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Modelling potential success of conservation translocations of a specialist grassland butterfly

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ABSTRACT

Success rates for conservation translocations of species are low and there is a need for increased understanding of how this activity is best applied. Here, using static species distribution models and a spatially-explicit dynamic simulation model, RangeShifter, we examine the impacts of habitat cover in recipient landscapes, allocation of individuals into multiple sites and species trait characteristics on the long-term fate of hypothetical translocations of a grassland specialist butterfly, *Maniola jurtina*, in Finland. While persistence of populations introduced to climatically suitable locations northwards of the current range can be increased by selecting sites with increasing habitat cover and by allocation of individuals to multiple release sites, local population growth rate is shown to be the key parameter in determining likely translocation success. We conclude that the long-term persistence of translocated habitat specialist butterflies, particularly with low growth rates, appears to be uncertain in modern-day fragmented grassland networks and that translocation activities should prioritize management that improves local growth rate.

1. Introduction

Conservation-oriented translocations (Seddon et al., 2007), i.e. assisted movements of organisms from one area to another, are a controversial tool (McLachlan et al., 2007; Loss et al., 2011) which nevertheless hold much potential for species conservation (Chauvenet et al., 2013a). In particular, carefully planned translocations can aid habitat specialists with limited mobility to track spatial changes in suitable areas (Willis et al., 2009a; Gallagher et al., 2015).

The two main types of conservation translocations are (i) reintroductions where species are released within their indigenous range and (ii) assisted colonization (referred to also as assisted migration and managed relocation) where species are moved beyond their historical range (McLachlan et al., 2007; Seddon et al., 2014). These have certain common key features (Olden et al., 2011). First, the success rate of both reintroductions (Griffith et al., 1989; Armstrong and Seddon, 2008) and assisted colonization (Gallagher et al., 2015) has been low, resulting from insufficient consideration of species biology and ad hoc selection of release sites (Seddon et al., 2007; Schultz et al., 2008; Chauvenet et al., 2013b). Second, translocation resources are often limited and only a few options can be implemented. Thus potential success of different alternatives should be scrutinized with appropriate tools (Rout et al., 2007; Schultz et al., 2008; Lewis et al., 2012). Indeed, increasingly sophisticated approaches are available for assessing factors determining the success of population establishment (Fordham et al., 2012; Chauvenet et al., 2013a). Systematic application of such tools helps in developing both reintroduction and assisted colonization planning (Armstrong and Seddon, 2008; Chauvenet et al., 2013b). A promising avenue is the use of species distribution models (SDMs) to determine the broad-scale suitability of recipient areas in conjunction with dynamic population models, which provide estimates of the translocation success (Fordham et al., 2012; Lewis et al., 2012).

In this study we examine the potential success of butterfly translocations at the northern range margin. We consider a habitat specialist, *Maniola jurtina*, which inhabits sparsely occurring managed grasslands in SW Finland (Heikkinen et al., 2014). With SDMs we determine the climatically suitable area for the species which is currently unoccupied, apparently due to difficulties in dispersing across fragmented landscapes (Warren et al., 2001; Pöyry et al., 2009). Within this focal area we use the dynamic model RangeShifter (Bocedi et al., 2014a) to explore potential success of simulated introductions in relation to (1) regional availability of suitable habitat (Chauvenet et al., 2013a; Seddon et al., 2014) and (2) allocation of introduced individuals in one vs. multiple sites (Rout et al., 2007; Armstrong and Seddon, 2008). We also examine the role of three key life-history parameters, growth rate, carrying capacity and length of long-distance dispersal events, in determining the introduced populations' persistence and spread. We conclude with recommendations for

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the development of reintroduction and assisted colonization programmes for habitat specialist species in modern-day agricultural landscapes.

2. Materials and methods

2.1. Study species

The Meadow Brown butterfly, *M. jurtina* (Linnaeus, 1758) (Lepidoptera, Nymphalidae) is a grass-feeding grassland generalist in many parts of Europe (Van Swaay, 2003; Dennis, 2004). However, the northern range margin of *M. jurtina* is in southernmost Finland (Fig. 1) where the species favors sparsely occurring managed dry unimproved (i.e. semi-natural, unploughed, non-fertilized, traditionally managed) grasslands over other types of grasslands (Schulman et al., 2005). Thus in our study area the species behaves as a grassland habitat specialist.

Despite possibilities provided by recent climatic warming (Pöyry et al., 2009) the species has not managed to expand its range northwards. As such, it represents a suitable candidate for an experimental climate change-related translocation (cf. Carroll et al., 2009). We used the National Butterfly Recording Scheme in Finland (NAFI) (Saarinen et al., 2003) data for 2001–2010 to determine 10 × 10 km cells with recent populations of *M. jurtina* in our study area (Fig. 1; Supplementary material, Text A1).

2.2. Recent climatically suitable areas

We determined the area that had recently become climatically suitable for *M. jurtina* by generating three SDMs (generalized linear models (GLM), generalized additive models (GAM) and generalized boosting method (GBM)). These SDMs were based on European-wide butterfly (Kudrna et al., 2011) and climate data, recorded using a regular 30′ × 30′ grid system and averaged across the time period of 1971–2000 (for details see Supplementary material, Text A1). In SDMs, the European range of *M. jurtina* was related to four climate variables, found to be ecologically important predictors for the broad-scale distributions of butterflies: mean temperature of the coldest month (MTCO), annual daily temperature sum above 5 °C (growing degree days, GDD5), annual water deficit (WD) and mean annual precipitation (PREC). The calibrated SDMs were then fitted to 10 × 10 km resolution climate data for Finland for the period 2001–2010, providing three different (GLM-, GAM- or GBM-based) projections of climatic suitability across the whole country. These model-based probabilities of suitability were converted into three maps where each 10 × 10 km cell was predicted to be either climatically suitable or unsuitable, and climatically favorable cells were determined by agreement of at least two of the models (see Supplementary material). Overlaying these 10 × 10 km cells with NAFI records revealed climatically suitable but currently unoccupied areas in SW Finland (Fig. 1).

