

The response of sward-dwelling arthropod communities to reduced grassland management intensity in pastures

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Abstract

We compared arthropod taxon richness, diversity and community structure of two replicated grassland husbandry experiments to investigate effects of reduced management intensity, as measured by nutrient input levels (390, 224 and 0 kg/ha per year N in one experiment, and 225 and 88 kg/ha per year N in another). Suction sampling was used to collect Araneae, Coleoptera, Hemiptera and Hymenoptera, with Araneae and Coleoptera also sampled with pitfall trapping. Univariate analyses found no significant differences in abundance and species density between treatments. However, with multivariate analysis, there were significant differences in arthropod community structure between treatments in both experiments.

Reducing N input and associated stocking rates, as targeted by agri-environment schemes, can significantly alter arthropod communities but without increasing the number of species present. Other approaches that may be necessary to achieve substantial enhancement of sward arthropod biodiversity are suggested.

Keywords

Rural Environment Protection Scheme (REPS) • agri-environment • insect • biodiversity • pasture

Introduction

In the Republic of Ireland, about 65% of the total land area is agriculturally managed and of this, approximately 92% (4.2 million ha) is devoted to grass-based farming (CSO, 2013). Although intensively managed agricultural grasslands are unlikely to ever be species-rich habitats, their status as a nationally significant habitat type means that it is important to understand how their management is likely to impact on biological diversity. In particular, there is a need to understand the effects of agri-environment measures on biodiversity aimed at reducing the intensity of grassland management.

Increased grassland management intensity has generally been found to decrease arthropod biodiversity, and practices such as fertilizer and pesticide use, grazing, cutting, ploughing and reseeded are likely to reduce biological diversity (Morris 2000; Plantureux, Peeters and McCracken 2005). Heavy grazing produces short swards that reduce foraging opportunities and habitat availability for many invertebrates, whilst lower stocking rates favour many species, particularly those whose incidence is strongly dependant on vegetation structure, such as spiders (Bell, Wheater and Cullen 2001; Morris 2000; Plantureux *et al.* 2005; Tscharrntke and Greiler 1995). Nitrogenous fertilizer input can have a marked influence on grassland plant and arthropod

communities, with a generally negative effect on species richness (Haddad, Haarstad and Tilman 2000; Kleijn *et al.* 2009; Klimek *et al.* 2007; Prestidge 1982; Zechmeister *et al.* 2003). In a recent study of 117 European grasslands, Klimek *et al.* (2007) concluded that a reduction in both nitrogenous fertilizer input and stocking rates might be particularly important in conserving plant diversity within agricultural grasslands. Such insights are already built into existing agri-environmental policy; in Ireland, attempts have been made to limit both nutrient inputs and stocking rates. This was the case in the Grassland and Soil Management Plan (Measure 2), part of the Rural Environment Protection Scheme (REPS) that was Ireland's agri-environment scheme from 1994 until being closed to new applicants in 2009 (Department of Agriculture Food and the Marine, 2012; Finn and Ó hUallacháin, 2012). The primary environmental objective for this measure was to improve nutrient management for the purpose of improving water quality (Department of Agriculture, Food and the Marine, 2003). In general, however, the greater the environmental gains (even if they were not the primary objective) from a measure, the more cost-effective it is. Even though the REPS is no longer in operation, the principle of reduced intensity

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benefitting biodiversity is still very relevant, as reflected in the low-input permanent pasture in the list of Tier 3 General Actions within the current Irish agri-environment scheme, that is, Green, Low-Carbon, Agri-Environment Scheme (GLAS) (Department of Agriculture, Food and the Marine, 2015).

The development and assessment of the impact of agri-environment schemes has been limited by methodological difficulties when seeking to compare farms in different areas. Difficulties include the non-independence of farm history, landscape and current agri-environmental practice (Kleijn and Sutherland 2003). One approach to avoid such problems is to use designed experiments with randomly assigned treatments. This approach, however, is rarely logistically possible at a farm scale but is very suitable for studies at a plot or field scale.

Owing to their small size and their generally greater responsiveness to patch-scale effects (relative to other wildlife groups), arthropods are very suitable subjects for plot-scale field studies to investigate the effects of specific agricultural practices on biodiversity (Mazerolle and Villard 1999).

The aim of this study was to assess the likely changes in arthropod biodiversity that result from the reduction in N application and associated reduction in grassland management intensity. We hypothesised that reduced management intensity would be associated with an increase in arthropod abundance and number of taxa present and would significantly alter arthropod community structure. Two separate grassland experiments at the Teagasc Grange Research Centre (the Irish Agriculture and Food Development Authority) and Teagasc Johnstown Castle Research Centre were used to investigate the effects of reduced management intensity on the arthropod communities in the grassland sward (sampled by suction sampling and pitfall trapping).

Materials and Methods

Experimental design

Two different field experiments in the Republic of Ireland were sampled for grassland arthropods: Teagasc Grange Research Centre, County Meath (longitude 6°40'4", latitude 53°31'14"N, Irish grid reference N884530), and the Tower Field experiment at the Teagasc Johnstown Castle Research Centre, County Wexford (longitude 6°30'45", latitude 52°17'56"N, Irish grid reference T015174).

The treatments established at the two sites represent different farming systems, which for ease of reference have been characterised in the following description as different inorganic N input levels. However, it must be realised that there are consequent differences in variables such as sward productivity, stocking rates, trampling and poaching, dung and urine input as well as N availability.

