Natural enemy abundance and pest density at difference scales of crop diversification

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MSc Thesis

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February 2015

Acknowledgement

I would like to thank all those who supported and helped me in this thesis period. First, I are heartily thankful to my supervisors: Dirk van Apeldoorn and Felix Bianchi in Farming Systems Ecology chair group for organising and supervising my thesis project. Their guidance, encourage and literature support led me to develop thesis proposal and conduct research successfully. I am really grateful to Felix and Dirk for passing on R statistics analysis skill. I did learn much from them and improve my scientific research skill and independence. Special thanks our technician Dine Volker who helped me get sampling facilities and materials. The most laborious and hardest part was my field sampling work and natural enemy identification. Special thanks again to Dine Volker for field work and deification. Special thanks to Bas Allema who spent personal time on helping me identify ground beetles and literature supports. I would also like to thanks my MOA classmates and friends (Yulin Yan, Shuang Liu etc.) who sacrificed their valuable personal time to help me with field sampling and identification. Last but not least, I want to express my gratitude to all of my families and friends for mental and emotional supports.

Abstract: The aim of this study was to find the appropriate scale of crop diversification with regard to pest density, natural enemy abundance and natural enemy conservation in cropping systems through field experiments in Wageningen, the Netherlands. The spatial and temporal distribution of natural enemies were determined by visual assessment, beat sampling and pitfall trap sampling at three scales of crop diversification including field, strip and plant scales. Results suggest that crop diversification is positively related to biological control potential while the difference of plant and strip scales of crop diversification need further study. It is still vital to figure out mixing crop to the appropriate scale rather than blindly pursue the more diverse the better. The Biological control function of non-crop habitats was also tested by abundance and movement of natural enemies. It demonstrated that non-crop habitats like hedges can conserve natural enemies as beneficial habitats especially after crop harvest. It is recommended that those non-crop habitats are installed in cropping systems for promoting pest control potential.

Key words: crop diversification, appropriate scale, non-crop habitats, biological control, aphid density, natural enemy abundance

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1 Introduction

1.1 Research background

In agricultural production, yield losses worldwide are not decreasing, despite of increased use of pesticides (Rusch et al., 2010). Since the green revolution has many adverse effects on environment and food safety, agricultural ecologists have therefore explored methods to reduce pesticide use while maintain high yield (Rusch et al., 2010; Letourneau et al., 2011). Agricultural and biological control methods that capitalize on biological interactions among insect pests, natural enemies and habitats, represent integrated pest management alternatives to reduce pesticides (Rand et al., 2006).,Therefore a better understanding of the relationships between pests, their natural enemies, plants and non-crop habitats is essential for the successful implementation of agricultural and biological control methods in practice.

The diversity-stability hypothesis states that the greater the biological diversity of a community of organisms, the greater is the stability of that community (Goodman, 1975). The hypothesis generated a broad interest in how to make better use of biodiversity to provide more ecosystem functions, including pest control. Indeed, establishing efficient biological pest control in crop monocultures can be challenging. Insect pests may colonize all the crop with one or few gene types (Andow, 1991). Besides, the resources such as prey and food in monocultures are insufficient to ensure that natural enemy populations perform well for the whole year (Rusch et al., 2010). To promote natural pest management in agro-ecosystems, two strategies are commonly practiced: increasing within-field crop diversity and creating semi-natural habitats near crop fields (Rand et al., 2006; Rusch et al., 2010). Within-field crop diversity (or polyculture) entails the mixing of multiple crops in the same space and/or in different time to mimic the diversity of natural ecosystems, and avoiding large stands of single crops in monocultures. Mixed cropping, intercropping, strip cropping, companion planting, weedy culture (crop with weed), nursery crop (crop with beneficial non crop), living mulches are different forms of polycultures (Andow, 1991). In polyculture, the greater extent of multifunctional agricultural biodiversity are found compared to monoculture (Gurr et al., 2003). In polycultures, generalist parasitoids and predators are typically more abundant than those in monocultures. Polyculture provide wider range of food resources for extended period during the growing season (Andow, 1991). Besides, polycultures conserve natural enemies better when facing disturbance, due to the temporal and spatial resource complementary advantages compared with large single stands crop in monocultures (Andow, 1991). In addition, literature is full of examples of experiments documenting that functional diversification of cropping systems often leads to reduced herbivore populations (Altieri, & Nicholls, 2004). In a comprehensive review Rusch et al. (2010) showed that higher crop diversity significantly reduces pest damage on crops. In explaining the potential mechanisms involved in interactions between within-field diversity and pest damage, two hypotheses have been put forward. Compared with monotypic stands, increasing vegetation diversity may suppress herbivore populations through the “dilution” of host plants which makes it more difficult for herbivore to find host plants. This hypothesis is the “Resource Concentration Hypothesis” (Tahvanainen, & Root, 1972; Root, 1973) and also bottom-up effect on pest suppression. The other hypothesis explains the herbivore pest control as the results of natural enemy that crop diversification promotes the success of natural enemies in terms of the abundance and prey/host finding efficiency. It is known as the as “Enemy Hypothesis” (Pimentel, 1961; Root, 1973) and also top-down effect.

Although increased within-field diversity is generally associated with more efficient natural control of pests in agro-ecosystems (Andow, 1991), “the more diverse the better” is not always true. It has been shown that increasing diversity can aggravate certain pest problems (Andow, 1991; Altieri, & Nicholls, 2004) due to increased crop species might provide favourable resource to herbivore pests. Besides,

simply increasing crop diversity may hinder beneficial insect activity. First, it might enhance interspecific competition or intraguild predation among natural enemies (Broatch et al., 2010). Second, natural enemies might experience difficulty to locate their prey/host insects due to the complexity of the searching environments (Sheehan, 1986; Rodriguez-Saona et al., 2012). Moreover, the research on cotton-wheat cropping system in China highlighted the importance the appropriate scale of crop diversification (Xia, 1997). Xia found cotton-wheat intercropping has an "overcapacity" for biological control of cotton aphid. It means that natural enemies are way more effective but not fully utilized in the current intercropping system, as the aphid populations are far below action thresholds. His results suggest that it is possible to increase distance between cotton and wheat from a few rows (e.g. wheat-cotton intercropping 3:2 pattern) in the current intercropping system to the "strip" scale (e.g. increasing strip width for wheat and cotton, optimum width did not be given), and maintain effective biological control of the cotton aphid. Strip cropping would be also advantageous with respect to fibre and seed quality, labour requirement, and allow more effective suppression of the cotton bollworm and verticillium wilt by cultural practices (Xia, 1997).

Therefore, low crop diversity in monoculture hold a high potential to cause pest outbreak and ineffective biocontrol due to uniform resource availability for pest and limited resources for natural enemies. However, “over diversity” of crop fields may cause interspecific competition or intraguild predation among natural enemies, more difficulty in herbivore searching and waste of mixing crops due to “overcapacity”. To find the appropriate scale of diversity of mixing crops is therefore of high importance to support functional diversity in terms of effective pest suppression and natural enemy promotion.

Both the pest and its enemies are often highly mobile and regulated at a much larger spatial scale than at the scale of the field, because they often require multiple resources, such as alternate food, hosts, and winter refuges to complete their life cycles (Tscharntke et al., 2007). Resources in agricultural landscapes vary strongly over time, as cultivated habitats provide high quality resources for only part of the year. The abrupt decline in habitat quality due to harvesting leads to the active emigration of natural enemies from the cultivated areas toward more stable non-crop habitats (Rusch et al., 2010). Understanding determinants of biological control management requires spatial scales exceeding the field scale, namely landscape scale (Schellhorn et al., 2014). Non-crop habitats, such as hedgerows, field margins, fallows, flower strips and meadows, support a large number of herbivore and natural enemy species, as they provide a more stable habitat than annual crops. Generally, these habitats host a larger proportion of neutral and beneficial arthropods than pests (Denys, & Tscharntke, 2002; Marshall, 2004; Thomas et al., 2002). Non-crop habitats are considered as important sources of natural enemy abundance, potentially enhancing the biological control of pests in crops if these are in enough proximity to the field (Tscharntke et al., 2007). Both empirical and modelling studies have demonstrated that the quality and quantity of semi-natural habitat patches adjacent to the crop may affect the natural enemy abundance and pest control in crop field (Bianchi, & Wäckers, 2008; Olson, & Wäckers, 2007). However, spillover effects of natural enemies from crop to non-crop habitats may also occur depending on the location of favourable resources (Rusch et al., 2010). The relationships between crop and non-crop habitats are complex and may be antagonistic (Rand et al., 2006). A further insight into the natural enemy movement between field and non-crop habitats is vital for non-crop habitats installation in agro-ecosystems and helps to make better use of pest control potential of those habitats.

1.2 Objectives

The aims of this study were twofold. One objective is to find the appropriate scale of crop diversification with regard to pest density, natural enemy abundance and enemy conservation in cropping systems. The term “conservation” means the performance of natural enemy after crop

harvest in this study. The spatial and temporal distribution of natural enemies were determined at three scales of crop diversification including field, strip and plant scales. Another objective is to get insight into bio-control function of non-crop habitats based on movement and distribution of natural enemies.

These aims led to the three following research questions:

I. What scale of mixing crops results is the most effective functional diversity to support pest suppression and natural enemy abundance?
II. What scale of mixing crops conserves natural enemies the best after harvest?
III. What is the effect of non-crop habitat on natural enemy movement in the crop growing season and after harvest?

Hypotheses were formulated based on above-reviewed literature to get "the more diverse the better" or "the appropriate is the best" with respect to crop diversification on pest control effect. The intermediate level of crop diversification at the strip scale in this study was expected to be the most effective among three scales, in view of above-mentioned problems for "low diversity" and "over diversity", and Xia's suggestion (Xia, 1997) as well. Besides, non-crop habitats would probably provide important favourable resources to natural enemies especially after crop field harvest (Rand et al., 2006 ; Rusch et al., 2010). On the basis of these research questions and previous findings, corresponding hypotheses were formulated:

I. Strip scale of mixing crops is the most effective for reducing pest population and increasing natural enemy abundance. The pest density at strip scale is lower than at field scale, but similar to that at plant scale; in contrast natural enemy abundance is higher at both strip and plant level than at field level, but are similar between strip and plant levels.

II. Strip scale of mixing crops conserves natural enemies effectively after crop harvest. The strip cropping system with hedge and flower strip is expected to have more abundant natural enemies after crop harvest than the large wheat field, but is similar at the strip-plant scales.

III. Non-crop habitats play a clear role on natural enemy movement in late season after crop harvest while not obvious in the crop growing season. Natural enemies that inhabit and move to hedge are more abundant than those in crop field after crop harvest, while in the crop growing season movement those from and to the hedge will be balanced.

