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High parasitoid diversity in remnant natural vegetation, but limited spillover into the agricultural matrix in South African vineyard agroecosystems

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ABSTRACT

The maintenance of remnant natural vegetation in agricultural landscapes is an important component of conservation programmes that promote farmland sustainability. Demonstrating the biodiversity value of remnant vegetation can support conservation initiatives in production landscapes. We assessed the diversity and assemblage structure of hymenopteran parasitoids in fragments of native scrubland (fynbos) within vineyard landscapes in the Cape Floristic Region of South Africa. We also aimed to detect positive effects of adjacent fynbos on vineyard parasitoids, such as elevated diversity at vineyard edges adjoining fynbos or evidence of parasitoid spillover into vineyards. Fynbos remnants had significantly higher parasitoid abundance and richness than neighboring vineyards, and supported assemblages distinct from those within vineyards. Parasitoid diversity in vineyards was not influenced by distance to remnant vegetation. Additionally, evidence for spillover was limited, as there were abrupt changes in assemblage structure at fynbos/vineyard boundaries. Surrounding vineyards therefore seem to have an isolating effect on parasitoids in remnants. This emphasises the need to increase the permeability of the vineyard matrix. Yet, our results show that remnants are important for retaining parasitoid diversity and provide refugia for certain species within the disturbed agricultural environment. Approaches that combine natural remnant conservation with arthropod-friendly activities in vineyards would be an effective way to support diverse and functional parasitoid assemblages at the landscape scale. Conservation of this diversity will be crucial for maintaining long-term ecological resilience in agricultural landscapes.

1. Introduction

Agricultural intensification and expansion is resulting in widespread biodiversity loss (Benton et al., 2003; Lindenmayer et al., 2013). Farmland conservation programs aim at improving the value of agricultural landscapes for biodiversity, and a key conservation strategy of these programs is the retention of remnant natural vegetation (Green et al., 2005; Kleijn et al., 2011; Phalan et al., 2011). The maintenance of remnants is considered to be one of the most effective measures for sustaining arthropod diversity in farmland (Attwood et al., 2008; Tscharntke et al., 2008). It allows native arthropods to persist in the transformed landscape by providing undisturbed refugia and supplementary resources within the agricultural mosaic (Benton et al., 2003; Landis et al., 2000; Duelli and Obrist, 2003).

Arthropod natural enemies are especially reliant on these natural habitats, as they need specific resources that are scarce in cultivated areas, such as overwintering sites, adult food sources and alternative hosts and prey (Altieri et al., 1993; Gurr et al., 2003; Landis et al., 2000). Remnant vegetation can therefore act as reservoirs for natural enemy diversity (Bianchi et al., 2006). They can also function as sources of natural enemy migration into cultivated fields through spillover across habitat edges (Blitzer et al., 2012; Tscharntke et al., 2005b), thereby enhancing enemy diversity throughout the landscape (Bianchi et al., 2006). The role of natural habitats in maintaining this diversity may have important implications for agroecosystem processes and services provided by natural enemies. For example, high enemy diversity in farmland has been shown to contribute to increased regulation of crop pests (Cardinale et al., 2003; Letourneau et al., 2009; Tscharntke et al., 2008). Conserving high species richness in a system also ensures that functional redundancy is retained, which can increase resilience in the agroecosystem by buffering against variability in ecological functioning (Tscharntke et al., 2005a, 2005b).

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However, there is a lack of information on the biodiversity value of most farmland habitat types, or on their interactions with the surrounding landscape (Bianchi et al., 2008; Landis et al., 2000). The effects of non-crop vegetation on biodiversity can vary between landscapes (Tscharntke et al., 2005b) and organisms (Chaplin-Kramer et al., 2011; Steffan-Dewenter, 2003), suggesting that further assessment is needed to more clearly understand this relationship (Tscharntke et al., 2005b). Additionally, information on how remnants influence diversity in the surrounding matrix will provide insight into their conservation significance in their local landscape context (Cunningham et al., 2013).

In the Cape Floristic Region (CFR) of South Africa, an area of exceptional biodiversity and endemism (Mittermeier et al., 2004), vineyard expansion is a major threat to the remaining natural vegetation in agricultural areas (Fairbanks et al., 2004; Rouget et al., 2003). Fortunately, over 140 000 ha of natural habitat is collectively protected on CFR wine farms through voluntary set-asides implemented as part of a partnership between the South African wine industry and the conservation sector (Viers et al., 2013; WWF, 2014). Conservation stewardship on wine farms contributes significantly to the protection of critical habitats and native plant species (Von Hase et al., 2010). However, few arthropod assessments have been done in these remnants, but earlier studies show that the diversity of beneficial arthropods in remnants is high (Gaigher and Samways, 2014; Kehinde and Samways, 2012) and that certain vineyard species are influenced by proximity to natural vegetation (Kehinde and Samways, 2012). Further assessment of the biodiversity value of remnant vegetation is an important step in promoting their conservation (Jackson et al., 2007; Kleijn and Sutherland, 2003; Viers et al., 2013) and can justify existing set-aside programmes.

