Received: 30 August 2021 | Accepted: 19 May 2022

DOI: 10.1111/icad.12593

ORIGINAL ARTICLE

Insect Conservation and Diversity

Royal Entomological Society

Does a short Pollard walk transect capture butterfly and bee diversity? A test to inform pollinator monitoring and community science initiatives

Leonardo Viliani[1] | Simona Bonelli[1] | Monica Vercelli[2] | David B. Roy[3] | Federico Riva[4,5]

[1]Zoolab, Dipartimento di Scienze della Vita e Biologia dei Sistemi, University of Turin, Turin, Italy

[2]Biodiversa, Turin, Italy

[3]UK Centre for Ecology & Hydrology, Benson Lane, Wallingford, Oxfordshire, UK

[4]Geomatics and Landscape Ecology Laboratory, Department of Biology, Carleton University, Ottawa, Canada

[5]Insectarium, Montreal Space for Life, Montreal, Montreal, Quebec, Canada

Correspondence
Leonardo Viliani, Zoolab, Dipartimento di Scienze della Vita e Biologia dei Sistemi, University of Turin, Via Accademia Albertina 13, 10123 Turin, Italy.
Email: vilianileonardo45@gmail.com

Editor: Laurence Packer
Associate Editor: Michael Garratt

Abstract

1. Widespread declines in insects will threaten ecosystem functioning and services. Nevertheless, a lack of data hinders assessments of population and biodiversity trends for many insect groups and thus effective conservation actions. Implementing cost-effective, unbiased, and accurate monitoring programmes targeting different groups across a larger geographical range has therefore become a key conservation priority.
2. We evaluated a sampling protocol designed for community science initiatives targeting butterflies and bees. Specifically, we tested how well a short (200-m long) version of traditional Pollard walk transects, designed to be accessible for large numbers of community scientists, captures changes in alpha and beta diversity of these two pollinator groups.
3. We used resampling methods to simulate and assess scenarios varying in sampling intensity and frequency. We found that alpha and beta diversity of butterflies and bees were estimated at similar accuracies across different scenarios, which suggests that even short transects can provide useful information on diversity patterns for both taxa. However, common sampling frequencies resulted in low accuracies (e.g. one sample every 10 days finds on average ~50% of the species present at a site).
4. We discuss our results in the context of developing large scale, structured monitoring systems for multiple insect taxa, and how information on biodiversity patterns can inform the expansion of monitoring schemes. We explain why, moving forward, even rapid sampling designs similar to the approach tested here will be useful given a higher potential to involve community scientists, data integration techniques, and the opportunities to sample under-represented habitat types

KEYWORDS
alpha diversity, beta diversity, citizen science, community science, EU pollinators initiative, monitoring, sampling design

INTRODUCTION

Global declines in biodiversity are threatening the functioning of ecosystems and their provision of ecosystem services (Ceballos et al., 2017; Wagner et al., 2021). For instance, over 70% of wildflower species and crops depend on insect pollination (Klein et al., 2007; Ollerton et al., 2011), and the role of different taxa in providing ecosystem services is often synergistic (Cusser et al., 2021; Winfree et al., 2018). Global, regional, and national policy initiatives (e.g. Potts et al., 2021; Wagner et al., 2021) aim to address growing concerns regarding a potential 'insectageddon' (Thomas et al., 2019). For instance, the Convention on Biological Diversity Post-2020 Biodiversity Framework will be characterised, among others, by the EU Pollinators Initiative in Europe and by the Agriculture Improvement Act in the United States (Wagner et al., 2021). Nevertheless, effective implementations of these and analogous policies require detailed information on insect conservation status that are, to date, often lacking (Thomas et al., 2019; Wagner et al., 2021).

Understanding changes in pollinator biodiversity requires extensive data in space and time that are rarely available for insects (Didham et al., 2020; Thomas et al., 2019; Wagner et al., 2021). Not only long-term data on distribution and abundance are rare for insects, but also the natural history of these taxa precludes more complex longitudinal assessments (e.g. typically fluctuating populations, different life forms, high diversity, small body size and thus generally low detectability; Didham et al., 2020). Therefore, while biodiversity loss has been well documented in vertebrates (Ceballos et al., 2017), trends in insect populations have been much harder to evaluate (Didham et al., 2020; Wagner et al., 2021). Systematic monitoring programmes have provided us with reliable information to estimate trends in abundance and distribution of insects (Crossley et al., 2020; MacGregor et al., 2019; Powney et al., 2019), but such programmes are usually limited to one group and a few areas (Buckland & Johnston, 2017). Indeed, systematic monitoring schemes provide just a rough picture of biodiversity trends in space and time. This is due to many reasons, including site selection bias (diverse sites overrepresented in monitoring programmes; Buckland & Johnston, 2017), spatial coverage bias (e.g. most sites sampled near roads; Didham et al., 2020), and imperfect detection (distribution and abundance of rare and/or hard to detect species often underestimated; Riva et al., 2018, Riva et al., 2020). Following these considerations, expanding ongoing monitoring programmes to cover larger spatial extents, at a higher spatial resolution, and for more taxa seems necessary to resolve when, where, and why we are experiencing insect declines. Because resources available for biodiversity conservation are limited, leveraging the infrastructures of well-established monitoring programmes to assess more insect groups could aid in optimising conservation efforts. Yet, trade-offs between sampling strategies and the ability to detect different taxa and their change must be carefully considered (Roy et al., 2007), particularly before expanding ongoing initiatives that were originally designed for a specific insect group. In other words, while leveraging ongoing initiatives would foster resource optimisation, how different sampling strategies translate to different taxa remains poorly understood (Didham et al., 2020; O'Connor et al., 2019).