2 Materials and Methods

2.1 Experimental site and design

The experimental site was located in the certified organic farm of Droevendaal (51°59'30 "N 5°39'5" E), an experimental farm of Wageningen University in Wageningen, the Netherlands (Appendix i). This research was a part of a multi-year project at the Droevendaal experimental farm. In the project, resilient farming system through strip cropping will be investigated using a 6 years rotation. In the experiment a minimum of five different crops have been grown as strip crops with crop rotation that fulfil the requirements of the European diet. In 2014, the first year rotation of crops were wheat, potato, maize, mustard and grass clover mixtures. Strip cropping strips were three-meter wide which is the working width of the machinery. The other large field with single wheat cropping (30m x 120m) has been implementing in 2014, which was regarded as field scale mixing crop/low diversity (Appendix ii).

One objective of this experiment is to identify appropriate spatial scale of mixing crops to obtain desired pest control effect and natural enemy conservation. Therefore, the strip cropping experiment was split in two treatments (Figure 1). One treatment (non-mix treatment) had limited mixing or a single crop within the strip as strip scale crop diversification in this study. The other treatment (mix treatment) the crop was grown in a mixed stand with two or more crops or different cultivars (Appendix ii) defined as plant scale crop diversification in this study. For example, wheat strip at non-mix treatment was only wheat single cropping while the mix treatment was an intercrop of wheat and fababean. Flower strip, mustard strip and hedge composition were the same in both treatments.

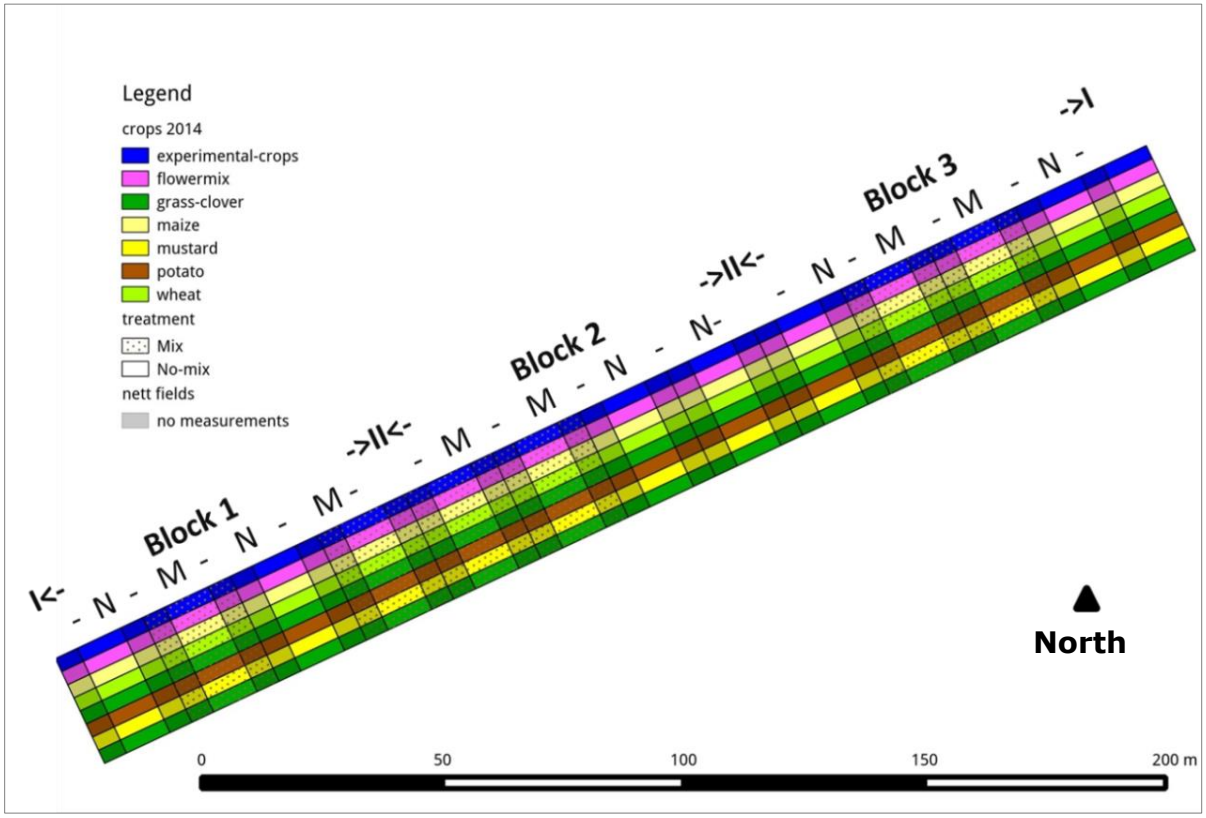

Figure 1 Arrangement of two treatments and crops in three blocks in strip cropping experiment, where 'N' refers non-mix treatment(strip scale), 'M' refers to mix treatment (plant scale); experimental-crops refer to test crops combinations for next year which are not included in this study. Crop species and composition in strips see Appendix ii, iii and iv.

There were six plots/replicates and two treatments resulting in twelve plots. In three block, two replicates of the two treatments per block were randomly located (Figure 1). Each crop plot was in total 3m x 20m, including 5 meter buffer at each side. The buffer had the same crop as the treatment but no measurement was conducted in this buffer. So the measurement area was 3m x 10m. To maximize potential biological control effect, one row of 3 meter was sown with a perennial flower strip mixture which constituted of selected flowers species that were regarded as beneficial habitat for parasitoids and predators (Appendix iii). These flowers were based on the work of Paul C.J. van Rijn (Institute for Biodiversity and Ecosystem Dynamics (IBED) University of Amsterdam). This flower strip is not part of the rotation. The opposite side of flower strip is a ten-year old hedge (Appendix iv) with field border.

In this experiment the herbivore pest in wheat strip was taken into account since crop of the large single cropping field was also wheat in this year of sampling. Besides, wheat is a major staple crop

which suffers from pest attack. Moreover, from a cropping system perspective, each strip and field border were taken into consideration.

Three aspects of cropping diversification were tested: 1) pest density and natural enemy abundance, 2) the conservation effect on natural enemies, and 3) natural enemy movement. Below the scale of study and season are summarized:

Table 1 Scale and season of study for three aspects of crop diversification

Aspect	Season and scale
1 Pest density & Natural enemy abundance	**pest density & natural enemy abundance at three scales of crop diversification/mixing crops in the crop growing season** Low diversity: large field single wheat system (field scale) Mid diversity: strip cropping Non-mix treatment (strip scale) High diversity: strip cropping Mix treatment (plant scale)
2 Conservation effect	**natural enemy abundance at three scales of mixing crops after harvest** Low diversity: large field single wheat system (field scale) Mid diversity: strip cropping Non-mix treatment (strip scale) High diversity: strip cropping Mix treatment (plant scale)
3 Arthropod movement	**natural enemy movement to non-crop habitat in early and late season at the strip scale** movement to hedge and to crop field in crop growing season movement to hedge and to crop field after crop harvest

2.2 Sampling methods

Pest and natural enemy abundance was quantified using different sampling methods including visual assessment, beating sampling and pitfall trap sampling. Because arthropods are more abundant or move more frequently on edges (Allema, 2014), the edge effect were excluded during sampling, and thus only the central row of plots were sampled (Appendix v).

2.2.1 Visual assessment

To find the most effective diversity scale of mixing crops, visual assessment was conducted at three scales of mixing wheat: single wheat cropping field (field scale), wheat strip cropping (strip scale) and wheat-fababean intercropping (plant scale).

Aphids (Hemiptera *Aphididae: Macrosiphum avenae, Metopolophium dirhodum, Rhopalosiphum padi , Aphis nasturtii and Macrosiphum euphorbiae*) are serious pest for wheat leading to yield loss, by direct damage due to sieve drain and plant reaction and by indirect damage, often the most important, due to virus transmission (Dedryver et al., 2010). Aphid parasitoid wasps (*Braconidae, Aphidiinae*) are important biocontrol agents on aphids (Müller, & Godfray, 1999). The aphids and parasitized aphids were objects of this sampling method.

The aphid density and parasitoid wasps were measured by visual assessment on wheat plants. For visual assessment 1 tiller per wheat plant and 10 plants per plot were randomly selected in R. The number of aphids and parasitized aphids (or mummies) on each plant were recorded through visual observation with a loupe. At strip and plant scales, there were 6 replicates for each scale. At the field scale, there were 3 replicates in the wheat single cropping field. In total 150 wheat tillers were visually assessed for aphids and parasitized aphids on 23rd July, 2014.

2.2.2 Beat sampling

To investigate aboveground natural enemies a beat sampling method was conducted, at three scales of mixing wheat: single wheat cropping field (field scale), wheat strip cropping (strip scale) and wheat-fababean intercropping (plant scale).

The aboveground important natural enemies of aphids are aphid parasitoid wasps (*Braconidae, Aphidiinae*), and aphidophagous predators: larvae and adults of ladybeetles (*Coleoptera, Coccinellidae*), larvae of hoverflies (*Diptera, Syrphidae*) and larvae of lacewings (*Neuroptera, Chrysopidae*) (Müller, & Godfray, 1999). Generalist insect predators are important agents in pest control because they consume wide range and large numbers of prey (Rotheray, 1989; Miranda et al., 2011). Generalist predators such as spiders (*Araneae*), harvestmen (*Opiliones*) and damsel bug (*Nabidae*) were also taken into account during beat sampling.

These aboveground natural enemies were sampled by beating the wheat plants 30 times with a stick (35cm long), along the middle row of each plot (Appendix v) parallel to the length (10m) of the field. The falling arthropods were collected in a white tray (30 cm x 30cm) and counted. Considering the beat range by hand (0.5m), the sampled area was estimated as $5m^2$ (0.5mx10m). The arthropods were subdivided over the following groups of natural enemies: spiders, harvestmen, damsel bugs, ladybeetles, lacewings larvae, hoverflies and their larvae. There were 6 replicates at strip and plant scales, and 3 replicates at field scale. In total, 450 beat samples were conducted for natural enemy groups on 30th July, 2014.

2.2.3 Whole-system pitfall trap sampling

Among ground dwelling predators, mainly spiders (*Araneae*), rove beetles (*Staphylinidae*) and ground beetles (*Carabidae*) have a great potential to suppress pest populations. They have a high abundance and wide prey spectrum on eggs, larvae and adults of different pests including aphids, caterpillars, leaf beetles, thrips, spider mites and whiteflies (Symondson et al., 2002).

Pitfall trap sampling has the advantage of being a quick and effective method that is commonly used for sampling ground-dwelling arthropods (Cheli, & Corley, 2010). Current literature shows that pitfall traps can be used in a variety of ways: to evaluate the distribution of macro-invertebrates in diverse ecosystems at different scales, to describe activity patterns, habitat associations as well as to establish relative species abundances, or the effects that disturbance can have on biodiversity (Niemelä et al., 1992; Noemí et al., 2006; Pekár, 2002). Therefore with the pitfall traps, ground arthropods abundance, conservation effect and movement were measured. Here the term “whole-system pitfall trap sampling” (2.2.3) means sampling the ground-dwelling enemies in all crop strips of agro-system which then is distinguished with bi-direction pitfall sampling (2.2.4).