The Grange experiment compared the agronomic performance of suckler beef production systems of different input intensities, with the lower intensity level representing farm management that was compatible with REPS measures. The experiment was established in 1997 with four blocks, each with the two treatments, and three 0.55-ha paddocks nested in each treatment (Fig. 1a). Prior to 1997, the experimental area had been used for intensive beef production receiving c.225 kg/ha per year N. The treatments established in 1997 were

- i) conventional standard suckler beef system with 1.5 livestock units per hectare (LU/ha) and 225 kg/ha per year of inorganic N;
- ii) REPS-compatible suckler beef system with 1.2 LU/ha and 88 kg/ha per year of inorganic N.

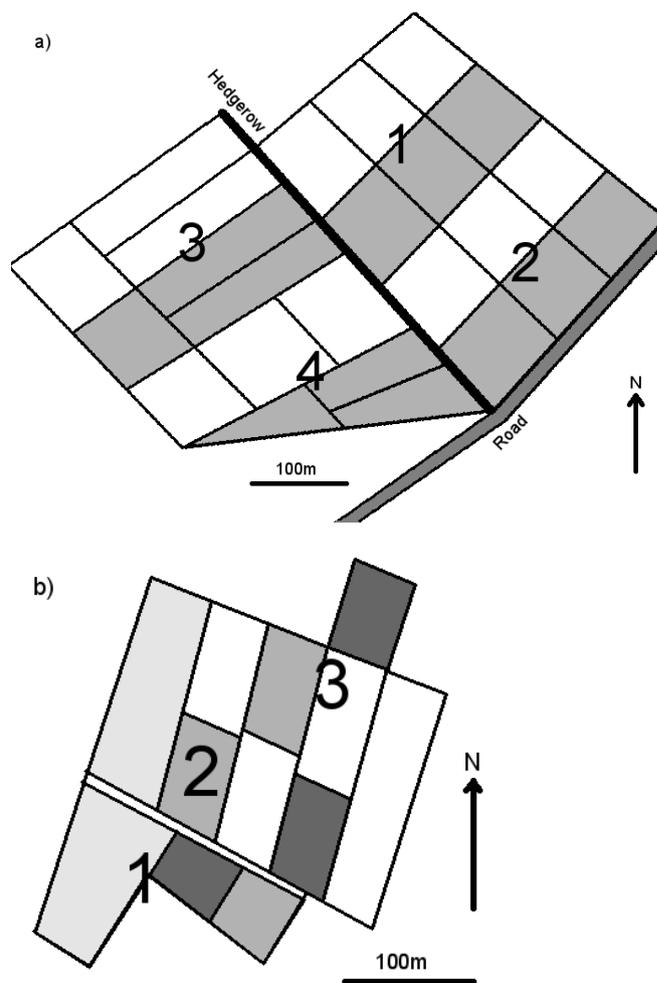


Fig. 1. Experimental plot layout at (a) Teagasc Grange (shaded, conventional; unshaded, REPS) and (b) Teagasc Johnstown Castle (pale grey, 0 N treatment; mid-grey, 225 N treatment; dark grey, 390 N treatment). Numbers indicate the different experimental blocks.

The treatments were managed with separate, self-contained herds. Individual paddocks were grazed between April and November, rotationally on an approximate 21- to 28-day cycle.

The Tower Field experiment was established at Johnstown Castle, Co. Wexford in 2001, primarily to study the effects of different N fertilizer rates on N₂O emissions (Hyde *et al.* 2006). Prior to this, the field contained a sward dominated by perennial ryegrass (*Lolium perenne*) that had been established for more than 10 years and had been intensively managed for commercial beef production with fertilizer applied at a rate of c. 350 kg/ha N per year. The experiment was arranged in a randomised block design. There were three blocks each containing the three N input treatments (Fig. 1b). Individual replicates were subdivided into three grazing paddocks. The three treatments differed in management intensity in terms of both N input and associated stocking density. Plots were given inorganic N fertilizer at rates of 0, 225 and 390 kg/ha per year (0 N, 225 N and 390 N treatments, hereafter). The two higher treatments corresponded, according to Teagasc advice at the time (Coulter 2001; Hyde *et al.* 2006), to an intermediate and maximum N fertilizer application rate for grazed grassland. Paddock size varied with treatment (from 0.4 ha for the 390 N treatment to 1.0 ha for the 0 N treatment) in order to accommodate a common 21-day rotational grazing cycle (7-day grazing and 14-day recovery) by a self-contained herd of 10–15 steers within each treatment. This equated to stocking rates of 1.0, 2.4 and 3.0 LU/ha, respectively, for the 0 N, 225 N and 390 N treatments. Paddocks were cyclically strip grazed with each main paddock divided into three strips with back fencing for this purpose. Unfortunately, after the experiment had been established for only one year, one of the three 0 N paddocks was found to be unrepresentatively waterlogged and so was removed from the experiment (thus providing only two true replicates for this study). Full details of the experimental design can be found in Hyde *et al.* (2006).

Arthropod sampling

Arthropods were sampled at both sites using the Vortis suction sampler (Burkard Manufacturing Co Ltd, Rickmansworth, Hertfordshire, UK) (Arnold 1994) and additionally at Tower Field with pitfall trapping.