Here, we evaluated how an adaptation of the traditional 'Pollard walk' monitoring protocol ('PW'; Pollard, 1977) would perform in sampling butterflies (Lepidoptera: Papilionoidea) and bees (Hymenoptera: Apoidea). Specifically, our objective was assessing whether a short (200-m long) version of traditional butterfly transects ('PW'; Pollard, 1977) is efficient in capturing biodiversity metrics of butterflies and bees, and thus its potential for integration in large-scale monitoring scheme. We focused on these two groups because they are important pollinators (Cusser et al., 2021; Winfree et al., 2018). We measured alpha and beta diversity patterns (Whittaker, 1962) using incidence data, because they provide the first and most intuitive baseline as a precursor of monitoring trends in biodiversity in space and time. Assessing alpha and beta diversity (rather than, e.g. more specific patterns in the abundance of different species) is often a first step in characterising new sites when establishing and expanding a monitoring programme. We chose a short transect length because an increasing number of volunteers contribute data to community science programmes (Theobald et al., 2015), and a short sampling protocol could be appealing to many community scientists, potentially resulting in more contributions, and thus in a larger spatial coverage (Freitag et al., 2016; Roy et al., 2007). As a comparison, classic butterfly monitoring designs take approximately three to four times longer than the approach tested here (Sevilleja et al., 2019), including for bees (Nielsen et al., 2011).

We assessed (i) whether the same sampling design (i.e. 200-m PW sampled in 15 min) provides different levels of accuracy in estimating alpha and beta diversity of butterflies and bees; and (ii) how accurate estimates of alpha and beta diversity are at increasing sampling effort (number and frequency of PW at a site). We extensively sampled five sites in a 20-day period ($n = 122$ transects; mean number of PW per site = 24.4; SD = 2.07) and used all samples to characterise a 'best estimate' of the diversity of our sites. We then randomly resampled the 122 transects following a virtual experimental design with eight factorial scenarios (one or two transects sampled in periods of 20, 10, 7 or 5 days). By comparing diversity metrics calculated on the best estimate versus those measured using random subsets of the dataset, we evaluated how well more common sampling designs (i.e. from 1 to 8 visits of each site in 20 days) describe the diversity of our study area.

METHODS

We summarise in Figure 1 the workflow of our study and describe it in more detail in the following sections and in Appendix S1.

Study area and sampling design

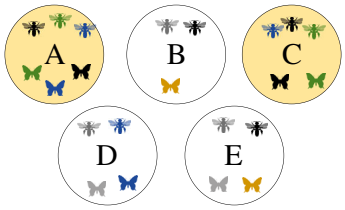
Data were collected within La Mandria Regional Park (ZSC IT1110079; permit 0002499), a protected area in the province of

Insect Conservation and Diversity

1

We tested a 200-m long transect, walked twice for 15 minutes (butterflies and bees), within recommended sampling conditions

2



We sampled two semi-natural (A, C) and three managed (B, D, E) meadows between July 13th to 31st 2020 (n = 122 transects)

3

Transect ID	Site	Sampling day	Butterfly sp. 1	Butterfly Sp. 2	Bee Sp. 1	Bee Sp.2	Bee Sp. 3	…
1	A	1	0	1	1	1	1	…
2	B	1	1	0	0	0	1	…
…	..		…	…	…	…	…	…
122	E	20	1	0	0	1	0	…

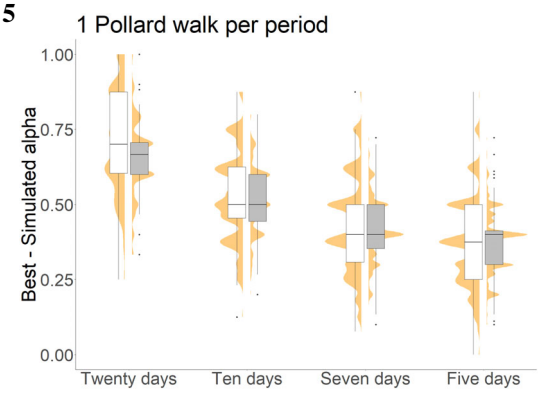
We compiled the full dataset containing 122 transects (rows), and 41 species (columns; 28 butterfly and 13 bee taxa)

4

Transect ID	Site	Sampling day	Butterfly sp. 1	Butterfly Sp. 2	Bee Sp. 1	Bee Sp.2	Bee Sp. 3	…
1	A	1	0	1	1	1	1	…
17	A	20	0	0	0	0	1	…

For each site, we randomly selected transects (rows) based on a factorial experimental design (sampling frequency × intensity: one or two Pollard walks every 5, 7, 10 or 20 days)

5



We compared alpha and beta diversity using simulated samples that represent realistic sampling frequencies and intensities

FIGURE 1 Summary of the study design

Turin, Piedmont, Italy (45.1631 N, 7.5739 E). Here, *Querco carpinetum* forests are intermixed with meadows at different stages of seral succession. We targeted five sites expected to differ in their diversity of bees and butterflies – two semi-natural meadows characterised by a prevalence of *Molinia caerulea* and *Lythrum salicaria* (A and C) and three meadows annually mowed (sites B, D, and E) – because we were interested in assessing whether the diversity of a site affects the efficacy of the evaluated sampling protocol. Sites were separated by forest strips and separated by at least 400 m, and we thus assume that we largely sampled independent assemblages.

We established in each site a 200-m long 'PW' transect (Pollard, 1977). Each transect was walked twice (back-and-forth) per sampling event, dedicating one direction and 15 min first to butterflies and then to bees. We sampled butterflies first because butterflies tended to be more reactive than bees to the presence of the observer (LV), and we aimed to reduce as much as possible the effects of the first 200-m walk on the second walk. At the time of data collection, LV was a Master's student who received a 4 days training session on butterfly and bee identification. We considered these conditions similar to the case of a volunteer approaching community science with minimal training. We sampled the five transects within recommended sampling conditions (temperatures >13°C with cloud cover <50%, and >17°C with cloud cover >50%, at wind speeds <5 Beaufort units, between 9.30 h and 17.00 h; Van Swaay et al., 2019) between 13 and 31 July 2020, randomising visit order, as many times as possible in 17 days (n = 122; mean number of PW per site = 24.4; SD = 2.07). We recorded in each

transect the presence of all butterfly species within an imaginary box of side 5 m (Sevilleja et al., 2019; Van Swaay et al., 2008), and the presence of bees visiting flowers within an imaginary box of side 4 m (D'Antoni et al., 2020). Recommended sampling conditions differ slightly between butterflies and bees, and for simplicity we used the slightly more stringent conditions recommended for butterflies (Figure 1; supplementary information S1.1). When identifying individuals in the field was not possible, we captured them with an entomological net and preserved them for later identification in the laboratory at species or morphospecies level (supplementary information S1.2). Six bee species for which identification was not possible even in the laboratory were classified at morphospecies level (supplementary information S1.2).