Roofed pitfalls were used to reduce the effect of rain and the arthropods falling from plants. Following the method of Allema (2014) a trap contained 100 ml of preservative (propylene phenoxetol, propylene glycol, and water in the ration 1:9:90) and some unscented detergent to break the surface tension and accelerate drowning of the arthropods. Many preservatives are available for pitfall trapping, the preservative mentioned above were chosen because they were least toxic for humans and gave good performance when conserving specimens. Propylene phenoxetol is also used as relaxing agent and propylene glycol is used, among others, as antifreeze (Allema, 2014).

Pitfall trap sampling was used for ground dwelling predators at three scales of mixing crops from whole system perspective: a mono cropping wheat cropping system (field scale), a strip cropping of non-mix treatment (strip scale) and a strip cropping of the mix treatment (plant scale) (Figure 2). One pitfall trap (Ø 8 ½ cm) with roof (Ø 12 ½ cm) was installed per plot in each crop strip including the

field border of the three treatments. The pitfalls in the strip cropping experiment were randomly located in the middle of the strip by using R. In the large wheat mono cropping system, the pitfalls were placed perpendicular to the field margin with a 3m distance between the pitfalls (Figure 2). Measurement took place on 27th July (mid growing season) and 9th October (two weeks after harvest). The sampling locations were kept the same during two sampling times. Each time there were 1 pitfall x 8 strips x 2 treatment x 6 replicates = 96 pitfalls in the strip cropping experiment and in the large wheat field 1 pitfall x 8 x 3 replicates = 24 pitfalls, summing up to120 pitfalls in the all sampling fields. The pitfall traps were put in the fields for two days and collected to identify in laboratory.

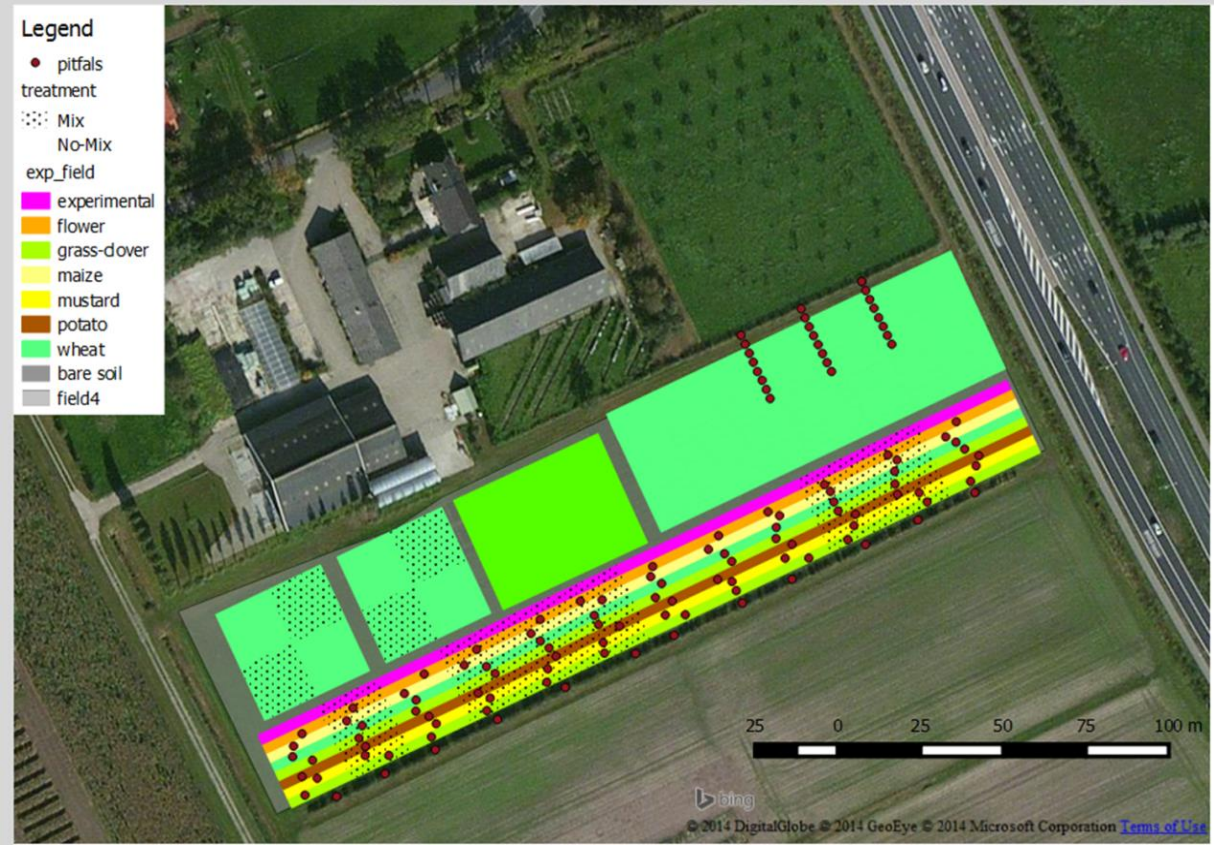

Figure 2 Pitfall trap locations for three scales of crop diversification

After crop harvest in September, the fields were sown with green manures in harvested crop strips (Appendix vi). At field scale a mixture of three species was sown, at the strip scale one species of green manure was sown in each strip, and at plant scale a mixture. Still, from the whole system perspective, plant scale, strip scale and field scale had high, mid and low plant heterogeneity respectively, which means most kinds of green manure species were at plant scale, middle at strip scale and least at large wheat field. The green manure at field scale was sown earlier than those at strip and plant scales. The hedge and flower strip were not disturbed during the harvested in the strip cropping experiment.

2.2.4 Bi-direction pitfall trap sampling

The amount of natural enemies moving to and away from the hedge was measured in a grassy edge between the hedge and crop field. In the interface of hedge and crop field, one set of bi-direction pitfall trap consists of four pitfalls and one screen (Figure 3 and Appendix vii). The two pitfalls on the same side (hedge or crop field) were combined as one sample. The sampling was conducted only at strip cropping non-mix treatment (strip scale). Measurements were conducted on 31st July and 13th October. The sampling locations were kept the same for the two samplings (Appendix viii) resulting in 1 interface x 6 replicates x 4 pitfalls =24 samples per sampling event in field border. The pitfalls were placed in the field for four days.

Figure 3 Bi-direction pitfall set

2.2.5 Natural enemy identification

Natural enemies by beat sampling (2.2.2) were identified in the field and afterwards released. All the pitfall trap samples (2.2.3 and 2.2.4) were taken to laboratory for identification. Natural enemies were identified to different groups and levels: spider (*Araneae*) and harvestman (*Opiliones*) to order level, ground beetles (*Carabidae)* to species or genus level (e.g. *Clivina fossor*), rove beetles (*Staphylinidae*) to family level, other groups at least to family level (e.g. hoverflies (*Syrphidae*) and lacewing (*Chrysopidae*)) (Rotheray, 1989; Chinery, 2005; Luff, &Turner, 2007). In this study, species richness of natural enemy was also taken into account. Because natural enemies were identified to different scales, "natural enemy richness" refers to the number of natural enemy groups.

2.3 Statistics analysis

For the statistical analysis, the aphid density data (2.2.1) and above-ground natural enemy data (2.2.1 and 2.2.2) were used to identify the most effective scale of mixing wheat.

For whole-system pitfall data (2.2.3), the first time sampling data on 27th July was used for ground natural enemy abundance to identify the most effective scale of mixing crops and tailor key factors that result in enemy abundance. Sampling data of two sampling periods were analysed to get insight into essential factors of crop diversification that retain ground-dwelling enemies, especially after disturbance by harvest. Natural enemy abundance, distribution and enemy group richness were analysed.

Natural enemy movement (2.2.4) and enemy distribution from data (2.2.3) were analysed to investigate the effect of the hedge (non-crop habitat) on the spatial distribution of arthropod natural enemies.

The statistics analysis was conducted with R. The initial data exploration showed that the count data were not normally distributed. Normality of the count data was also tested with log and squared root transformations, ending with no much improvement. Generalized linear modelling was considered in this data analysis with R. Generalised linear models (GLM) are commonly used for ecological experiments with count data, proportional data, and zero-inflated count data etc. (Zuur et al., 2009).

Because the data were counts, Poisson, quasi-Poisson and negative binomial error distributions were tested sequentially to select the best model. The model with the lowest AIC value was selected as the

best fit. Besides, if there were many zeros (e.g. in aphid density data), an extra test with GLM Zero-inflated negative binomial regression was performed. Proportional data (i.e. fraction of parasitized aphids) in this study was tested by GLM with binomial error distribution. For model selection, treatment effect and block effect were both taken into consideration. Block effect is excluded in the final model when it has insignificant effect ($P>0.1$). When there are more than 2 treatments, multi-comparison of pairwise treatments by post-hoc test with Tukey Contrasts was conducted for a more detailed difference among treatments (Hothorn, et al., 2008). Mean and SEM values are reported throughout the report.

3 Results

3.1 Aphid density

Blocks showed to have no significant (*P*=0.8745) effects on aphid density (Appendix ix). Therefore, the model excluded the block effect. The result of crop diversity effect on aphid density is shown as aphid density (aphid individual/ plant) of every measurement in three treatments (Figure 4). For the aphid density at three diversity scales of wheat cropping, the highest density (4.13±0.75) was found in the large field with single wheat cropping. When compared with aphid density at field scale (Table 1), the aphids density was lower in wheat strip cropping (2.52±0.30) and in wheat-fababean intercropping (2.60±0.49).