At Grange, arthropods were sampled on 6 August 2003, and 27 June and 26 August 2005, with a single sample taken from each paddock, giving three samples nested within each treatment. Each sample consisted of the pooled catch from 10, randomly placed, 10-s suction samples, covering a total area of 0.2 m². To enable a more complete assessment of community structure using ordination, two additional samples (each consisting of five pooled 10-s suction samples) were taken on the same sampling dates from each paddock in 2005; one

from areas of short grazed sward and one from the patches of longer sward that develop around dung pats (Helden *et al.* 2010).

At Tower Field suction, sampling was conducted on six occasions in 2004, three in May (12, 18 and 25) and three in July/August (28, 4 and 9). The repeated sampling within the two seasons was designed to minimise the effect of sward height differences generated by differential timing of grazing, as sward height can affect invertebrate catches. One suction sample, consisting of the pooled catch from four randomly placed 10-s samples, with a total area sampled of 0.08 m² was taken from each paddock on each date. Therefore, there were three nested samples within each experimental replicate, within each date.

Pitfall traps were used to collect Araneae and Coleoptera at the Tower Field. The traps consisted of clear plastic cups (8 cm in diameter and 11 cm deep) inserted into a short piece of plastic drainpipe and sunk into the ground such that the lip of the cup rested in the rim of the drainpipe at ground level. The traps were partially filled with a mixture of water and detergent. In the centre of each paddock, three pitfall traps were placed 10 m apart in a line in an approximately north-west to south-east orientation. The traps were installed on 5 May, then emptied after two weeks and then on a further two occasions at two-week intervals, with the final sample collected on 14 June 2004. Sampling was repeated later in the year, with the traps being set on 31 August and emptied on 14 and 28 September and 12 October.

Arthropods were preserved in 70% ethanol prior to identification. Four orders of arthropods were identified as follows: Araneae to species, Coleoptera to species (except for some of the Aleocharinae which were identified to genus), Hemiptera to species (except for some of the Aphidoidea which were identified to morphospecies) and Hymenoptera to genus. Literature used in the identification of arthropods is referenced in Anderson *et al.* (2008a; 2008b) and Helden, Anderson and Purvis (2008a, b).

Sward height measurement

On the same dates as suction sampling, the sward height in each paddock was measured using a Filips Folding Plate Pasture Meter manufactured by Jenquip (www.jenquip.co.nz). Sward height was recorded in each paddock at Grange from 20 randomly placed points in 2003 and from 50 points in 2005. At Tower Field, 10 sward height readings were taken from each plot.

To investigate whether there was any evidence at Grange of a difference in sward structural characteristics between the treatments through the grazing season, sward height was measured in one paddock of each treatment in each of the four blocks on 10 dates between May and September

2003. In each paddock, 25 randomly placed sward height measurements were made. The dates of sampling were 7 and 27 May; 11 and 17 June; 3, 15 and 30 July; 14 and 26 August; and 9 September.

Statistical methods

Analyses were carried out using R version 2.10.1 (R Development Core Team, 2009). The data were investigated using both generalised linear mixed models and non-metric multidimensional scaling (NMDS).

Mixed effects models

The abundance and number of taxa recorded in the Grange experiment were investigated with generalised linear mixed models using the lmer function from the lme4 package (Bates and Maechler 2009). The lmer function fits generalised linear mixed models by maximising the log likelihood, approximated using the Laplace method. The response variables were abundance (total number of individuals of all invertebrate groups combined) and taxon (species) richness. The latter term was used as a measure of the number of taxa uncorrected for sampled area. This being distinct from rarefied species (taxon) richness (Gotelli and Colwell 2001). Given the sampling methodology used, it was not possible to use rarefaction to correct for the number of individuals and thereby gain a measure of rarefied taxon richness. Only the random sample data were used in the models. Fixed effects tested were treatment (nutrient input), mean of the sward height and their interaction. To account for the nested sampling and plot designs, random effects tested were sampling date, nested within paddock, nested within treatment. In all models, Poisson errors were defined using the family directive.

To investigate whether mean sward height and sward height variance differed between treatments, a repeated measures analysis was carried out, using the linear mixed effect models, with lme, from the nlme package (Pinheiro *et al.* 2007). Sward data from eight of the plots (one plot from each treatment/block combination), on 10 dates between May and September were modelled. Both response variables were log transformed, as untransformed values did not fulfil assumptions of normality, and subsequently, tested for normality using the Shapiro–Wilk test. Date was included as a continuous random effect, and normal (Gaussian) error structure was defined. The model was fitted by maximising the restricted log likelihood using restricted maximum likelihood (REML).

For the Tower Field treatment (nutrient input), comparisons were made separately for suction sample and pitfall data, using linear mixed models fitted to three different response variables. These were taxon richness, rarefied taxon richness (i.e. corrected for abundance) and abundance. For each paddock, the rarefied taxon richness was calculated from

the species-abundance data collected on the six sampling dates by using rarefaction using species accumulation curves generated by EstimateS version 7.5.0 (Colwell 2005). The use of taxon richness calculated in this way corrected for differences in the number of individuals (Gotelli and Colwell 2001). As there was both spatial and temporal non-independence of errors, generalised linear mixed models, using the lmer function (Bates and Maechler 2009), were fitted to the data. For abundance and species density response variables, treatment, sward height and their interaction were included as fixed effects. Date nested within season, nested within paddock and nested within treatment were random effects. In models with rarefied taxon richness as the response variable, season and date were not included, because rarefaction combined the six sample dates to provide a single estimate of species number per paddock. For pitfall sample data, sward height was not used as an explanatory variable, as this had not been recorded. As the response variables were of count data, Poisson error structure was used in models.