Diversity of butterflies and bees

We measured the alpha and beta diversities of butterflies and bees in the study area, that is, the diversity of each site and its variation across sites (Whittaker, 1962). We focus on incidence data, measuring alpha diversity as the number of species observed in each site, and beta diversity as the multi-site Sorensen dissimilarity index proposed by Baselga (2012). There are several ways to calculate alpha and beta diversity (Riva & Mammola, 2021); we chose an incidence-based approach because, in our experience, one of the first aspects appreciated when exploring a new site is the diversity of species within that site, and incidence data more easily convey this aspect. Furthermore, we chose a multi-site dissimilarity index because it provides a single measure of how different the sites in a set are in a range between 0 and 1 (which is preferable to describe a system in comparison to, e.g. averaging of pairwise dissimilarity metrics; Baselga, 2012). Note that alpha diversity is calculated at the site level, whereas the beta diversity presented here is calculated at the 'set of sites' level, summarising the degree to which the five sites differ in their species composition, with one value for five sites.

The values of alpha and beta diversities calculated on the full dataset, that is, on 122 PWs across the five sites, are assumed to be the best estimate of diversity patterns in our study system. We sampled our sites extensively, and for both butterflies and bees, coverage-based rarefaction (Chao & Jost, 2012) indicates coverage of ≥0.98 for all sites (see supplementary information S1.3). Given this high coverage, we will assume in our analysis that we sampled all species in each site and compare simulations representing more typical sampling designs (e.g. one visit per week, equalling three transects randomly selected in each site) to the best estimates of diversity calculated in these sites using the full dataset (122 transects). For consistency, we always refer to the diversity calculated on the full dataset as the 'best estimate' of the diversity of the site and to the diversity calculated from the resampled dataset as the 'simulated diversity'.

Simulations

We used resampling methods to simulate and assess how sampling effort, represented by intensity and frequency, affect our estimates of alpha and beta diversity of butterflies and bees. We followed a factorial experimental design, with eight virtual strata representing the combinations of four sampling frequencies and two sampling intensities. Here, we refer to 'intensity' as the number of PW sampled during a given sampling period, and to 'frequency' as the number of these sampling periods (and thus as their total temporal span, expressed as how often each site is sampled by dividing the study period in increasingly short subsets). Specifically, we divided the sampling window (13–31 July 2020) in 'one 20-day period', 'two 10-day periods', 'three 7-day periods', 'and four 5-day periods' (i.e. four frequencies), and randomly sampled either one or two PW per sampling period (i.e. two intensities). Note that we incorporated the frequency component in our analysis to assess whether diversity estimates responded to temporal trends, particularly in relation to species turnover in time. If the assumption of closure (i.e. that all species were available for sampling during all sampling periods) is valid, then differences between simulations that include the same number of PW should be minimal regardless of the sampling frequency, which is supported in our dataset (supplementary material S1.4, Figure S2). For instance, we found the same accuracy in estimating alpha and beta diversity in the two strata of one PW every 5 days versus two PW every 10 days.

We simulated 1000 random sub-samples per site for each of the eight experimental strata (frequency * intensity), removing duplicates. We retained for analysis any unique combination of the IDs associated with each PW (i.e. sampling site, date, and hour). The number of PW randomly selected in each simulated sample of each site varied from one to eight (lowest vs. highest intensities and frequencies); when the stratum included more than one PW, they were summed to create a virtual sample of the sites. Because the number of possible combinations varies depending on the frequency and intensity in different scenarios, we obtained a different number of unique random samples in each of the eight strata (e.g. ranging from 22 random samples for one PW every 20 days to 625 random samples per site for one PW every 5 days for the butterflies; supplementary information S1.5 and Table S3). Ultimately, for each stratum, we obtained multiple samples in each of the five sites, each representing one or more PW obtained at the frequency and intensity specific to the stratum. These samples were used to calculate alpha and beta diversity across multiple simulations and to compare the simulated values to the diversities calculated on our full dataset.

Analysis

Our inference is based on how the empirical distributions obtained in the simulated sub-samples compare to the best estimates of the diversity of our system. Specifically, we compared the 25th percentile, mean, and 75th percentile obtained from the differences computed between the best diversity estimates and each simulated diversity from our simulations, to obtain a value of similarity between sub-samples and best estimates. We assessed (i) alpha diversity, that is, the proportion of species missing when comparing simulated richness with its best estimate, and (ii) beta diversity, calculated as the absolute

value of the difference between the best estimate and the diversity obtained from the resampled dataset. Specifically, these variables were calculated as follows: (i) 1 – simulated richness/best estimate of richness and (ii) absolute value of the difference between best estimate and simulated multi-site similarity. In variable (i), the simulated alpha diversity calculated for each site is divided by the alpha diversity best estimate i, to compare sites differing in their species richness. Both variables tend to zero when samples approach our best estimate of the system state because (i) as more of the species at a site are observed, the ratio between simulated and best richness estimate tends to 1 and (ii) simulated estimates of beta diversity can be larger or smaller than the best beta diversity estimate, but converge towards the best value as intensity and frequency increase.