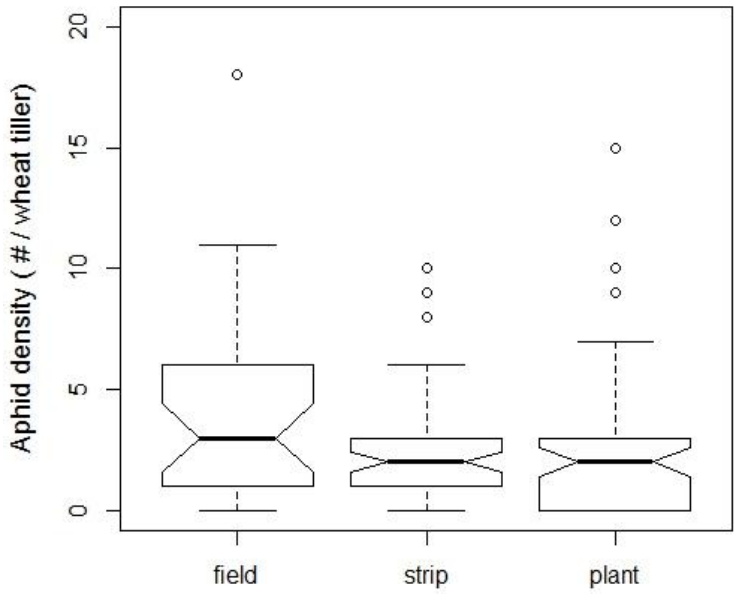

Figure 4 Aphid density in three treatments where 'field' refers to large field single wheat cropping, 'strip' refers to wheat strip cropping and 'plant' refers to wheat-fababean intercropping. Lines extending vertically from the boxes (whiskers) indicate variability of measurements outside the upper and lower quartiles. Outliers are observation points outside 1.5 times the interquartile range above the upper quartile and below the lower quartile plotted as individual points.

On the basis of the optimal GLM model for aphid density, the pairwise comparison between treatments was performed by post-hoc analysis with Tukey's procedure. Using this conservative criterion, aphid density was only marginally significant lower at strip scale mixing wheat than at field scale (*P*=0.0918). Plant-field comparison gave no significant difference (*P*=0.1231), although the *p*-value was close to 0.1. However, the contrast between the strip-plant treatment (*P*=0.9857) was not significant with a *p*-value close to 1.

Table 2 Multi-comparison of treatments on aphid density by post-hoc test with Tukey Contrasts, on the GLM, negative binomial error distribution

Pairwise comparison	Estimate	Std. Error	Pr(>|z|)	95% CI		Sig.
				lwr	upr	
strip - field== 0	-0.50	0.24	0.0918	-1.05	0.06	.
plant - field== 0	-0.46	0.24	0.1231	-1.02	0.09	
plant - strip== 0	0.03	0.20	0.9857	-0.44	0.51	

Significance codes: *P* < 0.001 = '***', P< 0.01 = '**', *P*< 0.05 = '*', *P*< 0.1 = '.' CI= Confidence interval

3.2 Natural enemy abundance

The plant diversity effect on natural enemy abundance was tested with parasitized aphid via visual assessment, aboveground enemies by beat sampling and ground-dwelling enemies through pitfall samples.

3.2.1 Parasitized aphid by visual assessment

Parasitized aphid mummies indicate presence of parasitoid wasps. Due to the variable sum of sampled aphids per wheat tiller, the fraction of parasitism was tested in different treatments based on binomial GLM model (Appendix x). 50% of the samples at plant scale were found with parasitized aphids, while strip and field scale ended up with the presence of aphid parasitism at only no more than 20% of sampled wheat tillers (Figure 5). Parasitism fraction at the plant scale was significantly higher than mixing at the strip and field scales ($P< 0.01$) (Table 3). When mixing crops at the plant scale parasitism was on average 18.90%±4.08%, at the strip scale 4.21%±2.01% and at field scale 7.78%±3.87%. Parasitism at the strip and field scales displayed no marked difference according to pairwise comparison of treatments on the fitted model (Table 3).

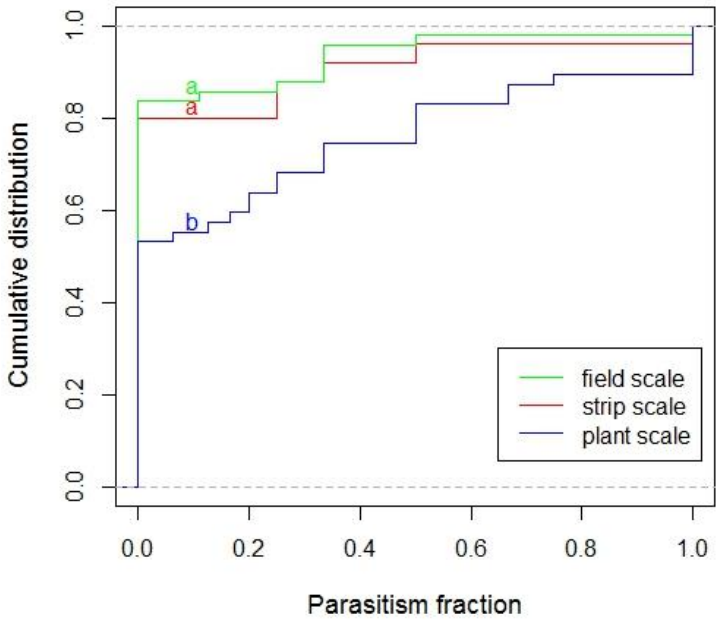

Figure 5 Cumulative distribution of parasitism fraction in three treatments where 'field' refers to large field single wheat cropping, 'strip' refers to wheat strip cropping and 'plant' refers to wheat-fababean intercropping. Different letters above the lines indicate significant difference ($P<0.01$) among treatments (Table 3)

Table 3 Multi-comparison of treatments on parasitism fraction by post-hoc test with Tukey Contrasts, on GLM binomial (logistic) regression

Pairwise comparison	Estimate	Std. Error	Pr(>|z|)	95% CI		Sig.
				lwr	upr	
strip - field== 0	0.00	0.47	0.9999	-1.08	1.09	
plant - field== 0	1.24	0.39	0.0040	0.33	2.14	**
plant - strip== 0	1.23	0.35	0.0017	0.39	2.07	**

Significance codes: $P < 0.001$ = '***', $P< 0.01$ = '**', $P< 0.05$ = '*', $P< 0.1$ = '.' CI= Confidence interval

3.2.2 Aboveground natural enemy from beat sampling

Beat sampling data showed a positive relationship between natural enemy abundance and crop diversity (Figure 6). The analysis of a GLM with Poisson error distribution (Appendix xi) indicated that the pooled enemy amount per replicate/plot was clearly more abundant (P<0.001) at both plant scale and strip scale than that at field scale (Table 4). Besides, the pairwise comparison showed the pooled enemies individuals were higher at plant scale than that at strip scale (P=0.0249).

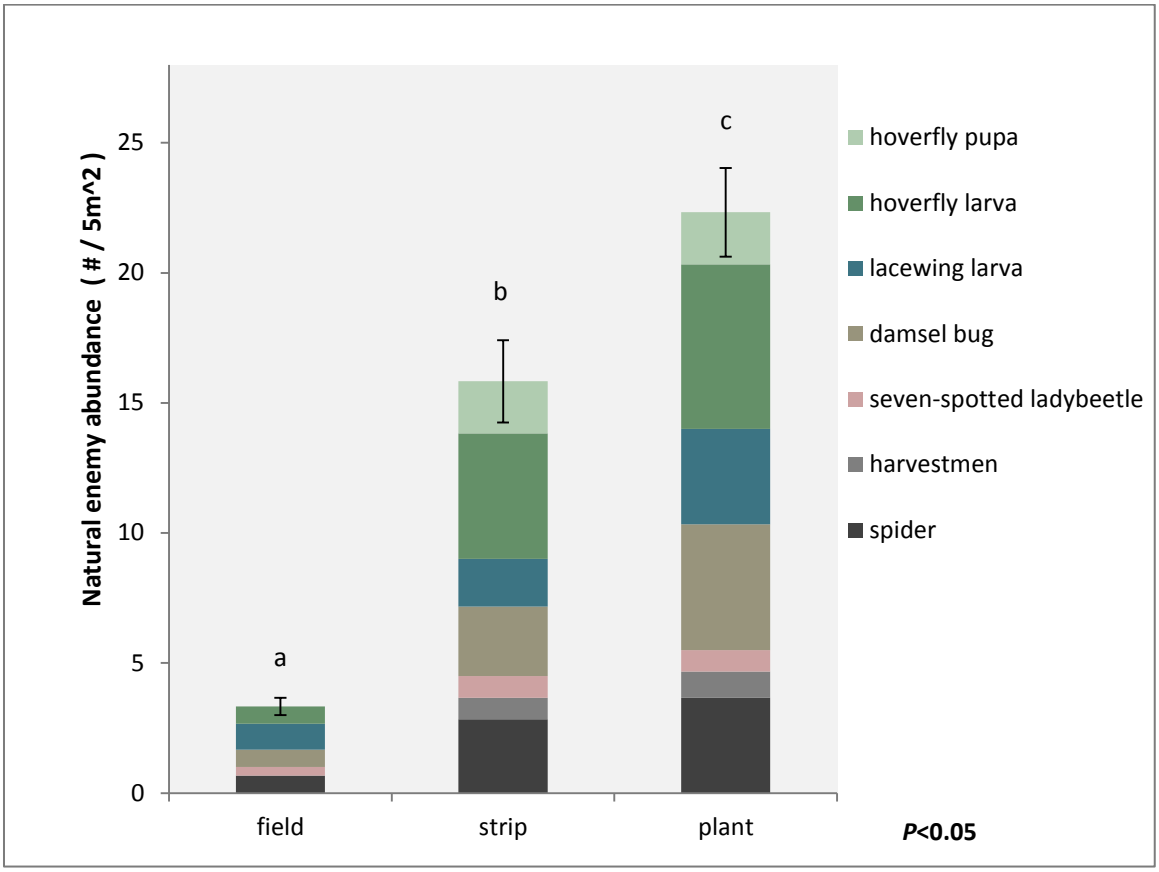

Figure 6 Aboveground natural enemy abundance and enemy groups composition in different crop diversification treatments where 'field' refers to large field single wheat cropping, 'strip' refers to wheat strip cropping and 'plant' refers to wheat-fababean intercropping. 5m^2 is the calculated beat area with stick in one sampled plot. The absence of certain color suggests that enemy group has not been found during sampling. Different letters above the bars indicate significant difference of enemy abundance (P<0.05) among treatments (Table 4).

