.539	0.695	0.515	0.649	0.568	0.705	0.568	0.706	0.545	0.705	0.524	0.687	0.548	0.702	0.568	0.705	0.567	0.705
HT	-0.032	0.049	-0.067	0.059	-0.017	0.081	-0.031	0.049	-0.031	0.049	-0.107	0.026	-0.099	0.043	-0.098	0.021	-0.031	0.048	-0.032	0.046
Time	-0.131	-0.076	-0.162	-0.086	-0.129	-0.073	-0.131	-0.076	-0.131	-0.076	-0.144	-0.062	-0.153	-0.067	-0.140	-0.065	-0.131	-0.076	-0.129	-0.076
HT:Time	-0.036	-0.006	-0.041	0.005	-0.026	0.000	-0.037	-0.006	-0.036	-0.007	-0.033	0.017	-0.033	0.019	-0.030	0.014	-0.036	-0.007	-0.035	-0.006
Trait			-0.025	0.084	-0.029	0.021	-0.019	0.033	-0.021	0.032	-0.042	0.074	-0.017	0.101	-0.035	0.073	-0.031	0.020	-0.033	0.019
HT:Trait			-0.054	0.095	-0.019	0.067	-0.034	0.037	-0.040	0.032	-0.006	0.145	-0.030	0.130	0.004	0.148	0.006	0.072	-0.078	-0.010
Time:Trait			-0.009	0.072	-0.031	0.011	-0.032	0.007	-0.030	0.009	-0.043	0.043	-0.036	0.054	-0.042	0.040	-0.026	0.012	0.013	0.050
HT:Time:Trait			-0.032	0.022	-0.017	0.007	-0.014	0.012	-0.002	0.024	-0.047	0.010	-0.048	0.009	-0.048	0.004	-0.030	-0.006	0.004	0.029

Table S2. The 95 % credibility intervals of the coefficients associated with the different models. Each pair of columns gives the results from the model of the specific trait in interaction with latitude, climate and time. Numbers in brackets in the latitude section correspond to the effects depicted in Fig. 1, from (1) at the bottom to (7) at the top. This numbering also applies to the sections for Temp (temperature), Rain and HT (Hygrothermic Index). The lower four rows of each section are reproduced in the colour chart in Figure 3 of the main text.

Key to column headers: Nutri: Nutritional mode (ECM or saprotroph); Cap A: Cap area; Stipe: Maximum height of stipe; Sp pale: spore colour; Sp smo: spore smoothness; Sp wall: spore wall thickness; Fruit M: fruiting season mean; Fruit sd: fruiting season standard deviation (log).

The cap size is defined as the area of an average sized cap, and for the stipe height used the maximum height recorded. The average fruiting day is mean ordinal day, and the standard deviation of fruiting day describe the length of the fruiting season for the individual species.

```
#####
```

```
#Summary of analyses for nutritional mode using INLA for the full trait-specific model as presented in Gange et al. , Trait-dependent
distributional shifts in fruiting of common British fungi
```

```
#####
```

```
#dag.df = dataframe with the observational data
```

```
#y = number of records per species per VC per year
```

```
#qE = expected number of records per species per VC per Year
```

```
#Sp1 = as.numeric(dag.df$Sp)#index the different species
```

```
#N.sp = nlevels(dag.df$Sp) #number of species
```

```
#Sp2 = Sp1+N.sp #Index of species to identify additional random contributions associated with species, interaction species and Latitude
```

```
#Sp3 = Sp2+N.sp #Index of species to identify additional random contributions associated with species, interaction species and Time
```

```
#Sp4 = Sp3+N.sp #Index of species to identify additional random contributions associated with species, interaction species and Lat:Time
```

```
#Latitude = latitudinal desimal degree
```

```
#Time = year
```

```
#LatitudeTime = Latitude*Time
```

```
#VC = vice county number
```

```
#UK.adj = a list of neighbouring VC's
```

```
inla.Nutri <- Inla(y~offset(log(qE))+
```

```
  f(Sp1,model="iid")+f(Sp2,Latitude,model="iid")+f(Sp3,Time,model="iid")+f(Sp4,LatitudeTime,model="iid")+
```

```
  f(VC,model="bym",graph=UK.adj)+f(Time,model="iid")+Latitude*Time*Nutri,
```

```
  family="nbinomial",control.compute=list(waic=T),data=dag.df)
```

```
summary(inla.Nutri)
```

```
Call:
```

```
c("inla(formula = y ~ offset(log(qE)) + f(Sp1, ", " model = \"iid\") + f(Sp2, Latitude,
model = \"iid\") +      f(Sp3, Time, ", " model = \"iid\") + f(Sp4, LatitudeTime, model =
\"iid\") + f(VC, model = \"bym\", ", " graph = UK.adj) +      f(Time, model = \"iid\") +
Latitude * Time * ", " Nutri, family = \"nbinomial\", data = dag.df, control.compute =
list(waic = T))" )
```

```
Time used:
```

Pre-processing	Running inla	Post-processing	Total
1.5906	75579.0516	7.5242	75588.1665

## Fixed effects:

	mean	sd	0.025quant	0.5quant	0.975quant	mode	kld
(Intercept)	0.6012	0.0462	0.5104	0.6012	0.6920	0.6012	0
Latitude	0.0196	0.0520	-0.0829	0.0198	0.1213	0.0201	0
Time	-0.1153	0.0215	-0.1576	-0.1153	-0.0731	-0.1154	0
Nutrisap	0.0360	0.0296	-0.0223	0.0360	0.0942	0.0360	0
Latitude:Time	0.0477	0.0118	0.0245	0.0477	0.0708	0.0477	0
Latitude:Nutrisap	-0.0070	0.0382	-0.0824	-0.0069	0.0683	-0.0069	0
Time:Nutrisap	0.0326	0.0239	-0.0145	0.0326	0.0798	0.0326	0
Latitude:Time:Nutrisap	-0.0539	0.0146	-0.0827	-0.0540	-0.0251	-0.0540	0

## Random effects:

Name	Model
Sp1	IID model
Sp2	IID model
Sp3	IID model
Sp4	IID model
VC	BYM model
Time	IID model

## Model hyperparameters:

	mean	sd	0.025quant	0.5quant	0.975quant	mode
size for the nbinomial observations	5.43	0.0642	5.303	5.430	5.556	5.431
Precision for Sp2	52.07	10.4329	32.691	51.913	73.084	52.460
Precision for Sp1	89.33	17.2561	57.630	88.858	124.781	88.962
Precision for Sp3	141.29	28.6123	94.227	138.121	206.168	131.816
Precision for Sp4	471.08	118.5723	284.721	455.161	747.564	424.411
Precision for VC (iid component)	10.03	2.2620	6.229	9.813	15.079	9.420
Precision for VC (spatial component)	16.42	12.4821	4.283	12.873	49.455	8.583
Precision for Time	211.03	52.8077	120.903	206.975	326.282	200.250

Expected number of effective parameters(std dev): 368.33(2.982)

Number of equivalent replicates : 192.10



Watanabe-Akaike information criterion (WAIC) ...: 306946.32  
Effective number of parameters .....: 401.01  
  
Marginal log-Likelihood: -153970.39  
Posterior marginals for linear predictor and fitted values computed

Figure S1