We observed the diversity metrics of butterflies and bees were more similar in variable (i) than in variable (ii). Therefore, we evaluated a third variable, that is, (iii) 1 – simulated beta diversity between five samples of the same site. This third model controls for the true beta diversity that we are attempting to estimate (i.e. a value of 1, because five samples from the same site should sample the same assemblage). We did so to assess whether the differences between butterflies and bees in variable (ii) depended on characteristics of the assemblages (e.g. if the species rarity distribution differed between the two groups) or depended on the different observed beta diversities between the two groups. If the difference between butterflies and bees in variable (ii) were due to characteristics of the assemblages, then we would expect a similar pattern between the two groups in variable (iii), with the two groups behaving differently. Conversely, if butterflies and bees follow the same trend in variable (iii), this would suggest that the difference observed in variable (ii) is not due to the characteristics of each assemblage, but rather to the fact that the five sites differ in their beta diversity for bees and butterflies. Basically, we treated five samples from the same site as five hypothetical sites with the same assemblages, testing whether differences in the assemblages of bees and butterflies affected how sampling effort and intensity affect beta diversity estimates. The true distributions of our simulations are shown in Figures 2 and 3.

RESULTS

We conducted 122 PW observing 28 species of butterflies and 13 of bees. The best estimates of species richness (alpha diversity) of butterflies and bees were, respectively, 18 and 11 in site 'A', 17 and 10 in site 'B', 15 and 13 in site 'C', 10 and 8 in site 'D', and 10 and 8 in site 'E'. Similarity across the five sites (beta diversity) was higher for bee than for butterfly assemblages, with 0.73 and 0.45 as best estimate values of multi-site similarity, respectively. Differences between best estimates and simulated values, between butterflies and bees, were smaller for alpha than for beta diversities (Figure 2). Trends in accuracy were similar for butterflies and bees for alpha diversity (Figure 2, top row), whereas simulated beta diversities were more similar to the best beta diversity estimates for butterflies than for bees (Figure 2, bottom row). Differences in the accuracy of beta diversity estimates between butterflies and bees largely disappeared when comparing five samples from the same site, effectively imposing the same beta diversity (Figure 3). Mean differences between best and simulated diversity estimates are presented in S1.5 and Table S4.

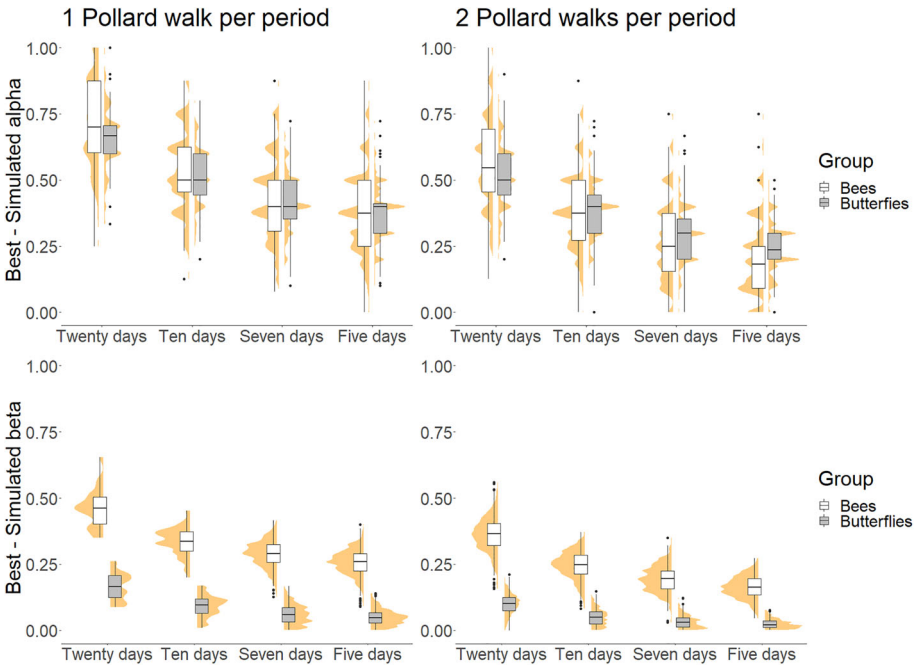


FIGURE 2 Differences between best and simulated alpha diversity estimates (top row) and beta diversity (bottom row) at different sampling frequencies and intensities. Increasing sampling effort, differences between the best estimate of metrics and simulated metrics tend to zero because samples approach the true state of the system.

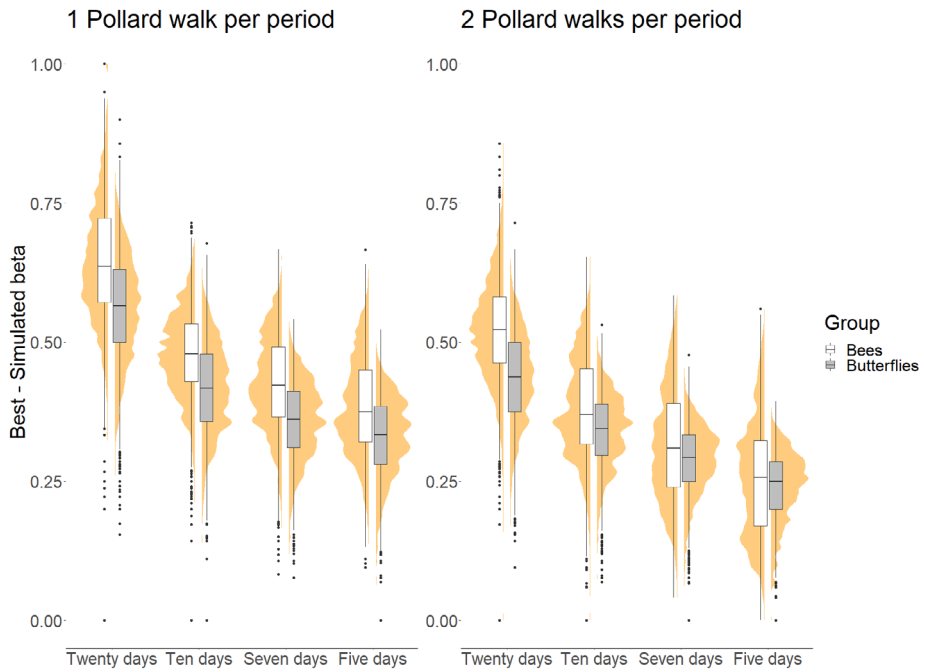


FIGURE 3 Similarity between five samples of the same site obtained at different sampling frequencies and intensities. This analysis suggests that the differences observed between estimates of beta diversity for butterflies and bees are due to the fact that bee communities were more similar in our sites (see Figure 2 and the methods).