Table 4 Multi-comparison of treatments on aboveground natural enemy abundance by post-hoc test with Tukey Contrasts, on GLM, Poisson error distribution

Pairwise comparison	Estimate	Std. Error	Pr(>|z|)	95% CI		Sig.
				lwr	Upr	
strip - field== 0	1.56	0.33	<1e-04	0.79	2.32	***
plant - field==0	1.90	0.33	<1e-04	1.15	2.66	***
plant - strip== 0	0.34	0.13	0.0249	0.04	0.65	*

Significance codes: P < 0.001 = '***', P< 0.01 = '**', P< 0.05 = '*', P< 0.1 = '.' CI= Confidence interval

With regard to natural enemy richness, there were 5 different natural enemy groups found in the large wheat field, while 7 groups were found at strip and plant scales in the strip cropping system (Figure 6). During beating sampling, neither hoverfly larva nor harvestmen were found in the large wheat field. On average three enemy groups per replicate were found at the field scale and, six groups at both strip and plant scale of mixing crops. However, the pairwise comparison showed no significant difference in enemy richness among treatments (Appendix xi)

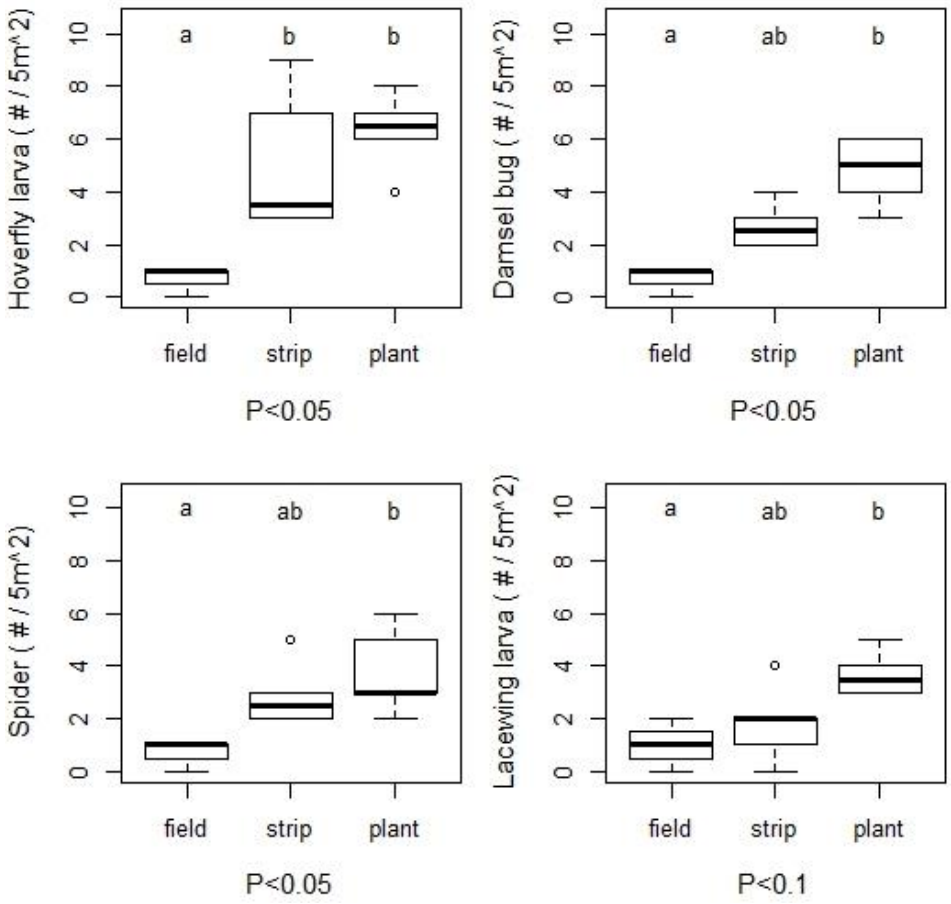

Figure 7 Abundance of four most abundant natural enemy groups in three treatments where 'field' refers to large field single wheat cropping, 'strip' refers to wheat strip cropping and 'plant' refers to wheat-fababean intercropping. 5m^2 is the calculated beat area with stick in one sampled plot. Different letters above the boxes indicate significant difference of natural enemy abundance among treatments within boxplot. Lines extending vertically from the boxes (whiskers) indicate variability of measurements outside the upper and lower quartiles. Outliers are observation points outside 1.5 times the interquartile range above the upper quartile and bellow the lower quartile plotted as individual points.

A more detailed analysis on the four most abundant enemy groups from beat sampling indicated that increased crop diversification positively influence the abundance of hoverfly larva, damsel bug, spider and lacewing larva, However, differences between crop diversity at the strip and plant scale were not significant (Figure 7).

An interaction, of treatment and block effects on natural enemy abundance for pooled natural enemy revealed that natural enemy in the strip cropping system showed higher abundance in block 2. However, this block effect was not included (*P*=0.2030) in final model based on insignificant influence (Appendix xi).

3.2.3 Ground-dwelling enemy by whole-system pitfall sampling

The Generalized Linear Model with a negative binomial error distribution (Appendix xii) indicated that a significant higher abundance of natural enemies at the strip (P<0.01) and plant scale (P<0.001) in comparison with the field scale on July (Figure 8). Besides, the plant scale system had higher natural enemy abundance than the strip scale (Figure 8). However, the pairwise Tukey contrasts between plant-strip scales indicated the difference (P=0.2835) was not significant (Table 5).

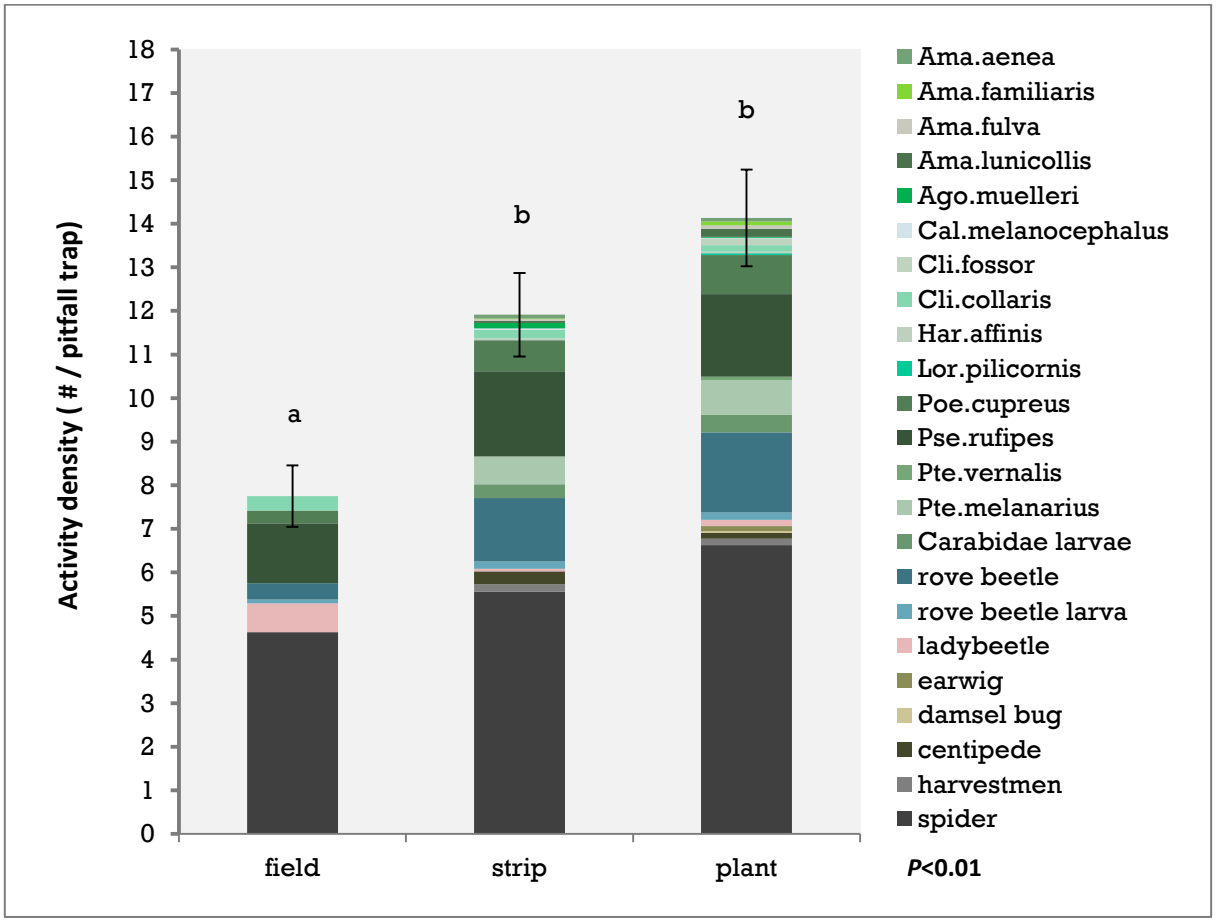

Figure 8 Activity density (number of individuals collected) and composition of ground-dwelling natural enemies by pitfall sampling in July in different crop diversity treatments, where 'field' refers to large field single wheat cropping system, 'strip' refers to strip cropping non-mix system and 'plant' refers to strip cropping mix system. Absence of certain colour suggests that enemy group was not found during sampling. Different letters above the bars indicate significant difference (P<0.01) of both natural enemy abundance and richness among treatments (Table 5 and Table 6).

Table 5 Multi-comparison of treatments on activity density of ground-dwelling enemies by post-hoc test with Tukey Contrasts, on GLM, negative binomial error distribution

Pairwise comparison	Estimate	Std. Error	Pr(>|z|)	95% CI		Sig.
				lwr	upr	
strip - field== 0	0.43	0.15	0.0099	0.08	0.77	**
plant - field==0	0.60	0.15	0.0001	0.26	0.94	***
plant - strip== 0	0.17	0.11	0.2835	-0.09	0.44	

Significance codes: P < 0.001 = '***', P< 0.01 = '**', P< 0.05 = '*', P< 0.1 = '.' CI= Confidence interval

As to natural enemy richness, only 7 different natural enemy groups were found in total at field scale, while 18 groups found at strip scale and 23 groups at plant scale (Figure 8). For whole-system pitfall

sampling, enemy groups per pitfall (2.54±0.23) at field scale was found significantly lower (P<0.01) than the other two treatments, while enemy groups per pitfall at strip (4.00±0.22) and plant scales (4.40±0.27) did not show significant differences (Table 6).

Table 6 Multi-comparison of treatments on ground-dwelling enemy richness by post-hoc test with Tukey Contrasts, on GLM Poisson error distribution

Pairwise comparison	Estimate	Std. Error	Pr(>|z|)	95% CI		Sig.
				lwr	upr	
strip - field== 0	0.45	0.15	0.0056	0.11	0.80	**
plant - field==0	0.55	0.15	0.0005	0.21	0.89	***
plant - strip== 0	0.09	0.10	0.6058	-0.14	0.33	

Significance codes: P < 0.001 = '***', P< 0.01 = '**', P< 0.05 = '*', P< 0.1 = '.' CI= Confidence interval

Detailed analysis on four enemy groups of pitfall sampling indicated that the increased crops diversity was positively related to the abundance of spiders, rove beetles and ground beetle *Poecilus cupreus* (Figure 9). However, ladybeetle abundance was significant higher at the field scale than at the other treatments. The abundance of these four enemy groups was no significant difference in strip-plant comparison.

