



Congruency in fungal phenology patterns across dataset sources and scales

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ABSTRACT

As citizen science and digitization projects bring greater and larger datasets to the scientific realm, we must address the comparability of results across varying sources and spatial scales. Independently assembled fungal fruit body datasets from Switzerland and the UK were available at large, national-scales and more intensively surveyed, local-scales. Phenology responses of fungi between these datasets at different scales (national, intermediate and local) resembled one another. Consistently with time, the fruiting season initiated earlier and extended later. Phenology better correlated across data sources and scales in the UK, which contain less landscape and environmental heterogeneity than Switzerland. Species-specific responses in seasonality varied more than overall responses, but generally fruiting start dates were later for most Swiss species compared with UK species, while end dates were later for both. The coherency of these results, across the data sources, supports the use of presence-only data obtained by multiple recorders, and even across heterogeneous landscapes, for global change phenology research.

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1. Introduction

Long-term species observation records are commonly used in ecology to determine changes in phenology that are correlated with global change. Historical datasets (maintained by museums and scientific societies) which note the presence of a particular species in a particular locality are considerably more spatially and temporally comprehensive than are the data currently available in

published scientific literature, atlases and websites (Boakes et al., 2010). The former sources are considered the ‘gold-standard’ for phenology research due to their high accuracy when processed appropriately to reduce biases (Davis et al., 2015). For some organisms (e.g. many plants and vertebrates) observations are relatively straightforward and ground-truth methods can be utilized to verify historical dataset accuracy (Primack et al., 2004; Robbirt et al., 2011; Calinger et al., 2013). However, for other organisms, such as fungi, it is difficult because they are largely hidden from sight. A fruit body indicates presence, but absence of a fruit body does not imply absence of the fungus, whose mycelium may remain hidden in soil, wood or within whatever it is feeding on. DNA-based analyses may better solve this problem in the future, but currently there are no comparable long-term large-scale datasets with highly precise and also widely distributed taxonomic and temporal resolution data available for DNA-based analyses. Large numbers of

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macroscopic fruit body records are cost-effective to obtain, and have greater and/or more positive public perceptions, hence their major contributions by citizen scientists to ecological data (Halme et al., 2012). For these reasons, the scientific value of these types of records to ecological research is unlikely to decrease in the near future. In fact, as the ecological and economic benefits of understanding climatic change effects on organisms outweigh the potential pitfalls of multi-source observational data, these data are likely to increase in their ecological use (Graham et al., 2004; Halme et al., 2012; Miller-Rushing et al., 2012).

While the importance of presence-only datasets to science is unequivocal, there are nonetheless numerous potential biases that may affect the results and interpretation of analyses of such data, even after parsing to reduce addressable biases (e.g., Boakes et al., 2010; García-Roselló et al., 2015; Andrew et al., 2017). Direct assessments of biases between differing sources of presence-only datasets have occasionally been investigated (Davis et al., 2015). Difficulties in recording methods can arise as a result of multiple recorders (recorder bias), from recording at different scales (spatial bias), or due to inequalities in timespans or temporal sampling intensities (temporal bias) (Boddy et al., 2014; Davis et al., 2015). Further issues within these groupings include: taxonomic mis-identifications; bias in recording favoured taxonomic groups; tendencies to under or over-report very common or rare taxa; lack of a standardised sampling regime and collection effort; temporal and spatial gaps in records; and preference for certain recording sites (Graham et al., 2004; Halme et al., 2012; Boddy et al., 2014; Davis et al., 2015; Isaac and Pocock, 2015).

Recent approaches to minimizing bias in presence-only data have focused on statistical manipulations or data filtering procedures prior to analysis (Geldmann et al., 2016; Stropp et al., 2016). While helpful up to a point, these can drastically reduce the number of samples and, thus, the reliability of the data, and introduce further statistical problems (Isaac and Pocock, 2015). There are, then, reasons to forego bias removal techniques. The question remains in these cases: how robust are results when data are minimally treated for bias? This is important to understand, as we must endeavour to explain ecology within the context of global change with what data are available, which will likely never have all potential biases completely removed. While resources are available to help with concern over data quality and filtering, there is also considerable ambiguity to the best practices (e.g., Graham et al., 2004; Boakes et al., 2010; Robbirt et al., 2011; Miller-Rushing et al., 2012; Davis et al., 2015; García-Roselló et al., 2015; Isaac and Pocock, 2015; Geldmann et al., 2016; Stropp et al., 2016). Thus, here we shift the focus from exploring bias techniques to whether ecologically informative results can be gained across data sources and scales, despite any potentially remaining biases (after basic filtering of multi-source data; e.g., Andrew et al., 2017).