Best estimates versus simulated alpha and beta diversities

The difference between best and simulated alpha diversity estimates for butterflies (Figure 2, top row) decreased from a mean value of 0.66 (25th PCTL: 0.60, 75th PCTL: 0.71) at the sampling frequency and intensity of 1 PW every 20 days, to a mean value of 0.24 (25th PCTL: 0.20, 75th PCTL: 0.30) at the sampling frequency and intensity of 2 PW every 5 days. For bees, alpha diversity decreased from a mean value of 0.71 (25th PCTL: 0.60, 75th PCTL: 0.88) to a mean value of 0.19 (25th PCTL: 0.09, 75th PCTL: 0.25). For instance, the common sampling design of one PW every week finds on average 60% of the species present at the sites for both pollinator groups, and half of the times between 50% and 65%. Doubling the sampling intensity (2 PW every week), the proportion of species rises to approximately 70% of the species present at a site for both butterflies and bees (supplementary information S1.5 and Table S4), with approximately half of the simulations ranging between 65 and 80 percentiles. On average, the two groups never differed across the eight scenarios by more than 0.05.

The predicted difference between best and simulated beta diversity estimates for butterflies (Figure 2, bottom row) decreased from a mean value of 0.17 (25th PCTL: 0.12, 75th PCTL: 0.21) at the lower sampling frequency and intensity of 1 PW every 20 days, to a mean value of 0.02 (25th PCTL: 0.01, 75th PCTL: 0.04) at the higher sampling frequency and intensity of 2 PW every 5 days. For bees, beta diversity decreased from a mean value of 0.46 (25th PCTL: 0.40, 75th PCTL: 0.50) to a mean value of 0.16 (25th PCTL: 0.13, 75th PCTL: 0.19), as sampling frequency and intensity increased. Butterflies and bees approximate the best estimates of beta diversity differently, with the simulated beta diversity of butterflies converging towards the best value more than was observed for bees. For instance, the common sampling design of one PW every week, finds on average a difference between best and simulated beta diversity of 0.06 for butterflies and 0.29 for bees (supplementary information S1.5 and Table S4), with approximately half of the simulations ranging between 0.03 and 0.09 for butterflies and 0.26 and 0.33 for bees.

Last, the difference between best and simulated similarity estimates between five samples of the same site (Figure 3) ranged from a mean value of 0.56 (25th PCTL: 0.50, 75th PCTL: 0.63) to a mean value of 0.24 (CI: 0.20–0.29) for butterflies and from a mean value of 0.64 (25th PCTL: 0.57, 75th PCTL: 0.72) to a mean value of 0.26 (25th PCTL: 0.17, 75th PCTL: 0.32) for bees, as sampling frequency and intensity increased. The two groups never differed across the eight scenarios by more than ~0.08 (Figure 3). On average, the difference between best and simulated similarity estimates found with the common sampling design of one PW every 7 days, was approximately 0.4 for both groups (supplementary information S1.5 and Table S4), with approximately half of the simulations ranging between 0.30 and 0.50.

DISCUSSION

Monitoring insect biodiversity across large spatial extents has become a conservation priority under the threat of catastrophic insect declines

(Thomas et al., 2019; Wagner et al., 2021). To this end, community science will be fundamental to collect large amounts of data (Theobald et al., 2015). Because the number of volunteers participating in a community science project is inversely related to the time required to participate (Freitag et al., 2016), evaluating trade-offs between fast sampling designs and their ability to accurately depict changes in biodiversity for multiple groups is key to optimise this sort of monitoring programme.

Here, we tested how a quick sampling protocol (i.e. a 200-m long transect walked twice in 30 min; Figure 1) performs in estimating key biodiversity metrics for butterflies and bees. We tested this approach to evaluate whether it can provide a rapid assessment of the diversity of sites and as a baseline for monitoring schemes. Our analysis demonstrates that this short PW approach provides similar, although relatively low, accuracies when estimating alpha (Figure 2) diversity of the two pollinator groups. For instance, one sample every 7 days finds on average ~60% of the species present at a site (Figure 2). This result was consistent for butterflies and bees, and independent of the number of species found at a site (supplementary information S1.5). Conversely, the accuracy of beta diversity estimates differed between the two groups (Figure 2). This difference in accuracy was not due to differences between bee and butterfly assemblages, for example, to the higher species richness and proportion of rare species in butterflies (supplementary information S1.2 and Figure S1), but rather to a higher similarity of bee assemblages across the five sites. Indeed, when comparing five samples of the same sites in both groups (i.e. when controlling for differences in beta diversity between the two groups), differences between bees and butterflies virtually disappeared, and the accuracy in estimating beta diversity decreased (compare Figures 2 and 3). Therefore, multi-site beta similarity seems more difficult to estimate when considering a set of similar sites, not when assessing bees rather than butterflies. Comparing beta diversity of different sets of sites with equal sampling effort likely holds biased estimates for both butterflies and bees, underestimating the similarity of sites that have more similar assemblages.

Overall, our analysis suggests that the short sampling design tested here, by itself, is unlikely to provide sufficient information to assess biodiversity across a set of sites, assuming traditional sampling frequencies. In turn, the tendency to detect only a subset of the species present at a site is likely to result in a general overestimation of species turnover either in space (as shown here) and/or in time. However, we found that results are similar for both butterflies and bees, suggesting that there is potential to leverage similar data for both taxa in the context of data integration within more intensive sampling protocols. In other words, the short sampling design tested here could be useful to complement initiatives that are already ongoing, from which one could borrow information on, for example, the detectability of species and their habitat association. This will allow increasing the accuracy of inferences made using the short design data (e.g. using hierarchical models; Isaac et al., 2020; Pagel et al., 2014). It has been already shown that sampling designs with shorter periods of sampling could aid in ameliorating the issue of poor representativeness for some habitats in monitoring systems (Roy et al., 2007) or provide robust estimates of butterfly population trends (Dennis et al., 2017). Here, we show that 200-m transects could also be effective in gathering information for bees. Butterfly monitoring programmes are well-developed worldwide (van Swaay et al., 2008), and the benefits and costs of including bees in these monitoring efforts should be evaluated quickly as we attempt to understand population declines in insects. Key considerations for a successful implementation of these approaches include the creation of many new sampling sites, of which at least some will target habitat types that have been historically underrepresented in monitoring schemes (i.e. not in protected areas or sites of conservation interest). Furthermore, this protocol can easily consider trade-offs between sampling design, variability between and within sites, rarity of target species, and the number of sites integrated in ongoing monitoring networks (Roy et al., 2007).