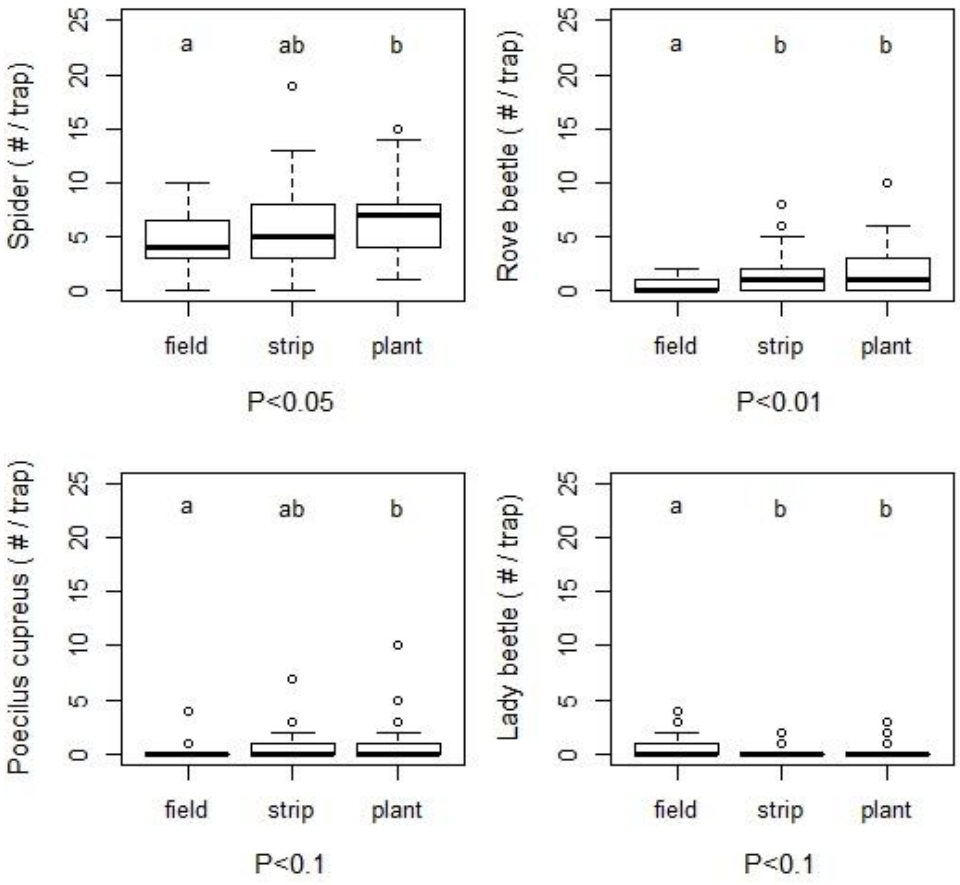

Figure 9 Activity density of four natural enemy groups by pitfall sampling in different crop diversity treatments in July. Different letters above indicate significant difference among treatments within boxplot Lines extending vertically from the boxes (whiskers) indicate variability of measurements outside the upper and lower quartiles. Outliers are observation points outside 1.5 times the interquartile range above the upper quartile and bellow the lower quartile plotted as individual points.

Natural enemy abundance in the pitfalls at the same distance of the hedge of three treatments were performed by pairwise Tukey contrasts for 8 different distances, respectively (Figure 10). Firstly, natural enemy activity density was significantly (P<0.01) higher in hedge, the first and second grass-clover strips of strip scale and plant scale than that in the same distance from the hedge at field scale, while the difference between strip scale and plant scale was not statistically significant for these three strips. Secondly, mustard and flower strips at the field scale had a significant lower natural enemy abundance than at the plant scale. Meanwhile, differences were not obvious in plant-strip scale comparison or field-strip scale comparison. Thirdly, neither the wheat strip nor maize strip in three treatments had significant difference on activity density of natural enemies. Only in the strip 4 where there was wheat at field scale, potato at both strip and plant scale, natural enemy abundance at field scale was slightly higher than that at strip and plant scale with significant difference (P<0.05). Again, no significant difference between potato strip at strip and plant scale.

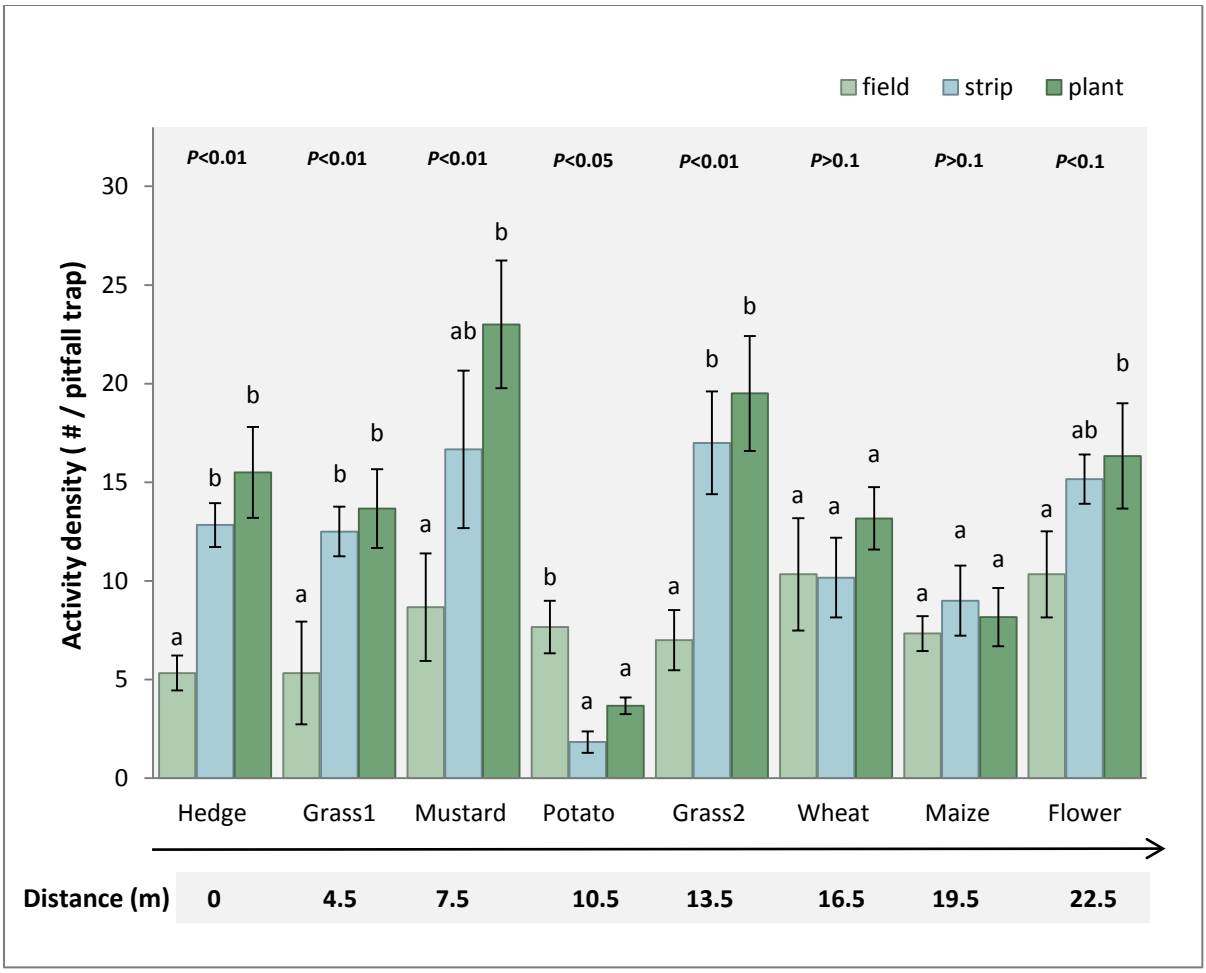

Figure 10 Activity density (number of individuals collected) of ground-dwelling natural enemies in the same strip among three treatments by pitfall sampling in July, where 'field' refers to large field single wheat cropping system, 'strip' refers to strip cropping non-mix system and 'plant' refers to strip cropping mix system. From strip 1 to strip 8 at strip and field scale, the strip element is hedge, grass1, mustard, potato, grass2, wheat, maize, flower mix respectively. At field scale, only strip 1 is hedge, the rest 7 strips are all wheat. Different letters above the bars indicate significant difference of the same strip among treatments.

In the strip 6 where crop element is wheat for all treatments, there was no significantly different according to pairwise comparisons (Table 7). The activity density was 10.33±2.84, 10.16±2.02 and 13.17±1.58 at field, strip and plant scale, respectively.

Table 7 Multi-comparison of treatments on collected ground-dwelling enemy individuals from wheat strip by post-hoc test with Tukey Contrasts, on GLM Poisson error distribution

Pairwise comparison	Estimate	Std. Error	Pr(>|z|)	95% CI		Sig.
				lwr	upr	
strip - field== 0	-0.02	0.22	0.9970	-0.53	0.50	
plant - field==0	0.24	0.21	0.4841	-0.25	0.74	
plant - strip== 0	0.26	0.17	0.2800	-0.14	0.66	

Significance codes: *P* < 0.001 = '***', *P*< 0.01 = '**', *P*< 0.05 = '*', *P*< 0.1 = '.' CI= Confidence interval

Comparison of mean of collected enemy individuals per pitfall was performed with Tukey contrasts in different strip elements within treatment for the three treatments (Figure 11). Firstly, within large wheat single cropping system, natural enemy individuals were not significantly different in the wheat field and the adjacent hedge. Secondly, in the strip cropping system, enemy abundance was significantly lower in potato strip than that in the other seven strips. Natural enemies in the maize strip were significant less abundant than those in mustard strip and the second grass-clover strip. Except for comparisons mentioned above, paired comparisons showed no significant difference of other paired plant elements at strip scale. Thirdly, in the most crops-diverse cropping system, enemy abundance was significantly lower in the potato strip than those in other strips. Enemy individuals in maize strip were significant less abundant than those in hedge, mustard, the second grass-clover and flower strip. Significant less enemy individuals were found in wheat strip than in mustard strip. Except for these comparisons, other paired plant elements at plant scale showed no significant difference (Figure 11).

Additionally, the analysis on best model selection for pooled natural enemy abundance indicated an interaction of treatment and block effects on natural enemy individuals (Appendix xii). It showed that difference between plant-strip comparisons was larger in block 2 and block 3 than that in block 1. Nevertheless, the final model (GLM, negative binomial model, Figure 9) took only treatment effect (*P*=0.0002) rather than also adding block effect (*P*=0.1546) on the basis of their *p*-values.

