Original Articles

Higher-taxon and functional group responses of ant and bird assemblages to livestock grazing: A test of an explicit surrogate concept

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ABSTRACT

Biodiversity monitoring programs are routinely established to quantify changes in biotic communities in response to land management. Surrogacy is implicitly used in many such monitoring programs whereby the measurement of a component of biodiversity is used to infer responses of broader biodiversity. Yet rarely is this surrogacy validated by demonstrating that measured variables and the target variable of interest have matching responses to management treatments. Here we examined the responses of higher-taxon and functional groupings of ants and birds (our surrogate variables) two years after the implementation of experimental livestock grazing treatments, and compared these with the responses of total ant and bird species richness (our target variables) to the same treatments. We found significant and strong correlations between surrogate and target variables, but this did not predict corresponding similar response to treatments. For ants, we found that the genus *Monomorium* had a negative response to the grazing exclusion treatment, but there was no matching response of species richness, and so no surrogacy was identified. For birds, total species richness had a weak positive response to spring/summer grazing exclusion, and the abundance of honeyeaters (Meliphagidae) showed a similar positive response, suggesting surrogacy. Our study highlights that correlations among variables do not necessarily lead to surrogacy, and indeed that different sub-components of biotic assemblages can respond in ways that contrast with overall species richness. Careful assessment of the matched responses of surrogate and target variables to management can provide a simple and robust way to critically assess biodiversity surrogacy.

1. Introduction

Biodiversity monitoring programs are routinely established to quantify changes in biotic communities in response to different land management practices (Lindenmayer and Likens, 2010; Vackar et al., 2012). Acquiring and analysing monitoring data requires considerable time and effort. Using surrogate variables to make inferences about other unmeasured variables of interest is one approach to reducing monitoring costs (Caro, 2010; Lindenmayer and Likens, 2011). This can be, for example, in the form of higher-taxon surrogacy, where patterns occurring at a higher taxonomic level, such as family or genus, are used to infer patterns of species-level responses (Williams and Gaston, 1994; Brennan et al., 2006; Driessen and Kirkpatrick, 2017). Functional surrogacy can also be used, whereby individuals are grouped by their shared ecological attributes, such as diet or body size, and used to infer broader assemblage responses to the environment (Gollan et al., 2010;

Bhusal et al., 2014; Barton and Moir, 2015). Each of these approaches can offer potentially simple, cheap, and ecologically meaningful ways to quantify broader biotic patterns, but nevertheless require proper evaluation before surrogacy can be attributed.

Biodiversity surrogates can be used to provide information about the response of biota to management interventions aimed at conserving broader biodiversity (Lindenmayer et al., 2002; Gonzalez et al., 2013; Barton and Moir, 2015). For example, increased abundance of a particular species following altered land management might be used to infer a broader community response to management intervention (Gollan et al., 2010; Barton and Moir, 2015). However, it is important to distinguish between studies that identify a simple correlation between a target and its surrogate from those that show matched responses of these variables to a shared treatment. This difference is essential to moving beyond establishing an association and towards establishing surrogacy within a particular context (Barton et al., 2015; Pierson et al.,
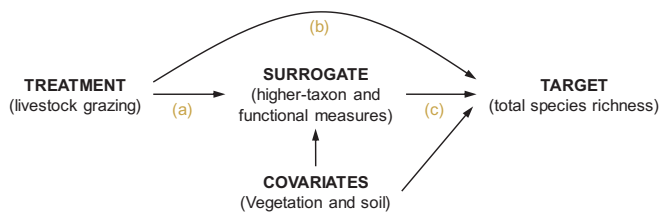
Fig. 1. A surrogate concept that incorporates the relationships between treatment, surrogate, and target, as well as covariates. (a) We quantified the effects of the grazing treatments on a range of candidate surrogate variables, as well as (b) treatment effects of the target for both bird and ant assemblages. Environmental covariates were also considered in separate models. (c) We then examined the correlations between surrogate and target variables to see if this gave any insight into which surrogate and target responses to the treatment were similar.

2016). The additional step of identifying matched responses is needed because target and surrogate variables may not necessarily respond to an intervention in the same way, despite themselves being correlated, yet few studies acknowledge or empirically test this (Pierson et al., 2016).

In this study, we used an explicit surrogate concept to guide our evaluation of surrogates of biodiversity responses to livestock grazing treatments (Fig. 1). This concept is adapted from the medical sciences (Atkinson et al., 2001; Barton et al., 2015) and shows how a surrogate variable is placed between a treatment and its target, while accounting for covariates. Monitoring of different taxa was subsequently undertaken to assess the effects of grazing treatments on biodiversity, and this provides the basis of our current study. We examined the responses of a suite of higher-taxon and functional groupings of ants and birds (our surrogate variables) and see if any match the response of overall species richness (our target variables) to the livestock grazing treatments. Our questions were: (1) Which surrogate and target variables respond to the grazing treatments? (2) Which surrogate and target variables are correlated? (3) Which variables are both strongly correlated *and* show similar responses to the grazing treatments? These analyses provide the basis for an objective assessment of matched responses of surrogate and target variables to a common treatment and are hence a simple, but important, test of surrogate validity.