Most data collected via monitoring programmes assume constant detection within recommended sampling conditions and suffer from imperfect detection, which affects estimates of species occurrence and abundance, and therefore of beta diversity patterns (Riva et al., 2018, 2020). It is likely that longer transect lengths would, to some extent, increase the accuracy of biodiversity estimates due to a higher sampling effort. We did not assess this aspect in our analysis but suggest this to be an interesting question for future studies. We also note that our transects were conducted in five grasslands, each homogenous in habitat and surrounded by a forest matrix, and thus that our study does not evaluate whether short PW are efficient in describing heterogeneous sampling sites. It is a truism of ecology that increasing sampling effort – either via sampling intensity and/or frequency as evaluated here or by increasing transect length – improves accuracy in describing the community found at a specific site. Increased sampling effort can also increase the likelihood of detecting dispersing species and provide information on variation in biodiversity due to processes that occur across large spatial scales (e.g. landscape moderation of biodiversity; Tscharntke et al., 2012).

We recognised some caveats to our analyses. First, when performed across the entire summer season (vs. the 3 weeks sampled here), the accuracy of 200-m PW in describing patterns in alpha and beta diversity would likely increase, because some species persist in the adult stage for longer than the duration of this study. This would result in a higher probability of detection, and thus short PW might give more accurate alpha diversity estimates (at least in some cases). Yet, information obtained on the identity of species using a 200-m transect at traditional sampling frequencies would likely remain sparse, and the applications of the quick sampling design tested here for assessments of beta diversity patterns (i.e. changes in species in space and/or time) is especially limited due to the differences observed between the two taxa. Second, PW typically provide abundance data, which allow a deeper focus on, for example, species' relative abundance, population trends, and the calculation of diversity indices that account for the species-abundance distribution (e.g. Hill numbers; Riva & Mammola, 2021; Roswell et al., 2021). Here, we focus on incidence data to evaluate the accuracy of a short and simple sampling protocol in providing a first baseline for the monitoring of new, unknown sites. Indeed, patterns in species richness and

dissimilarity are perhaps the easiest and most intuitive aspects to characterise an expanding monitoring system based on community science. Communicating with and training community scientists is important, and the number of species at a site is a very simple concept that can aid in involving them in the process of collecting and analysing data, especially when more taxa are monitored at the same time. PW are only one of many sampling methods designed to monitor insect populations and biodiversity, and it is likely affected by the different level of qualification of operators in detecting species (O'Connor et al., 2019). Therefore, this potential bias must be considered when the protocol is implemented, and appropriate preventive measures should consequently be considered (e.g. brief training session for non-expert volunteers; a discussion of alternative approaches, and why PW are ideal for expanding current efforts in monitoring insect biodiversity, is provided in S1.6). Lastly, in our analyses, we distinguish sampling frequency and intensity as two different components of sampling efforts, with both components showing positive effect on the accuracy of diversity estimates (supplementary information S1.5 and Table S4). Nevertheless, our analysis does not resolve whether increasing sampling intensity might replace higher frequencies when seeking higher accuracies. We suggest that this trade-off is typically context dependent. For instance, in the Mediterranean area, the flight period of butterflies and bees lasts from April to September and capturing all species will require spreading a given number of samples across the entire time window. Conversely, a higher sampling intensity might be a plausible choice when the samples are conducted in system where all species of butterflies and bees fly for a temporal window of only a few months, such as high altitudes or latitudes.

CONCLUSIONS

Many conservation programmes will target pollinator insects in the coming decades (Wagner et al., 2021). For instance, monitoring butterflies and bees will be crucial to inform their conservation policy in Europe moving forward, particularly because IUCN Red Lists are here only available for these two groups (Bonelli et al., 2018). Furthermore, the European Pollinator Monitoring Scheme (Eu-PoMS) will integrate community science data and professional monitoring to assess the status of bees, butterflies, moths, and hoverflies across Europe (Potts et al., 2021). Therefore, assessing different sampling approaches for both groups is a priority for safeguarding pollinators across the European Union.

With some caveats, the integration of short PW targeting both butterflies and bees could contribute to large-scale monitoring programmes. A notable result is that patterns in beta and alpha diversity of butterflies seem to mirror those of bees, at least in our systems. If this holds true across many more system, one could leverage large amounts of data already available for butterflies to better understanding diversity patterns in bees. More tangibly, our study assessed how accurate diversity estimates are for these two pollinator groups for a sampling design that is already in use. For instance, the Austrian Butterfly Monitoring System integrates 50-m transects sampled by volunteers with more intensive samples from experts (Rüdisser et al., 2017), and a similar design was used in an Italian monitoring programme within agroecosystems (D'Antoni et al., 2020). These simple designs can provide general information on the habitat quality for pollinators at a site (Rüdisser et al., 2017). To the best our knowledge, this is a first attempt to evaluate in more detail how accurate similar approaches are, which is important given that uncertainty in baseline conditions hinder efforts to quantify the effectiveness of conservation actions (Buckland & Johnston, 2017).

