



Geometrid moth assemblages reflect high conservation value of naturally regenerated secondary forests in temperate China



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ABSTRACT

The widespread destruction of mature forests in China has led to massive ecological degradation, counteracted in recent decades by substantial efforts to promote forest plantations and protect secondary forest ecosystems. The value of the resulting forests for biodiversity conservation is widely unknown, particularly in relation to highly diverse invertebrate taxa that fulfil important ecosystem services. We aimed to address this knowledge gap, establishing the conservation value of secondary forests on Dongling Mountain, North China based on the diversity of geometrid moths – a species-rich family of nocturnal pollinators that also influences plant assemblages through caterpillar herbivory. Results showed that secondary forests harboured geometrid moth assemblages similar in species richness and phylogenetic diversity, but with a species composition distinctly different to assemblages in one of China's last remaining mature temperate forests in the Changbaishan Nature Reserve. Species overlap between these sites was about 30%, and species did not form separate phylogenetic clusters according to site. Species assemblages at Dongling Mountain were strongly differentiated according to forest type; a pattern not found at Changbaishan. Our results indicate that protected naturally regenerated secondary forests in northern China provide suitable habitats for species-rich and genetically diverse geometrid moth assemblages, highlighting the potential importance of these forests for conservation and ecosystem function provision across the wider landscape.

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1. Introduction

Widespread deforestation across China has led to dramatic biodiversity losses since the 1950s. These triggered severe population declines and local extinctions in more than 200 plant species, and in over half of the country's large mammals (see Zhang et al., 2000). In response to the widespread ecological degradation associated with this deforestation, the Chinese government established a variety of ecological protection programmes such as Nature Forest Protection Programme, Nature Reserve Development Programme and Desertification Reduction Programme. These programmes were aimed at both the protection of the last remaining mature forests and regenerating secondary forests, and at triggering re- and afforestation activities on a globally unprecedented

scale (Wang et al., 2007; Chinese State Forestry Bureau, 2011). These activities were chiefly focussed on erosion control, lacking clear objectives for biodiversity conservation and for the provision of associated ecosystem services (Cao et al., 2010; Ma et al., 2013; Ran et al., 2013). It is generally assumed that the recent net increasing in China's forest cover has had little positive impact on biodiversity in forest ecosystems (Lü et al., 2011), but very little evidence has been gathered about the actual conservation value of China's secondary and plantation forests.

Mature forests are crucial for global biodiversity conservation, as they harbour a unique and often highly specialized fauna and flora (Gibson et al., 2011; Ruiz-Benito et al., 2012; Adams and Fiedler, 2015). At the same time, the potential of both plantation and secondary forests to contribute towards ecosystem service provision and conservation of diverse species assemblages is being increasingly recognized (Brockhoff et al., 2008; Chazdon et al., 2009; Bremer and Farley, 2010; Martin and Blackburn, 2014; Zou et al., 2015). Comparative assessment of biological assemblages between mature and secondary forests can help to establish the

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relative importance of the latter for biodiversity conservation and ecosystem functioning across wider scale landscapes. Assessing the species richness of target taxa can give us direct insights into biodiversity values, whereas the assessment of species composition changes can indicate the sensitivity of target taxa to ongoing and historic changes in environmental conditions (Condit et al., 2002; McKnight et al., 2007).

Species-rich taxa fulfilling important functions in forest ecosystems are valuable targets of biodiversity assessments in mature and secondary forests. Geometrid moths (Lepidoptera: Geometridae) represent one such taxonomic group. With more than 35,000 described species (McLeod et al., 2009), geometrids are one of the most diverse monophyletic insect families. They provide a number of key ecosystem services, as an important pollinator group that can also contribute towards weed control, since caterpillar herbivory influences the composition and competitive balance in the vegetation (Scoble, 1999; Palmer et al., 2007; Grenis et al., 2015; Macgregor et al., 2015). In turn, their diversity and abundance in forest ecosystems makes them an important food source for predatory species like birds or spiders. Changes in forest geometrid diversity and assemblage structure can be expected to directly impact the ecosystem functioning of forest ecosystems at multiple trophic levels, with wide implications for ecosystem service provisions.

From an evolutionary perspective, the phylogenetic analysis of species assemblages allows us insights into evolutionary pathways and associated ecological traits. For example, species losses from species-poor, phylogenetically highly distinct clades are considered more detrimental than losses from species-rich, closely related clades (Mace et al., 2003; Mouquet et al., 2012). Phylogenetic diversity therefore reflects evolutionary information and can be used as a proxy for functional diversity (Winter et al., 2013). DNA barcoding-based phylogenetic analysis is increasingly promoted as a complementary approach to traditional species richness and composition-focused measures of conservation value (Lahaye et al., 2008; Smith and Fisher, 2009; Liu et al., 2015). DNA barcoding of geometrid

moths has been used in a number studies already (Hausmann et al., 2011; Sihvonen et al., 2011; Strutzenberger et al., 2011; Brehm et al., 2013, 2016; Zou et al., 2016).