2. Methods

2.1. Study area and design

Our study was conducted in south-eastern Australia, with sites spanning an area approximately 100 km east to west, and 150 km north to south (Fig. S1). Within this area, we established 78 sites, each of 40 × 200 m (0.8 ha), across 29 different farms from mid-2010. All sites were located in temperate grassy woodland, which is characterised by a patchy distribution of *Eucalyptus* trees in grassland largely dominated by native perennials (Lindenmayer et al., 2012; Barton et al., 2016). Grassy woodland was once widespread in south-eastern Australia, but has been subject to large-scale clearing or modification due to agricultural practices including grazing (McIntyre et al., 2014).

We grouped the 29 farms into three blocks, each representing a historical 'business as usual' grazing practice of either continuous grazing, short-term rotational grazing (conversion to rotational grazing practice within the last five years), or long-term rotational grazing (conversion to rotational grazing practice for greater than 10 years). Farms with continuous grazing allowed livestock access to sites all year round, whereas farms with rotational grazing typically rotate higher numbers of livestock through sites, but for a limited duration.

Sites were assigned within in each farm to one of three different treatments: (i) all-year exclusion, (ii) spring/summer exclusion, and (iii) 'business as usual'. All-year exclusion sites had little or no grazing

by livestock in the year prior to our study. Spring/summer exclusion sites were not grazed during the six month period of spring and summer prior to our study. The 'business as usual' sites continued grazing in line with the usual grazing practices of the farm (*viz.* continuous, short-term rotational, long-term rotational). We documented data on livestock numbers and duration of grazing events for each site as reported by landholders in the 12 months prior to this study, and provide grazing summary statistics in Table S1.

2.2. Soil and vegetation covariates

Soil and vegetation surveys were conducted on every site during January and February 2012, approximately two years after the grazing treatments commenced. We established two 20 × 50 m quadrats at 0–50 m and 150–200 m along the centre line of each site (Fig. S1). Within each quadrat, we recorded the number of tree stems > 10 cm in diameter. A 50 m transect was located down the centre of each plot with biometric step-count measurements (Gibbons et al., 2008) taken every metre to assess percentage cover of ground layer native and exotic grass cover, and leaf litter cover. In addition, ground-layer plant biomass was assessed using a rising plate pasture meter to determine average height of ground cover present (Filip's Manual Folding Plate Meter, Jenquip, New Zealand (Correll et al., 2003). Vegetation measures were averaged across the two quadrats to give one measure per site. We also collected soil cores of 10 cm diameter × 5 cm depth every 16.5 m (n = 12) along the 200-m centre transect of each site, following the careful removal of any surface plant and litter biomass present. We then pooled soil samples 1–4, 5–8, and 9–12 for each site to provide three bulked samples per site (see Fig. S1). We air dried samples at 35 °C for 48 h prior to processing, then crushed the dried samples and passed each through a 2-mm sieve. We quantified total carbon and nitrogen (%) in each sample using Dumas combustion analysis (Vario Max, Elementar, Germany) (Matejovic, 1997), and expressed results as a C:N ratio. We determined total phosphorus (%) using the Kjeldahl method (Diamond, 2006). All soil measures were averaged to give one value per site.

2.3. Ant sampling

We sampled ground-active ants using pitfall traps (250 ml plastic jars) dug in flush with the ground surface and half-filled with a 50% polyethylene glycol solution. Three pitfall traps were deployed in each site for a two-week period in December 2011 (Fig. S1), with ants removed and pooled to give one sample per site. Our sampling approach deliberately prioritised spatial replication across many sites over sampling intensity within sites, resulting in standardised bias towards the more active species of the ant community.

Specimens were sorted and identified to subfamily, genus, and species (or morphospecies) by a taxonomic specialist and assigned a functional group based on their genus membership using the classification scheme described by Andersen (1995a, 1997) (see Table S3). We used only the four most abundant functional groups in further analysis: the Dominant Dolichoderinae, Generalist Myrmecinae, Opportunists, and Hot Climate Specialists. Ant functional groups were first described as a way to improve prediction and generalisation of ant species responses to disturbance, and have been used previously to examine responses to livestock grazing (Hoffmann, 2010; Barton et al., 2016). The list of ant species and their functional groupings is given in Table S3.

2.4. Bird surveys

Birds were surveyed during spring of 2011 within a 25 m radius at both ends of every site. Surveys consisted of five-minute point counts with two repeat visits by highly skilled field staff. All bird species seen or heard during the four counts were pooled to give one sample per site. There were sufficient data for two families of birds (Acanthizidae and