In conclusion, there will be an increasing need for quick sampling designs in the context of insect monitoring programmes. While accuracy will inevitably be lower when collecting samples with quick designs such as the approach proposed here, methods to integrate this sort of data with more comprehensive datasets already exist (Isaac et al., 2020; Pagel et al., 2014). Perhaps an underestimated benefit of short sampling designs is the potential of involving more volunteers in community science programmes. Involving the public in conservation initiatives will be crucial not only to document and reverse insect declines but also to increase engagement, awareness, and education (Prudic et al., 2017). Designing quick monitoring protocols is also an important step towards inclusion and accessibility across a spectrum of physical abilities (Healey et al., 2002). Making citizen science accessible is not only a moral imperative but also a necessity amid the current sixth mass extinction (Ceballos et al., 2017). As the status of many pollinator insects remains highly uncertain across the planet (Thomas et al., 2019; Wagner et al., 2021), documenting where insects are and how their biodiversity is changing is crucial: Any additional datum will matter, and our results suggest that a shorter version of PW could contribute to understanding how biodiversity is changing in butterflies and bees.

AUTHOR CONTRIBUTIONS

All authors provided critical feedback and helped shape the research; Leonardo Viliani lead field work and conducted the analysis with assistance from Federico Rivad; Federico Rivad and Leonardo Viliani wrote the initial draft of the manuscript with critical feedback from Simona Bonelli, Monica Vercell, and David B. Roy.

ACKNOWLEDGEMENTS

The authors thank Christian Segreto for supporting field work activities. The authors thank Reto Schmucki and an anonymous reviewer for their helpful comments and helping to improve the manuscript.

Open Access Funding provided by Universita degli Studi di Torino within the CRUI-CARE Agreement.

CONFLICT OF INTEREST

The authors have no funding sources or conflict of interest to declare.

DATA AVAILABILITY STATEMENT

Data available on request from the authors.

REFERENCES

Baselga, A. (2012) The relationship between species replacement, dissimilarity derived from nestedness, and nestedness. *Global Ecology and Biogeography*, 21, 1232–1223.

Bonelli, S., Casacci, L.P., Barbero, F., Cerrato, C., Dapporto, L., Sbordoni, V. et al. (2018) The first red list of Italian butterflies. *Insect Conservation and Diversity*, 11(5), 506–521.

Buckland, S.T. & Johnston, A. (2017) Monitoring the biodiversity of regions: key principles and possible pitfalls. *Biological Conservation*, 214, 23–34.

Ceballos, G., Ehrlich, P.R. & Dirzo, R. (2017) Biological annihilation via the ongoing sixth mass extinction signaled by vertebrate population losses and declines. *Proceedings of the National Academy of Sciences of the United States of America*, 114(30), E6089–E6096.

Chao, A. & Jost, L. (2012) Coverage-based rarefaction and extrapolation: standardizing samples by completeness rather than size. *Ecology*, 93(12), 2533–2547.

Crossley, M.S., Meier, A.R., Baldwin, E.M., Berry, L.L., Crenshaw, L.C., Hartman, G.L. et al. (2020) No net insect abundance and diversity declines across US Long term ecological research sites. *Nature Ecology & Evolution*, 4, 1376–1368.

Cusser, S., Haddad, N.M. & Jha, S. (2021) Unexpected functional complementarity from non-bee pollinators enhances cotton yield. *Agriculture, Ecosystems and Environment*, 314, 107415.

D'Antoni, S., Bonelli, S., Gori, M., Macchio, S., Maggi, C., Nazzini, L. et al. (2020) La sperimentazione dell'efficacia delle Misure del Piano d'Azione Nazionale per l'uso sostenibile dei prodotti fitosanitari (PAN) per la tutela della biodiversità. ISPRA, Serie Rapporti, 330/2020.

Dennis, E.B., Morgan, B.J., Brereton, T.M., Roy, D.B. & Fox, R. (2017) Using citizen science butterfly counts to predict species population trends. *Conservation Biology*, 31(6), 1350–1361.

Didham, R.K., Basset, Y., Collins, C.M., Leather, S.R., Littlewood, N.A., Menz, M.H.M. et al. (2020) Interpreting insect declines: seven challenges and a way forward. *Insect Conservation and Diversity*, 13(2), 103–114.

Freitag, A., Meyer, R. & Whiteman, L. (2016) Correction: strategies employed by citizen science programs to increase the credibility of their data. *Citizen Science: Theory and Practice*, 1(2), 12.

Healey, M., Roberts, C., Jenkins, A. & Leach, J. (2002) Disabled students and fieldwork: towards inclusivity? *Planet*, 6(1), 24–26. https://doi.org/10.11120/plan.2002.00060024

Isaac, N.J.B., Jarzyna, M.A., Keil, P., Dambly, L.I., Boersch-Supan, P.H., Browning, E. et al. (2020) Data integration for large-scale models of species distributions. *Trends in Ecology & Evolution*, 35(1), 56–67.

Klein, A.M., Vaissiere, B.E., Cane, J.H., Steffan-Dewenter, I., Cunningham, S. A., Kremen, C. et al. (2007) Importance of pollinators in changing landscapes for world crops. *Proceedings of the Royal Society B: Biological Sciences*, 274(1608), 303–313.

MacGregor, C.J., Williams, J.H., Bell, J.R. & Thomas, C.D. (2019) Moth biomass has fluctuated over 50 years in Britain but lacks a clear trend. *Nature Ecology and Evolution*, 3, 1645–1649.

Nielsen, A., Steffan-Dewenter, I., Westphal, C., Messinger, O., Potts, S.G., Roberts, S.P. et al. (2011) Assessing bee species richness in two Mediterranean communities: importance of habitat type and sampling techniques. *Ecological Research*, 26(5), 969–983.

O'Connor, R.S., Kunin, W.E., Garratt, M.P.D., Potts, S.G., Roy, H.E., Andrews, C. et al. (2019) Monitoring insect pollinators and flower visitation: the effectiveness and feasibility of different survey methods. *Methods in Ecology and Evolution*, 10(12), 2129–2140.

Ollerton, J., Winfree, R. & Tarrant, S. (2011) How many flowering plants are pollinated by animals? *Oikos*, 120(3), 321–326.

Pagel, J., Anderson, B.J., O'Hara, R.B., Cramer, W., Fox, R., Jeltsch, F. et al. (2014) Quantifying range-wide variation in population trends from local abundance surveys and widespread opportunistic occurrence records. *Methods in Ecology and Evolution*, 5(8), 751–760.