For all models, the maximal model was fitted first and then non-significant terms were removed sequentially until the minimal adequate model was identified (Crawley 2007). For the lmer models, sequential models were compared using the anova command, which provides AIC (Akaike information criterion) values for each model, and a chi-squared deletion test to determine whether removal of terms from the model was justified. Random effects were retained in all models. Model parameters were considered significant at the $\alpha = 0.05$ level.

NMDS

NMDS was carried out using the metaMDS function in the vegan package of R (Oksanen *et al.* 2010). Bray–Curtis similarity was used in the ordinations, which were performed with several random starts to find the best solution. Only taxa with 10 or more individuals in total were used in the ordinations. Treatments (nutrient input) were compared using treatment as a categorical environmental variable in the NMDS. The significance of any patterns found was assessed by fitting the treatment levels to the ordination using the envfit function, which determines the goodness-of-fit statistic based on a number of random permutations of the data. In this case, 1,000 permutations were used. In the same way, species that showed a significant effect within the ordination were identified using the envfit function.

Prior to the NMDS, Grange data were combined by pooling all catches from each grazing paddock over the two years of sampling, including the additional samples from long and short swards. Similarly, the Tower Field data were pooled across the six sampling dates for each grazing paddock.

Results

In total, 9,492 adult arthropods from 227 taxa were collected at Grange and 4,850 adult arthropods from 198 taxa at Tower Field.

Grange

There was no significant effect of N level on either abundance or species density of arthropods in suction samples. The only significant effect was an increase in these variables with sward height (abundance: $z = 11.79$, d.f. = 53, $P < 0.001$; species density: $z = 3.47$, d.f. = 53, $P < 0.001$). The statistical models were as follows (because of the Poisson error structure, parameter estimates are given in \log_e values): $\log_e(\text{abundance}) = 3.42 + 0.06 \text{ sward height}$; $\log_e(\text{species density}) = 3.04 + 0.03 \text{ sward height}$.

Modelling the sward height in the eight paddocks on 10 dates between May and September indicated no difference ($t = -0.42$, d.f. = 69, $P = 0.669$) in the mean sward height showed between the treatments. In contrast, sward height variance was significantly greater in the REPS than the conventional treatment ($t = 2.33$, d.f. = 69, $P = 0.023$) (Fig. 2).

The output of the NMDS ordination analysis of community similarity in individual grazing paddocks (12 per treatment) produced a two-dimensional ordination with a final stress of 22.841 (Fig. 3). A clear but not complete separation of paddocks relating to the experimental treatments is apparent on the first axis. Permutation tests of treatment regime fitted to this ordination, indicated a significant difference in the arthropod

community structure of REPS and conventional paddocks ($r^2 = 0.398$, $P < 0.001$). Twenty-six taxa were found to show a significant pattern within the ordination (Fig. 3 and Appendix Table A.1). Of these, one Coleoptera species (*Acrotoma* C.G. Thomson species A) and two Hymenoptera genera (*Basalys* Westwood and *Diglyphus* Walker) were associated with the conventional treatment. One Coleoptera species (*Ptenidium nitidum* (Heer)) and one Hymenoptera genus (*Rhoptromeris* Förster) did not show any difference between treatments but were associated with the second axis of the ordination, which may relate to position within the experimental field. The other 21 significant species were associated with the REPS treatment.

Tower Field

There were no significant treatment effects on arthropod abundance, taxon richness or rarefied taxon richness in suction samples. There was, however, a significant positive relationship between taxon richness from suction samples and sward height ($z = 2.33$, $P = 0.02$, d.f. = 72) ($\log_e(\text{taxon richness}) = 2.96 + 0.02 \text{ sward height}$). There was also a positive sward height effect on arthropod abundance in suction samples, with significantly greater abundance in the 390 N treatment than the 0 N treatment, and a significant treatment*sward height interaction (Appendix Table A.2). The interaction indicated that although the increase in arthropod abundance with sward height was significant for all treatments, the slope of the relationship was significantly greater in 0 N and 225 N than in the 390 N treatment.