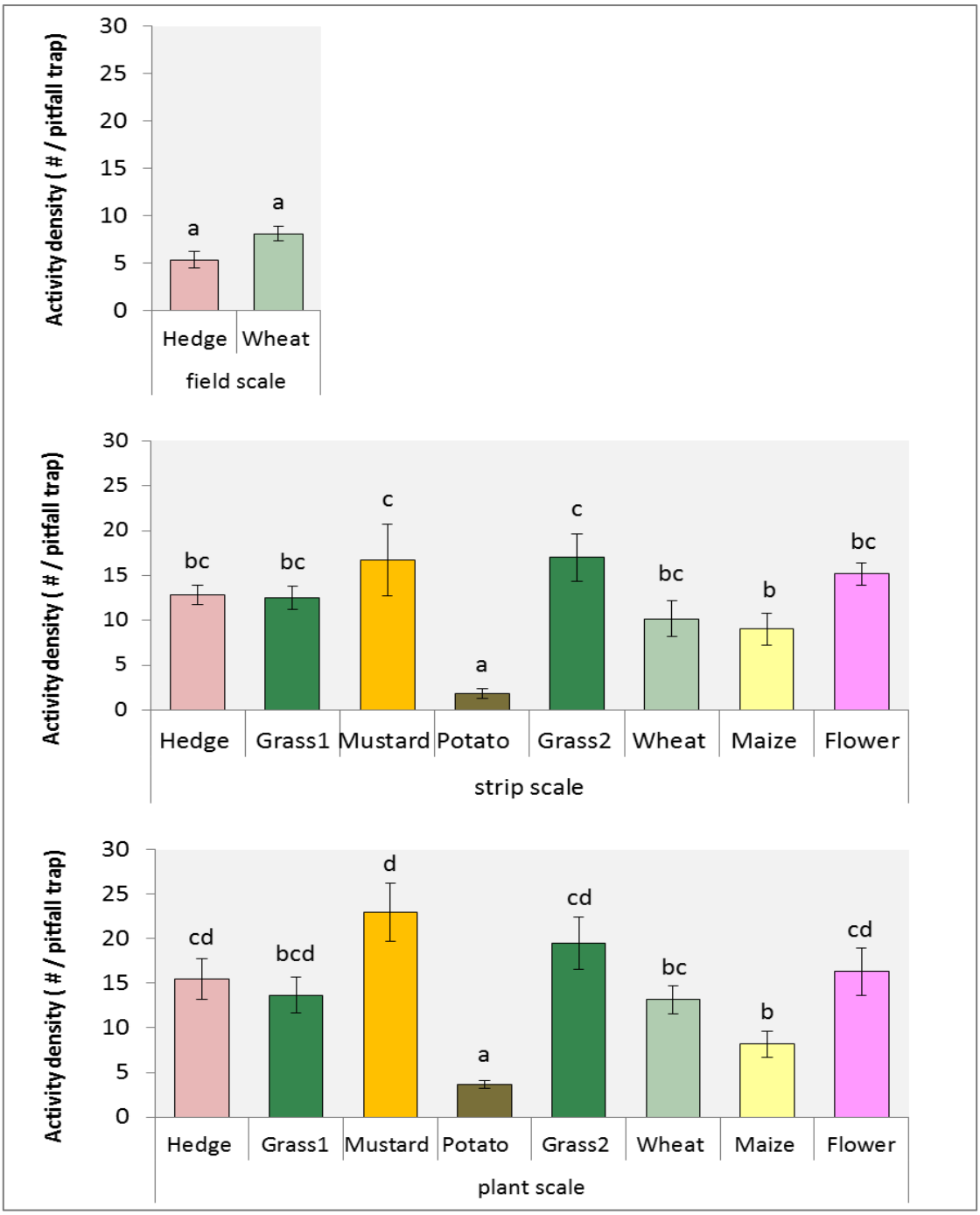

Figure 11 Activity density (number of individuals collected) of ground-dwelling natural enemies in different strip elements within treatment by pitfall sampling in July, where 'field' refers to large field single wheat cropping system, 'strip' refers to strip cropping non-mix system and 'plant' refers to strip cropping mix system. The absence of colors suggests that crop element did not be installed in that treatment. Different letters above bars indicate significant difference (at least *P*<0.1) among different crop strips within treatment (Appendix 12) .

3.3 Natural enemy conservation

Natural enemy abundance and composition were measured by whole-system trap pitfall sampling in October when crops had been harvest and re-sowed green manure had emerged (Appendix vi). The result showed no significant differences among treatments in terms of pooled natural enemy

abundance, enemy richness, and the abundance of four most abundant groups: spider *Carabidae* larvae, rove beetle and harvestmen (Figure 12 and Appendix xiii).

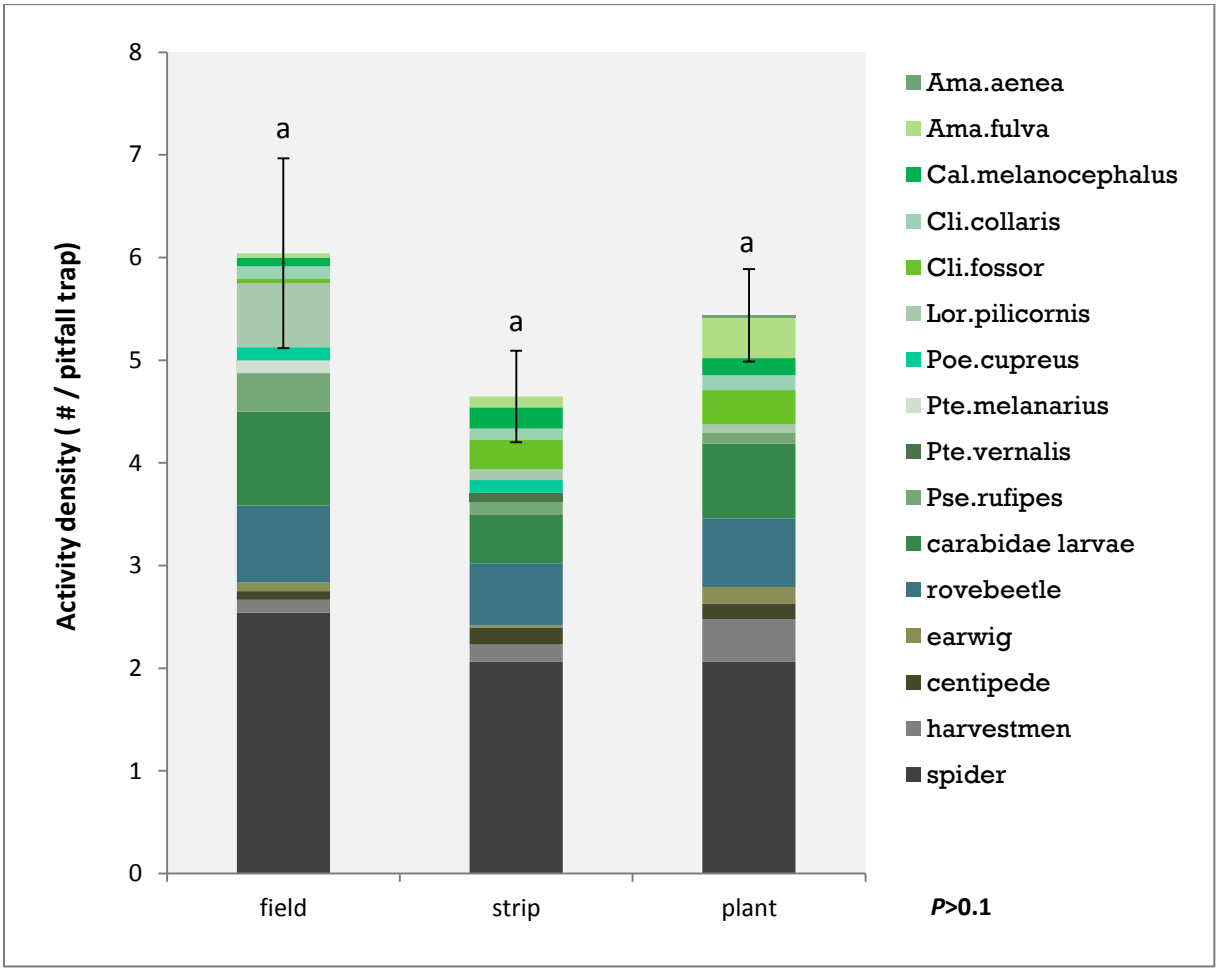

Figure 12 Activity density (number of individuals collected) and composition of ground-dwelling natural enemies by pitfall sampling on October in different crop diversity treatments, where 'field' refers to large field single wheat cropping system, 'strip' refers to strip cropping non-mix system and 'plant' refers to strip cropping mix system. Absence of certain colour suggests that enemy group was not found during sampling. Same letters above the bars indicate no significant difference (*P*>0.1) among treatments.

In more detail, comparing enemy average individuals per pitfall in same distance among three treatments showed no significant difference (*P*>0.1) in terms of hedge, mustard, potato, the second grass-clover, maize and flower strip (Figure 13). Only the first grass-clover strip and wheat strip at strip scale had lower natural enemy abundance than field scale, while no difference were found in plant-strip scale comparison or field-plant scale comparison.