Pollard, E. (1977) A method for assessing changes in the abundance of butterflies. *Biological Conservation*, 12(2), 115–134.

Potts, S.G., Dauber, J., Hochkirch, A., Oteman, B., Roy, D.B., Ahrné, K. et al. (2021) *Proposal for an EU pollinator monitoring scheme, EUR 30416 EN*. Ispra: Publications Office of the European Union. ISBN 978–92-76 23859–1.

Powney, G.D., Carvell, C., Edwards, M., Morris, R.K.A., Roy, H.E., Woodcock, B.A. et al. (2019) Widespread losses of pollinating insects in Britain. *Nature Communications*, 10(1), 1–6.

Prudic, K.L., McFarland, K.P., Oliver, J.C., Hutchinson, R.A., Long, E.C., Kerr, J.T. et al. (2017) eButterfly: leveraging massive online citizen science for butterfly consevation. *Insects*, 8(2), 1–12.

Riva, F., Acorn, J.H. & Nielsen, S.E. (2018) Distribution of cranberry blue butterflies (Agriades optilete) and their responses to forest disturbance from in situ oil sands and wildfires. *Diversity*, 10(4), 112.

Riva, F., Gentile, G., Bonelli, S., Acorn, J.H., Denes, F.V., Crosby, A.D. et al. (2020) Of detectability and camouflage: evaluating Pollard Walk rules using a common, cryptic butterfly. *Ecosphere*, 11(4), e03101.

Riva, F. & Mammola, S. (2021) The rarity facets of biodiversity: integrating zeta diversity and dark diversity to understand the nature of commonness and rarity. *Ecology and Evolution*, 11(20), 13912–13919 in Press.

Roswell, M., Dushoff, J. & Winfree, R. (2021) A conceptual guide to measuring species diversity. *Oikos*, 130(3), 321–338.

Roy, D.B., Rothery, P. & Brereton, T. (2007) Reduced-effort schemes for monitoring butterfly populations. *Journal of Applied Ecology*, 44(5), 993–1000.

Rüdisser, J., Tasser, E., Walde, J., Huemer, P., Lechner, K., Ortner, A. et al. (2017) Simplified and still meaningful: assessing butterfly habitat quality in grasslands with data collected by pupils. *Journal of Insect Conservation*, 21, 677–688.

Sevilleja, C. G., van Swaay, C. A. M., Bourn, N., Collins, S., Settele, J., Warren, M. S. et al. (2019). Butterfly transect counts: manual to monitor butterflies. *Report VS* 2019, 16.

Theobald, E.J., Ettinger, A.K., Burgess, H.K., DeBey, L.B., Schmidt, N.R., Froehlich, H.E. et al. (2015) Global change and local solutions: tapping the unrealized potential of citizen science for biodiversity research. *Biological Conservation*, 181, 236–244.

Thomas, C.D., Jones, T.H. & Hartley, S.E. (2019) "Insectageddon": a call for more robust data and rigorous analyses. *Global Change Biology*, 25(6), 1891–1892.

Tscharntke, T., Tylianakis, J.M., Rand, T.A., Didham, R.K., Fahrig, L., Batáry, P. et al. (2012) Landscape moderation of biodiversity patterns and processes-eight hypotheses. *Biological Reviews*, 87(3), 661–685.

Van Swaay, C.A.M., Dennis, E.B., Schmucki, R., Sevilleja, C.G., Balalaikins, M., Botham, M. et al. (2019) The EU butterfly indicator for grassland species: 1990–2017: technical report, Butterfly Conservation Europe, p. 23.

Van Swaay, C.A.M., Nowicki, P., Settele, J. & van Strien, A.J. (2008) Butterfly monitoring in Europe: methods, applications and perspectives. *Biodiversity and Conservation*, 17(14), 3455–3469.

Wagner, D.L., Grames, E.M., Forister, M.L., Berenbaum, M.R. & Stopak, D. (2021) Insect decline in the Anthropocene: death by a thousand cuts. *Proceedings of the National Academy of Sciences of the United States of America*, 118(2), 1–10.

Whittaker, R.H. (1962) Classification of natural communities. *The Botanical Review*, 28(1), 1–239.

Winfree, R., Reilly, J.R., Bartomeus, I., Cariveau, D.P., Williams, N.M. & Gibbs, J. (2018) Species turnover promotes the importance of bee diversity for crop pollination at regional scales. *Science*, 359(6377), 791–793.

SUPPORTING INFORMATION

Additional supporting information may be found in the online version of the article at the publisher's website.

Appendix S1: Supporting Information.

Figure S1: Species rarity of butterflies and bees.

Figure S2: Distribution of simulated alpha diversity (top row) and beta diversity (bottom row) obtained at different sampling frequencies but with the same intensity (four Pollard Walks).

Table S1: List of the taxa of butterflies observed in the study area and the number of Pollard Walks (tot 122) in which we found each taxon. Nomenclature according to the European checklist of Butterflies from Wiemers et al. 2018.

Table S2: List of the taxa of bees observed in the study area and the number of Pollard Walks (tot 122) in which we found each taxon. Nomenclature according to the European Red list of Bees from Michener 2007.

Table S3: Average number of unique random samples in each of the eight strata. Table S3 shows the mean (and the standard deviation) of the number of unique random samples between the five sites.

Table S4: Differences between best and simulated metrics estimates (top table shows the mean value (with 25th and 75th percentile) of the difference between best and simulated alpha and beta diversity estimates; the bottom part of the table shows the mean values (with 25th and 75th percentile) of the difference between best and simulated similarity estimates between five samples from the same sites).

How to cite this article: Viliani, L., Bonelli, S., Vercelli, M., Roy, D.B. & Riva, F. (2022) Does a short Pollard walk transect capture butterfly and bee diversity? A test to inform pollinator monitoring and community science initiatives. *Insect Conservation and Diversity*, 15(6), 645–654. Available from: https://doi.org/10.1111/icad.12593