In this study, we compare and contrast the species richness, species composition and phylogenetic diversity of geometrid assemblages in two forest regions of northern China that experience similar climatic conditions. The first, on Dongling Mountain (DLM), comprises a mosaic of naturally regenerated secondary forests and forest plantations. The second region is located in the Changbaishan Nature Reserve (CNR) at a distance of 1100 km from DLM. This reserve contains one of the largest remaining mature forests in temperate China. Due to historical clearance of the forest cover at DLM, forest specialist species are assumed to have been widely replaced by generalists in the regenerating secondary forests (Warren-Thomas et al., 2014). We hypothesised that this would lead to a depleted, homogenous geometrid moth assemblage in these secondary forests when compared to assemblages at CNR. In addition, we also hypothesised that the widely undisturbed forest cover at the CNR would support more phylogenetically distinct moth assemblages and hence a higher phylogenetic diversity, as a wider variety of historically consistently available niches in these forests should have allowed them to preserve assemblages containing more moth species with unique ecological traits. In combination, CNR was therefore assumed to have a higher conservation value in terms of species richness, species composition and phylogenetic diversity, compared to the secondary forests at DLM that have established following the near-complete clearance of forest vegetation at this region. In order to achieve the above goals, we compared geometrid moth assemblages at DLM and CNR with view of (1) number of genera rarefied to a standardized sample size as a proxy of diversity (Brehm et al., 2013), (2) expected species richness using the Chao1 estimator, (3) Shannon diversity, (4) extrapolated expected species richness, (5) species turnover pattern, (6) phylogenetic diversity rarefied for the standardized maximum common number of species for all samples and (7) the nearest-taxon index (NTI).

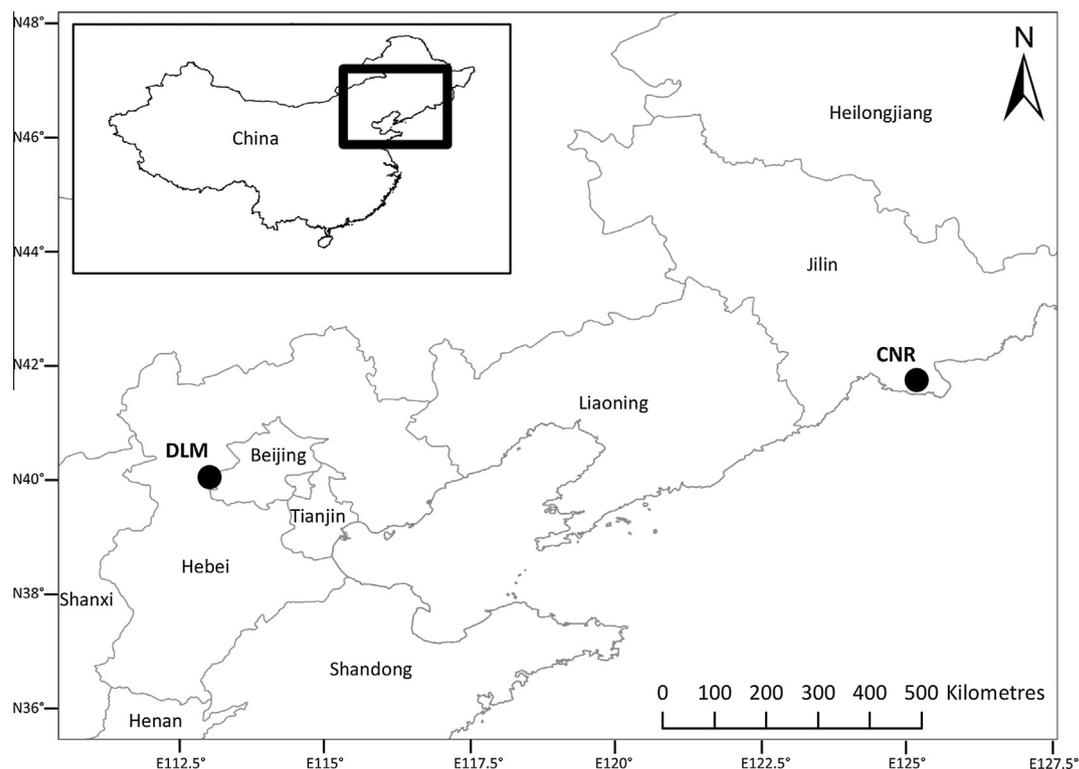


Fig. 1. Map of the study areas (DLM: Dongling Mountain; CNR: Changbaishan Nature Reserve).

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