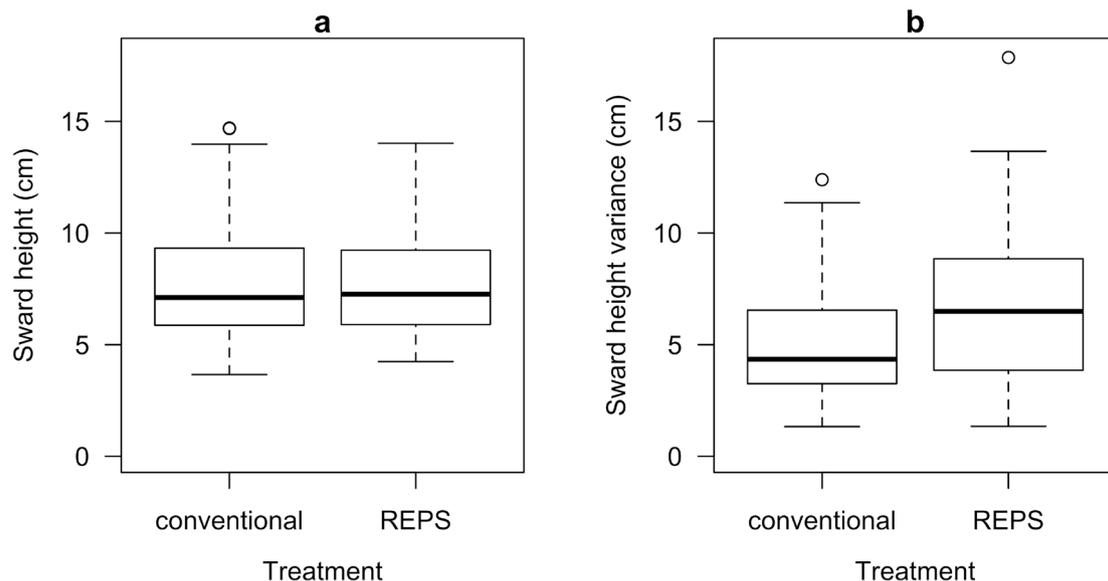


Fig. 2. Sward characteristics at Teagasc Grange over 10 sampling dates between May and September 2003: (a) showed no difference in sward height ($t = -0.42$, d.f. = 69, $P = 0.669$) and (b) a significant difference in sward height variance ($t = 2.33$, d.f. = 69, $P = 0.023$).

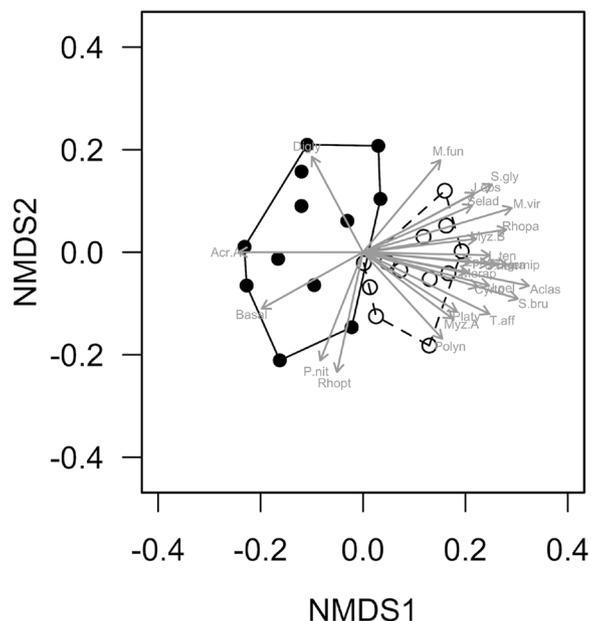


Fig. 3. NMDS plot of Grange arthropods. Data were square root transformed and then submitted to the Wisconsin double standardization. The NMDS solution had two dimensions and was derived after four runs. Final stress = 22.841. Fit of treatment to ordination $r^2 = 0.398$ and $p < 0.001$. Conventional paddocks are represented by filled circles and solid lines and REPS by open circles and broken lines. Species abbreviations: Araneae: *B.gra* *Bathyphantes gracilis*, *L.ten* *Lepthyphantes tenuis*; Coleoptera: *Acr.A* *Acrotona sp.A*, *M.fun* *Mocyta fungi*, *P.nit* *Ptenidium nitidum*, *S.bru* *Stenus brunripes*, *S.nan* *Stenus nanus*; Hemiptera: *J.obs* *Javesella obscurella*, *J.pel* *Javesella pellucida*, *M.vir* *Macrosteles viridigriseus*, *Myz.A* *Myzus sp.A*, *Myz.B* *Myzus sp.B*, *Rhopa* *Rhopalosiphum*, *S.gly* *Sipha glyceriae*, *T.aff* *Thecabius affinis*; Hymenoptera: *Aclas* *Aclastus*, *Basal* *Basalys*, *Cyrtog* *Cyrtogaster*, *Digly* *Diglyphus*, *Ephed* *Ephedrus*, *Hemip* *Hemiptarsenus*, *Merap* *Meraporus*, *Platy* *Platygaster*, *Polyn* *Polynema*, *Selad* *Seladerma*, *Rhopt* *Rhoptromeris*).

There were significant treatment differences in the grassland arthropod community structure (Fig. 4). Fitting management category onto the NMDS ordinations using the envfit function indicated that there were significant treatment differences for both pitfall ($r^2 = 0.538$, $P = 0.001$) and suction ($r^2 = 0.590$, $P = 0.001$) catches. In all cases, there was a consistent pattern of the 0 N treatment being clearly separated along the first NMDS axis from the 225 N and 390 N treatments, with the latter two showing considerable overlap in community structure.

For the pitfall data, 25 taxa showed a significant pattern (Fig. 4a and Appendix Table A.3). Six species of Araneae (*Pachygnatha degeeri* Sundevall, *Pardosa palustris* (L.), *Pardosa pullata* (Clerck), *Oedothorax retusus* (Blackwall), *Trochosa ruricola* (Degeer) and *Xysticus cristatus* (Clerck)) were significantly associated with the 0 N treatment and all other species of Araneae and Coleoptera were associated with 225 N and 390 N treatments.