In this study, we make direct comparisons of fungal fruiting phenology across datasets collected in different ways, with different recorder efforts and at different temporal and spatial scales. We focus on data of fruiting basidiomycetes, and more specifically agaricoid fungi that typically produce ephemeral fruit bodies, so that the date of a record is a good approximation of fruiting. While we follow the standard primary filtering steps to reduce biases as far as possible, we also purposefully have not drastically modified the data. Our goals are to assess the robustness of phenology results across multiple datasets and scales when the data are minimally treated for bias.

The analysis includes: (1) national scale datasets from the United Kingdom (1950–2008) and Switzerland (1975–2006) compiled from data submitted by multiple recorders, and collected in a non-structured manner in space and time, but with greater focus on the autumn fruiting season; (2) intensively collected local

datasets from a ca. 3000 km² area in the UK with a similar number of recording occasions throughout the year (1950–2008), and (3) from a <1 km² forest plot in Switzerland which was exhaustively sampled throughout the summer and autumn fruiting season (1975–2006); and (4) intermediate scale datasets extracted from the national datasets. For the UK, and provided mostly as [supplemental material](#) (as results were similar and only added complexity), an additional local-scale dataset was analysed which was extracted from the national-scale data (see Material and methods).

Dataset comparisons and hypotheses were as follows: (1) despite considerable variability derived from multiple collectors, the phenological trends in national datasets will be similar to those in the intensively collected datasets; (2) the comparability of all datasets from a single country will be relatively high (i.e. greater than by chance), and higher than between countries; (3) within-country datasets of similar-scaled sources will be more correlated than differently-scaled sources. Climatically-driven temporal effects on fungal fruit body seasonality (start, end, and mean fruiting days) were determined for all fungi as well as subsections by fungal nutritional modes (saprotrophic versus ectomycorrhizal fungi), thus placing these results within a global-change biology context.

2. Methods

2.1. Datasets

Four data sources were used in this study, and are described in detail below. All dataset sources had independent origins, but were expanded into six main dataset scales for comparison (Table 1, Fig. 1), plus one additional dataset for comparison within scales ([supplementary material](#); the results added too much complexity without any novelty to the overall results). Standard dataset combination and bias removal techniques first homogenized all of the data, and quality, across sources (Andrew et al., 2017). For example, the taxonomy across datasets was streamlined, temporal resolutions were equalized, discrepancies and duplicates were removed, records with dubious or missing data removed and georeferences verified.

The UK national (and matching, extracted intermediate) scale dataset was derived from multiple sources, including individual contributions, foray lists and fungarium data from the Royal Botanic Gardens, Kew, United Kingdom. Data were from The Fungal Records Database of Britain and Ireland (FRDBI; www.fieldmycology.net; <http://www.frdbi.info/>), available from 1760 to 2014, but only data from the mainland countries of England, Scotland and Wales, a region of approximately 209,331 km², were used. For the current study, data were limited in temporal (1950–2008) and spatial ranges, plus taxonomic groups to match the local dataset (see below).

The Swiss (CH) national (and intermediate) scale dataset was also a compilation of individual contributions, forays, scientific surveys and fungarium data. It is managed at the Swiss Federal Research Institute WSL in Birmensdorf/ZH (www.swissfungi.ch). Data are available from 1904 to 2014 across the country of approximately 41,285 km². Again, a narrower dataset timespan (1975–2006) and taxonomic coverage was used to filter and match the national and local data sources (Table 1).

In the UK, a local scale dataset (called the Gange dataset) was earlier compiled based on weekly fruiting records across 1424 locations within a 30-km radius (2828 km²) of Salisbury, Wiltshire, United Kingdom (Fig. 1). Now part of the UK national dataset, it was separated from that data for use as a local dataset (those records then removed from the national and intermediate data to avoid duplication). Fresh fruit bodies were recorded each week of every

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