This study focused on the value of natural scrubland (fynbos) remnants for maintaining a high diversity of hymenopteran parasitoids, an important natural enemy group, within vineyard landscapes in the CFR. It also provided an assessment of parasitoid spillover from fynbos remnants into vineyards. We assessed how biotope (fynbos or vineyard) and distance from habitat edges influence parasitoid abundance, richness and assemblage structure. To determine whether there are between-taxon differences in response to these landscape features, we also examined family-level distribution patterns. Assessing these distribution patterns allowed us to evaluate the importance of natural remnants as a source of natural enemy diversity within vineyard landscapes.

2. Methods

2.1. Study area and design

Surveys were undertaken on six wine farms (4–40 km apart) in the CFR during January 2014 (Fig. A1). Each farm had vineyards adjoining undisturbed fynbos vegetation. Three of the fynbos areas were not isolated fragments, but were connected to reserve areas (Figs. A1A, A1B and A1F). 150 m transects were laid out perpendicular to vineyard-fynbos edges, extending 50 m into the fynbos and 100 m into vineyards. Transects were placed where they could extend for the required distance without interference from surrounding landscape elements. A total of ten transects were done, which was limited by the number of farms in the area that had fynbos directly adjacent to vineyards. Where more than one transect occurred on a single farm, they were separated by at least 300 m. Samples were taken along the transects at 10 m and 50 m from the edge in fynbos areas (referred to as 10 N and 50 N respectively) and 10 m, 50 m and 100 m from the edge in vineyards (10V, 50V and 100V respectively) (Fig. A1). To include isolated locations, additional samples were taken at seven locations in vineyards that were at least 200 m from any non-vineyard habitats (200V).

2.2. Data collection

Vacuum samples were taken with a fuel powered leaf blower (Stihl SH 86), set to vacuum mode with a fine mesh bag attached to the 10 cm diameter nozzle. This technique has been shown to be suitable for collecting a high abundance and variety of parasitoids in the fynbos (R. Gaigher, unpublished data). At each sampling point, the vacuum nozzle was inserted into the vegetation 50 times, which included vines and cover crops at vineyard sites. Samples were transferred to plastic storage bags and kept at −15 °C before laboratory processing. Parasitoids were sorted to morphospecies and identified to family level using the keys in Goulet and Huber (1993), Prinsloo and Eardley (2012) and Prinsloo (1980). Taxonomy of parasitoids in this area is not sufficiently advanced to enable species-level identifications. However, the morphospecies approach provided valuable information at the species level. At each sampling point, we recorded the following environmental variables within a 1 m × 1 m quadrat: plant species richness, percentage plant cover, average plant height, percentage litter cover and number of flowering plant species.

2.3. Statistical analyses

Generalized linear mixed models (GLMMs) were used to determine how parasitoid abundance, species richness and family richness varied with environmental variables (Bolker et al., 2009). Data fitted a Poisson distribution when a likelihood ratio test was performed. Therefore, a GLMM fit by Laplace approximation and with Poisson error distribution (log-link function) was used (Bolker et al., 2009). Where Pearson's *R*-values identified correlated variables, only one was included in the models. Akaike's Information Criterion was used to select the best model from all possible combinations of remaining variables (Johnson and Omland, 2004). Where several models were equally good, the optimal model was selected based on ecological knowledge. To account for the locality-based nature of the sampling design, farm location was included as a random effect (Bolker et al., 2009). Interaction terms were excluded because it would have made the model too complex for the given sample size. χ^2 statistics and *P*-values were calculated using likelihood ratio tests as data did not show overdispersion (residual deviance/residual degrees of freedom: abundance = 6.05, species richness = 1.72, family richness = 0.94)(Bolker et al., 2009). GLMMs were performed in R (R Core Team, 2014) using the *lme4* package (Bates et al., 2014). Post-hoc Tukey tests were calculated on significant effects using the *multcomp* package in *R* (Hothorn et al., 2008).

Canonical analysis of principal coordinates (CAP) was performed in Primer 6 (PRIMER-E, 2008) to visualize differences in parasitoid assemblage structure between locations along sampling transects. CAP is a constrained ordination method that finds the axes that best discriminate among groups of interest defined a priori (Anderson and Willis, 2003). Permutational multivariate analysis of variance (PERMANOVA) was performed in PRIMER 6 (PRIMER-E, 2008) to test for differences between parasitoid assemblages at different locations along sampling transects (Anderson, 2006). *F*- and *P*-values, as well as pairwise differences between locations, were estimated using 9999 permutations. CAP and PERMANOVA analyses were based on Bray-Curtis similarities derived from square-root transformed abundance data.

As a high number of species occurred as singletons (>70%), it was not possible to examine species-level distribution patterns. This is a common limitation with parasitoid surveys, as parasitoids are a hyperdiverse group and are often present in high species