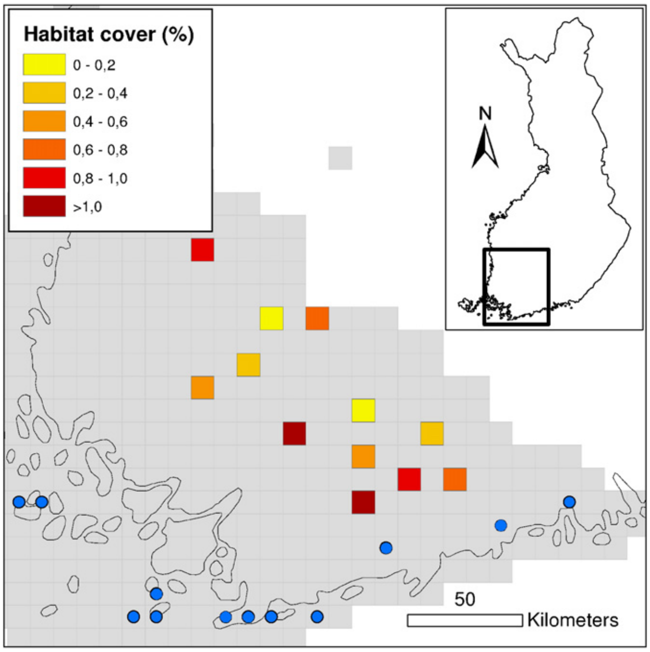

Fig. 1. Distribution of the selected twelve 10 × 10 km grid cells ("10 × 10 km landscapes") used in the modelling of translocation potential of *Maniola jurtina* butterfly in SW Finland. Cover of suitable habitat in the selected 10 × 10 km cells is shown using a 6-level scale. Grey shading indicates climatically suitable area for the species and blue dots (midpoints of 10 × 10 km grid cells) known occurrences in 2001–2010.

2.3. Land cover data and selection of recipient landscapes and sites

The amount of suitable habitat (i.e. 'habitat cover') for *M. jurtina* was determined for all unoccupied but climatically suitable 10 × 10 km cells and for all potential release sites (200 × 200 m cells) using CORINE 2006 Land cover data, available at 25 × 25 m resolution, by summing up the categories 'Pastures' and 'Natural grassland' — the two CORINE categories deemed suitable for *M. jurtina* (Heikkinen et al., 2014). In these calculations climatic suitability, as determined by SDMs, was not considered, only the habitat cover. Next we selected twelve 10 × 10 km cells as recipient landscapes, two for each of six habitat cover classes (<0.2%; 0.2–0.4%; 0.4–0.6%; 0.6–0.8%; 0.8–1.0% and >1.0% cover), in order to represent a gradient in habitat cover (Table A1). Two selection rules were used: no neighboring 10 × 10 km cells were selected for simulated release sites and all selected cells were located inland, separated by at least one empty 10 × 10 km cell from known occurrences (Fig. 1). From each of the twelve 10 × 10 km landscapes, we then selected as release sites, the one, four or eight 200 × 200 m cells with the highest habitat cover. Habitat calculations were conducted using ArcMap software (Version 10.2.2, ESRI Inc., Redland, CA, USA).

2.4. Species parameterization, founder population persistence and spread

The long-term persistence and spread of translocated *M. jurtina* populations were projected using RangeShifter v1.0, a platform for individual-based modelling of species' population dynamics and dispersal (Bocedi et al., 2014a). We used a female-only and non-overlapping generation population model, requiring information on growth rate (r_{max}) and carrying capacity (K; i.e. equilibrium population density) (Bocedi et al., 2014a). We assumed density-dependent dispersal probability (Heikkinen et al., 2014) and sampled the dispersal distance from a double negative exponential distribution in order to account for rare long distance dispersal events (i.e. simulating a combination of more common short dispersal events and rarer long distance dispersal events) (Nathan et al., 2012). We modelled population dynamics at a 200 × 200 m resolution, recording local population abundances for 50 years following each initial translocation. The 'released' butterfly populations were allowed to spread outside the focal 10 × 10 km cells, potentially throughout the whole climatically suitable area (grey-shaded grid cells in Fig. 1).

Biological parameters were extracted from literature, long-term butterfly monitoring surveys and expert assessments (for details see Supplementary material, Text A1 and Heikkinen et al., 2014). We conducted a sensitivity analysis to evaluate the effects of varying three key life-history traits on the simulated population dynamics (Carroll et al., 2003; Naujokaitis-Lewis et al., 2013): carrying capacity, population growth rate and the mean distances of long-distance dispersal events (McInerny et al., 2007; Willis et al., 2009b; Heikkinen et al., 2014). A default intermediate value and one alternative lower and one higher parameter value were used for each parameter, such as $K = 100/150/200$ individuals/ha ("K100", "K150" and "K200"), for $r_{max} = 1.5/2.0/2.5$, and mean long-distance dispersal = 1500/3000/5000 m ("D1500",