In the ordination of suction sample data (Fig. 4b and Appendix Table A.4), 28 taxa showed a significant pattern with one Hymenoptera genus (*Phaenocarpa* Förster), two Hemiptera genera (*Metopolophium* Mordvilko and *Rhopalosiphum* Koch) and six Coleoptera species (*Aloconota gregaria* (Erichson),

Atomaria nitidula (Marsham), *Cartodere nodifer* (Westwood), *Ephistemus globulus* (Paykull), *Mocyta fungi* (Gravenhorst), *Tachyporus pusillus* Gravenhorst) associated with the 225 N and 390 N treatments. Two Coleoptera species, *Calathus fuscipes* (Goeze), *Ptenidium pusillum* (Gyllenhal), were most strongly associated with the 225 N treatment with little or no difference between 0 and 390 N. The rest of the Coleoptera species were associated with the 0 N treatment.

Discussion

Treatment effects

In both experiments, there was evidence that a reduction in N application and associated change in stocking rate resulted in changes in arthropod community structure. However, these changes were not associated with any significant overall changes in abundance, taxon richness or rarefied taxon richness amongst the treatments. There was no indication of any treatment effects in terms of the rarefied taxon richness of either suction or pitfall sampled arthropods, or for suction sampled abundance. The only significant treatment effect

between abundance and species number (Magurran 2004). The greater abundance in longer swards may have some ecological explanations such as improved shelter or microclimatic conditions (Andrzejewska 1965; Curry 1987; Morris 2000; Purvis and Curry 1981). An additional physical explanation may be that in longer swards, a greater volume of sward habitat is sampled. Assuming an even density of arthropods in three-dimensional sward space, a greater height of vegetation should hold more individuals.

No specific attempts were made to explore the reasons for the contrast in community structure between the treatments at the two sites. However, given the apparent importance of sward height for arthropods, it may be informative to consider whether the treatments differed in sward height or its variance. Such an approach would be problematic if only the sward height on the dates of arthropod sampling is considered, as this varied markedly because of periodic grazing events, as cattle were rotated through the paddocks of the experiment. However, measurement of sward height at Grange on 10 separate occasions between May and September 2003 enabled an overall assessment of sward characteristics over the grazing season. The resulting data indicated that mean sward height did not vary between the treatments, but its variance did, and was significantly greater in the lower-input REPS treatment. This suggests that over the year, it is possible that the lower intensity of grazing in the REPS treatment allows a generally more varied sward structure to develop than in the conventional treatment. More varied sward structure is likely to provide a greater variety of niches for arthropods and thus promote a more diverse arthropod community to exist (Dennis, Young and Gordon 1998; Morris 2000; Woodcock *et al.* 2007b).

Significance for agricultural biodiversity

Our finding that a reduction in intensity, in terms of N input and stocking density, leads to significant change in arthropod communities is not in itself surprising, given the many previous studies that have found similar effects (Bell *et al.* 2001; Haddad *et al.* 2000; Klimek *et al.* 2007; Morris 2000; Plantureux *et al.* 2005; Tschardtke and Greiler, 1995). What is much more valuable here is the quantitative comparison of the influence of a relatively simple change in husbandry practice that is widely implemented in agri-environment schemes, the importance of which has been highlighted most strongly by Kleijn *et al.* (2001) and Kleijn and Sutherland (2003). This simple approach to reducing the intensity of grassland husbandry practice was adopted as part of the Irish scheme REPS. Our findings suggest that a relatively simple change of reduction in N input and stocking density can have significant arthropod community effects. Similar changes associated with agri-environment schemes in other countries, such as

the EK2 Permanent Grassland with Low Inputs option in the UK's Entry Level (ELS) of its agri-environment scheme, Environmental Stewardship, might be expected to similarly alter arthropod community structure.

However, it must be emphasised that the biodiversity effects reported here are clearly limited to a modest change in community structure with no evidence of an increase in biodiversity. Further work may well reveal that more radical changes of agronomic practice are necessary to achieve more rapid and far-reaching increases in biodiversity within managed grassland, for example, the maintenance of existing semi-natural habitat patches (Öckinger and Smith 2007) or the creation of new more botanically rich habitats outside the main sward, such as field margins (Anderson *et al.* 2013; Blake *et al.* 2011; Fritch *et al.* 2011; Fuentes-Montemayor, Goulson and Park 2011; Öckinger and Smith 2007; Woodcock *et al.* 2007a; Woodcock *et al.* 2009). These alternative approaches, albeit at a small-scale, may well be more cost-effective for biodiversity conservation than reducing management intensity. At both the Grange and Tower Field sites, the means of sward utilisation was not changed from the intensive practice of cyclical rotational grazing in electrically fenced paddock sections, with cattle moved on once the available fodder had been removed. Consequently, the extent and frequency of vegetation removal remained similar in all treatments. This may have severely limited the potential biodiversity benefit of reducing overall nutrient input levels, and consequently, different targeted measures such as the modification of sward use (grazing system) or sowing more botanically diverse swards may be necessary in a land-sharing approach. Additionally, the legacy of former intensive nutrient use in agricultural swards may mask for some considerable time the benefits of reducing nutrient use (Dennis *et al.* 2004). Even more substantial changes in practice, such as the establishment of new field margins may in some cases be of limited biodiversity value without careful management. In a separate experiment at Johnstown Castle, which investigated field margins, Fritch *et al.* (2011) concluded that simply fencing or reducing nutrient inputs would have limited conservation value for plants, although in contrast invertebrate diversity and abundance was significantly enhanced (Anderson *et al.* 2013; Ó hUallacháin *et al.*, 2014). Given this evidence, the adoption of the more targeted optional agri-environment measures within the current GLAS to maintain low-input permanent pasture and traditional hay meadows (Department of Agriculture Food and the Marine 2015) is very much to be welcomed. Indeed, it could be argued that such a land-sparing approach may be more cost-effective, particularly in hard economic times, in enhancing biodiversity. However, to realize the full potential of biodiversity within grass-based agriculture, a dedicated

programme of longer-term grassland husbandry research is needed to achieve an optimised and sustainable model for grass-based production systems that are customised to particular agronomic conditions (Purvis *et al.* 2011).

