Exposure time is an important variable in quantifying post-dispersal seed removal

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INTRODUCTION

Dylewski et al. (2020) presented a literature synthesis and concluded that intermediated-sized seeds had the highest proportion of seeds removed by small mammals. However, seeds in their dataset were exposed to predators for times ranging from half to 210 days (Figure 1a), and their analyses did not account for exposure time. They also failed to consider seed density and introduced biases by assigning removal data of middle times to species whose seeds were fully removed at the end of the experiments. Here, we re-analyse Dylewski et al. (2020)'s dataset, accounting for these potentially confounding factors.

We began by standardising seed removal data to 1 day of exposure to post-dispersal predators. We chose this time because it is commonly used in literature and captures the whole round of activities of diurnal and nocturnal animals. To determine the most appropriate model for seed removal through time, we extracted data for the 125 data points in Dylewski et al. (2020)'s dataset which presented time series for seed removal, and fitted them with linear and exponential decline models (following Blate et al., 1998; García-Castaño et al., 2006; Mittelbach & Gross, 1984). We found that an exponential decline in seed survival through time was the best or equal best fit for 87% of the time series (Appendix SI). Therefore, we standardised the dataset following this model.

In addition to failing to account for exposure time, Dylewski et al. (2020) used data from the mid-point time for species whose seeds were 100% removed at the end of the study (27% of the dataset; Appendix SI). The species to which this criterion was applied have 20-fold larger
seeds than do the other species (845.7 mg vs. 42.6 mg; Figure 2). That is, taking data from mid-point rather than the end-point of the experiment disproportionately reduced the apparent removal for large-seeded species, potentially contributing to the hump-shaped relationship in Dylewski et al. (2020). Our time-corrected dataset appropriately deals with these species, using the corresponding times for the mid-point data.

Another factor that might affect seed removal but was not considered in Dylewski et al. (2020) is seed density. In the dataset, small seeds tended to be presented at a higher number per depot than large seeds (Appendix SI). This is a potential source of bias, as seed density can affect seed removal (Wang, 2020). We, therefore, included a covariate for seed density in our analysis. We also corrected a few minor errors in the authors’ original dataset (Appendix SI).

Analysis of the standardised and corrected dataset showed that the effect of seed mass on removal remained significant, but became very shallow ($p = 0.025$; Figure 1b). The curve peak dropped from 60% removal in Dylewski et al. (2020) to 17% in our corrected analysis. The relationship between seed mass and post-dispersal seed removal becomes so weak after accounting for time that it is likely of limited biological significance, consistent with the finding of Moles et al. (2003).

Finally, we note that although Dylewski et al. (2020)'s synthesis purported to analyse seed removal by small mammals, their dataset included several studies where seeds were exposed not just to small mammals, but
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also to other predator guilds (e.g. birds), or even to the full suite of predators in the community (e.g. Boman & Casper, 1995; Cintra, 1997; Hulme, 1997; Blate et al., 1998; Edwards & Crawley, 1999).

While we appreciate the efforts of Dylewski et al. (2020) in their attempts to quantify a broad-scale pattern in post-dispersal seed removal by small mammals, our re-analysis has demonstrated that failure to appropriately resolve the presence of confounding variables and a lack of consistency can result in inaccurate findings in studies based on data compiled from the literature (Haddaway et al., 2020). Literature syntheses can be very powerful, but authors must apply consistent and unbiased data selection criteria and make efforts to standardise the data included in their studies. For this, we also need the authors of field studies to provide full details of their methods in addition to the raw data.

Key functional traits, such as seed mass, plant height and specific leaf area, can be easily measured and play an indispensable role in plant ecology studies (Perez-Harguindeguy et al., 2016). However, it is unrealistic to expect a single trait to explain the diverse spectrum of plant life strategies or to predict complex ecological processes (Paine et al., 2015). For seed predation, seed mass could be just one of the many factors in determining removal and fate. Other potential contributing factors likely include other seed traits (such as physical and chemical defences; Wang et al., 2018), the identities and traits of potential predators, and the scenarios in which the seeds are exposed to potential predators. In short, while single plant traits are incredibly useful in ecology, we must keep our expectations reasonable.

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AUTHORSHIP
S-CC initiated the idea, analysed the data and lead the writing. BW and ATM substantially participated in the discussion and writing.

PEER REVIEW
The peer review history for this article is available at https://publons.com/publon/10.1111/ele.13744.

OPEN RESEARCH BADGES
This article has earned an Open Data badge for making publicly available the digitally-shareable data necessary to reproduce the reported results. The data is available at: https://github.com/Si-Chong/Exposure_time

DATA AVAILABILITY STATEMENT
No new data were used. Appendix S1, R script, supplementary data and associated details are available on GitHub at https://github.com/Si-Chong/Exposure_time

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FIGURE 2 In Dylewski et al. (2020), species whose seeds reached 100% removal by the last or longest time point (end-point) of the experiment were not recorded as 100% removed, but rather had taken from the middle trial or median time point (mid-point). This is a potential source of bias, as the species for which the mid-point data were used have significantly larger seed mass than do species for which removal data were taken from the end-point ($p < 0.0001$). Dots and bars within violin plots show the mean and the standard deviations of each group, respectively. Values in parentheses stand for numbers of data points.
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SUPPORTING INFORMATION
Additional supporting information may be found online in the Supporting Information section.

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