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Appendix Table A.1. Species found to show a significant effect within the Grange NMDS ordination. Total numbers collected are given for conventional (Conv) and REPS treatments. Significance was assessed using the envfit function, which determined the goodness-of-fit statistic based on 1,000 random permutations of the data.

Species	Conv	REPS	r ²	P
Araneae				
<i>Bathypantes gracilis</i> (Blackwall)	93	161	0.388	0.009
<i>Lepthyphantes tenuis</i> (Blackwall)	58	89	0.344	0.013
Coleoptera				
<i>Acrotona</i> C.G. Thompson species A	11	4	0.331	0.015
<i>Mocyta fungi</i> (Gravenhorst)	368	462	0.309	0.022
<i>Ptenidium nitidum</i> (Heer)	9	9	0.289	0.028
<i>Stenus brunnipes</i> Stephens	2	17	0.560	0.002
<i>Stenus nanus</i> Stephens	22	43	0.342	0.012
Hemiptera				
<i>Javesella obscurella</i> (Boheman)	23	65	0.341	0.013
<i>Javesella pellucida</i> (Fabricius)	1	19	0.364	0.007
<i>Macrosteles viridigriseus</i> (Edwards)	13	47	0.516	0.001
<i>Myzus</i> Pass. species A	2	10	0.266	0.037
<i>Myzus</i> Pass. species B	27	84	0.279	0.039
<i>Rhopalosiphum</i> Koch	364	655	0.451	0.002
<i>Sipha glyceriae</i> (Kaltenbach)	42	109	0.454	0.001
<i>Thecabius affinis</i> (Kaltenbach)	2	23	0.423	0.004
Hymenoptera				
<i>Aclastus</i> Förster	25	94	0.612	0.001
<i>Basalys</i> Westwood	14	8	0.287	0.013
<i>Cyrtogaster</i> Walker	58	184	0.309	0.022
<i>Diglyphus</i> Walker	20	10	0.250	0.048
<i>Ephedrus</i> Haliday	5	77	0.254	0.050
<i>Hemiptarsenus</i> Westwood	7	37	0.448	0.001
<i>Meraporus</i> Walker	13	29	0.244	0.044
<i>Platygaster</i> Latreille	86	164	0.264	0.046
<i>Polynema</i> Haliday	15	48	0.294	0.029
<i>Seladerma</i> Walker	5	16	0.302	0.019
<i>Rhoptromeris</i> Förster	7	8	0.321	0.020

Appendix Table A.2 Results of generalised linear mixed models (lmer) of suction sampled arthropod abundance from Tower Field. Fixed effects used in the maximal models were treatment (0 N, 225 N or 390 N) and, for suction samples, mean sward height. Nested random effects were date within season, within grazing paddock within treatment. For each response variable, the minimal adequate model, derived from stepwise model simplification, is shown. Approximate degrees of freedom are 6 for treatment and 105 for the intercept, sward and interaction.

Response variable	Minimal adequate model (fixed effects)	Parameter	Parameter estimate	Standard error	z	P
Suction abundance	Abundance ~ treatment + sward + treat:sward	Intercept (0 treatment)	3.292	0.188	17.538	<0.001
		treatment (225)	0.149	0.242	0.614	0.539
		Treatment (390)	0.543	0.241	2.257	0.024
		Sward	0.078	0.015	5.103	<0.001
		Treatment (225) : sward	-0.016	0.017	-0.955	0.340
		Treatment (390) : sward	-0.058	0.017	-3.406	0.001

Appendix Table A.3. Species found to show a significant effect within the Tower field NMDS ordination of pitfall data. Mean numbers collected per treatment block are given for 0 N*, 225 N and 390 N treatments. Significance was assessed using the envfit function, which determined the goodness-of-fit statistic based on 1,000 random permutations of the data (* 0 totals are for six sample plots rather than nine in other treatments).

Species	0 N	225 N	390 N	r ²	P
Araneae					
<i>Erigone dentipalpis</i> (Wider)	51.5	72.0	86.0	0.283	0.031
<i>Lepthyphantes tenuis</i> (Blackwall)	0.5	10.0	12.7	0.315	0.011
<i>Oedothorax fuscus</i> (Blackwall)	193.5	326.7	332.0	0.249	0.046
<i>Oedothorax retusus</i> (Blackwall)	17.5	10.7	9.7	0.432	0.002
<i>Pachygnatha degeeri</i> Sundevall	45.5	26.3	17.0	0.654	0.001
<i>Pardosa palustris</i> (L.)	1205.5	516.0	407.3	0.624	0.001
<i>Pardosa pullata</i> (Clerck)	85.0	46.7	38.3	0.363	0.010
<i>Trochosa ruficollis</i> (Degeer)	5.0	0.3	1.3	0.334	0.021
<i>Xysticus cristatus</i> (Clerck)	6.5	2.0	0.7	0.639	0.001
Coleoptera					
<i>Aleochara lanuginosa</i> Gravenhorst	0	3.3	9.3	0.301	0.016
<i>Anchomenus dorsalis</i> (Pontoppidan)	1.5	8.3	16.0	0.333	0.016
<i>Bembidion lampros</i> (Herbst)	61.0	118.3	99.3	0.250	0.049
<i>Loricera pilicornis</i> (Fabricius)	22	37.3	46	0.423	0.002
<i>Megalinus glabratus</i> (Gravenhorst)	0	6.0	8.0	0.404	0.006
<i>Nebria brevicollis</i> (Fabricius)	134.5	308.7	325.7	0.462	0.004
<i>Oxytelus laqueatus</i> (Marsham)	0.5	1.3	1.7	0.382	0.004
<i>Philonthus carbonarius</i> (Gravenhorst)	15.5	57.0	48.3	0.472	0.003
<i>Philonthus cognatus</i> Stephens	118.5	306.0	345.3	0.483	0.002
<i>Philonthus laminatus</i> (Creutzer)	28.0	91.3	70.3	0.365	0.009
<i>Philonthus marginatus</i> (Müller)	2.0	22.3	12.3	0.268	0.022
<i>Philonthus varians</i> (Paykull)	0.5	5.0	2.3	0.301	0.015
<i>Pterostichus melanarius</i> (Illiger)	25.5	89.3	136.3	0.236	0.047
<i>Pterostichus strenuus</i> Panzer	11.5	33.0	33.7	0.368	0.010
<i>Quedius schatzmayri</i> Gridelli	1.0	1.7	2.7	0.477	0.002
<i>Xantholinus punctulatus</i> (Paykull)	2.5	3.0	3.3	0.303	0.023

Appendix Table A.4. Species (or genera) found to show a significant effect within the Tower field NMDS ordination of suction sample data. Mean numbers collected per treatment block are given for 0 N*, 225 N and 390 N treatments. Significance was assessed using the envfit function, which determined the goodness-of-fit statistic based on 1,000 random permutations of the data (* 0 totals are for six sample plots rather than nine in other treatments).

Species	0 N	225 N	390 N	r ²	P
Coleoptera					
<i>Aloconota gregaria</i> (Erichson)	0.0	2.7	3.7	0.320	0.021
<i>Atomaria nitidula</i> (Marsham)	4.5	7.0	7.0	0.575	0.001
<i>Calathus fuscipes</i> (Goeze)	3.0	5.0	2.0	0.304	0.030
<i>Cartodere nodifer</i> (Westwood)	0.5	1.7	1.0	0.334	0.019
<i>Cypha</i> Leach	5.0	0.0	0.0	0.512	0.001
<i>Ephistemus globulus</i> (Paykull)	0.0	1.7	5.0	0.279	0.031
<i>Mocyta fungi</i> (Gravenhorst)	31.0	37.7	28.0	0.319	0.017
<i>Protapion fulvipes</i> (Geoffroy in Fourcroy)	2.0	0.3	0.0	0.414	0.003
<i>Ptenidium pusillum</i> (Gyllenhal)	3.0	5.3	1.3	0.284	0.039
<i>Sitona lepidus</i> (Fabricius)	5.5	2.0	1.7	0.334	0.025
<i>Stenus brunnipes</i> Stephens	3.0	0.0	0.3	0.482	0.001
<i>Stenus clavicornis</i> (Scopoli)	5.0	1.0	0.3	0.419	0.003
<i>Stenus nanus</i> Stephens	5.0	1.0	0.7	0.425	0.004
<i>Tachyporus pusillus</i> Gravenhorst	3.0	4.0	8.3	0.324	0.015
Hemiptera					
<i>Acyrtosiphon Mordvilko</i> sp.A	16.0	2.7	2.7	0.372	0.007
<i>Macrosteles viridigriseus</i> (Edwards)	4.5	0.3	1.0	0.335	0.012
<i>Metopolophium</i> Mordvilko	6.5	17.7	19.7	0.522	0.001
<i>Myzus Passerini</i> sp.A	5.0	0.7	0.0	0.310	0.030
<i>Rhopalosiphum</i> Koch	2.5	36.0	39.7	0.715	0.001
<i>Sipha glyceriae</i> (Kaltenbach)	3.0	1.0	0.7	0.328	0.017
Hymenoptera					
<i>Anaphes</i> Haliday	21.0	6.7	4.0	0.345	0.010
<i>Aprostocetus</i> Westwood	13.0	6.3	2.0	0.429	0.003
<i>Gonatocerus</i> Nees	6.0	0.7	0.7	0.522	0.001
<i>Meraporus</i> Walker	7.5	1.3	1.0	0.396	0.006
<i>Phaenocarpa</i> Förster	1.0	3.3	7.3	0.375	0.014
<i>Platygaster</i> Latreille	20.0	7.0	12.0	0.266	0.033
<i>Polynema</i> Haliday	100.5	19.6	17.3	0.654	0.001
<i>Trimorus</i> Förster	71.5	27.0	17.7	0.753	0.001