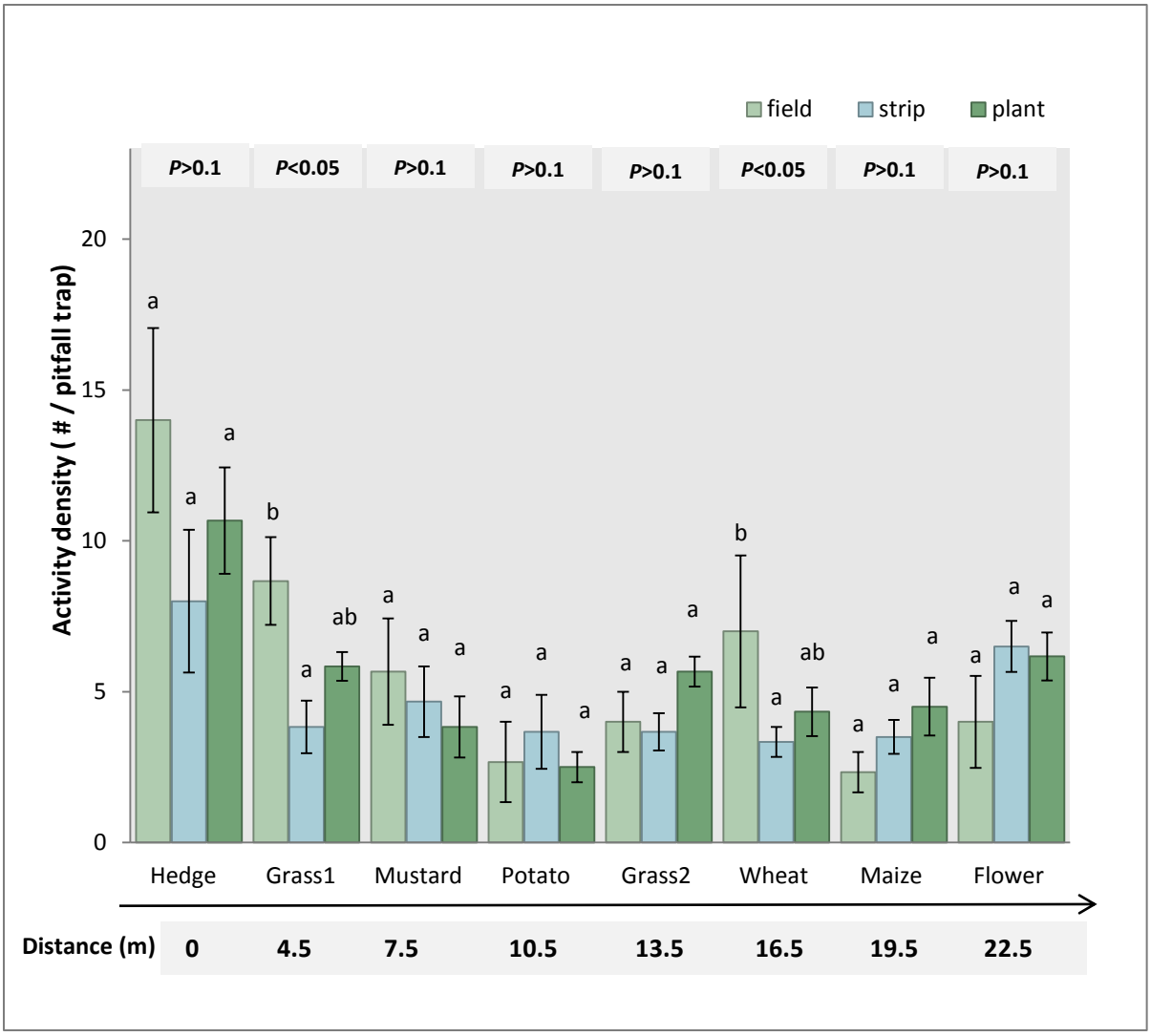

Figure 13 Activity density (number of individuals collected) of ground-dwelling natural enemies in the same strip among three treatments by pitfall sampling in October, where 'field' refers to large field single wheat cropping system, 'strip' refers to strip cropping non-mix system and 'plant' refers to strip cropping mix system. The name of bar came from the original strips' name. From strip 1 to strip 8 at strip and field scale, the strip element is hedge, grass1, mustard, potato, grass2, wheat, maize, flower mix respectively. At field scale, only strip 1 is hedge, the rest 7 strips are all wheat. Different letters above the bars indicate significant difference of the same strip among treatments.

Average enemy individuals per pitfall of different plant elements within treatment was performed with Tukey contrasts (Appendix xiii). At field scale, natural enemy individuals were highly significantly abundant (P<0.001) in the hedge than those in the adjacent field with green manure. At the strip scale, non-crop habitats (hedge and flower strip) also retained more enemy individuals than the crop field. However, natural enemy abundance in hedge were only marginally significantly higher (P<0.1) than in wheat strip, while there was no significant difference between enemy amount in hedge and flower strip. Other comparisons showed no significant difference at strip scale. At plant scale, enemy abundance in hedge was significantly higher (P<0.01) than in maize, wheat, potato and mustard strips, and slightly significant higher than that in grass-clover strips (P<0.1). Flower strip conserved more enemy with marginally significant difference (P<0.1) than that in potato strip. Except for comparisons mentioned above, paired comparisons showed no significant difference of other paired plant elements at plant scale.

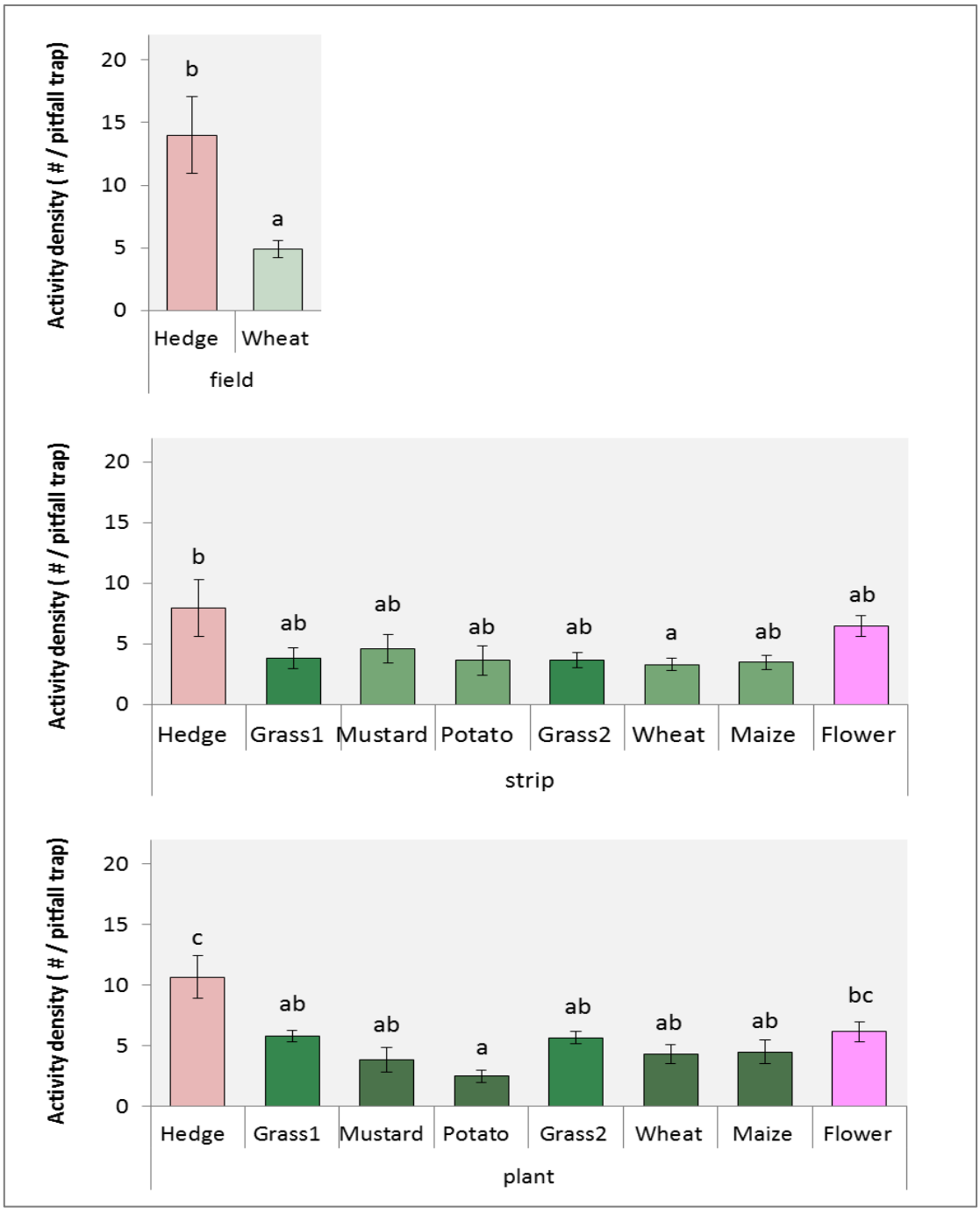

Figure 14 Activity density (number of individuals collected) of ground-dwelling natural enemies in different strip elements within treatment by pitfall sampling in October, where 'field' refers to large field single wheat cropping system, 'strip' refers to strip cropping non-mix system and 'plant' refers to strip cropping mix system. The name of bar came from the original strips' name. Except for unharvest hedge and flower strip, other strips are all green cover. The absence of colors suggests that crop element didn't be installed in that treatment. Different letters above bars indicate difference (at least $P< 0.1$) among different crop strips within treatment.

3.4 Natural enemy movement

The number of natural enemy individuals and groups that moved to the hedge and to the crop field were assessed by bi-direction pitfalls (Figure 17 and Figure 18) in July (crop growing season) and in October (after harvest) (Appendix xiv). In July during crop cropping season, natural enemy individuals and group number showed a relative balanced state where no significant difference was found

between enemy movements to hedge and to crop field. Nevertheless, after crop harvest in October, significantly more natural enemies moved from the field to the hedge (P<0.05) than vice versa. However, there was no statistically significant difference in natural enemy richness (in terms of group number).

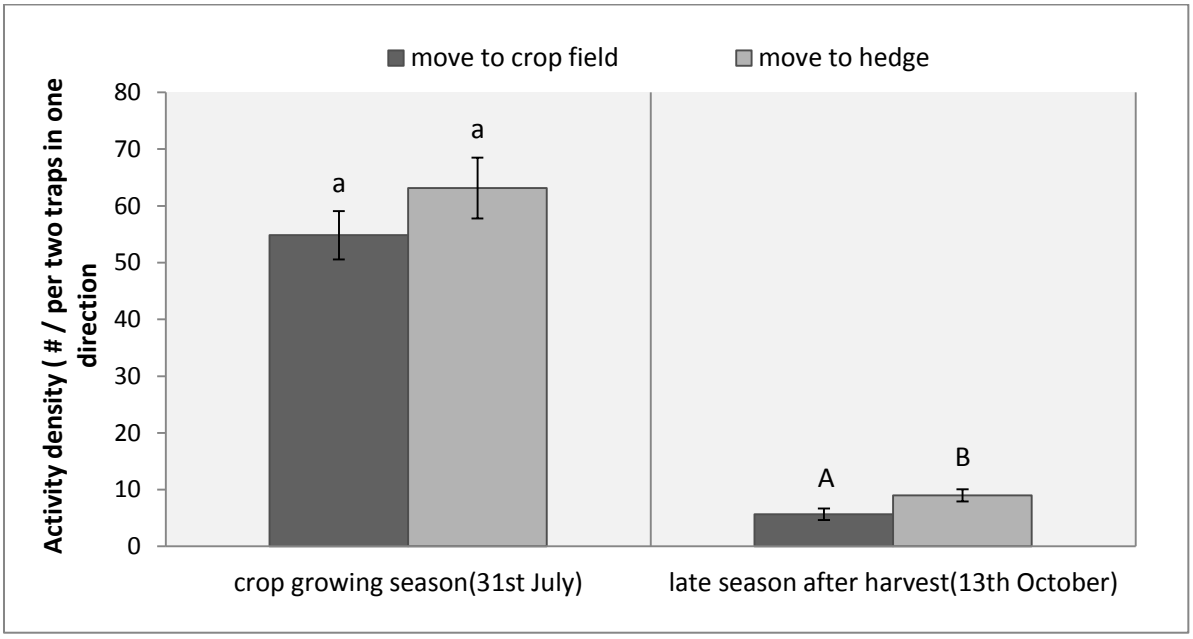

Figure 15 Activity density (number of individuals collected) of ground-dwelling natural enemies that moved to crop field and to hedge by bi-direction pitfall sampling in crop growing season and late season. Different letters above bars indicate significant difference (P<0.05) of natural enemy individual moving to crop field and hedge directions.

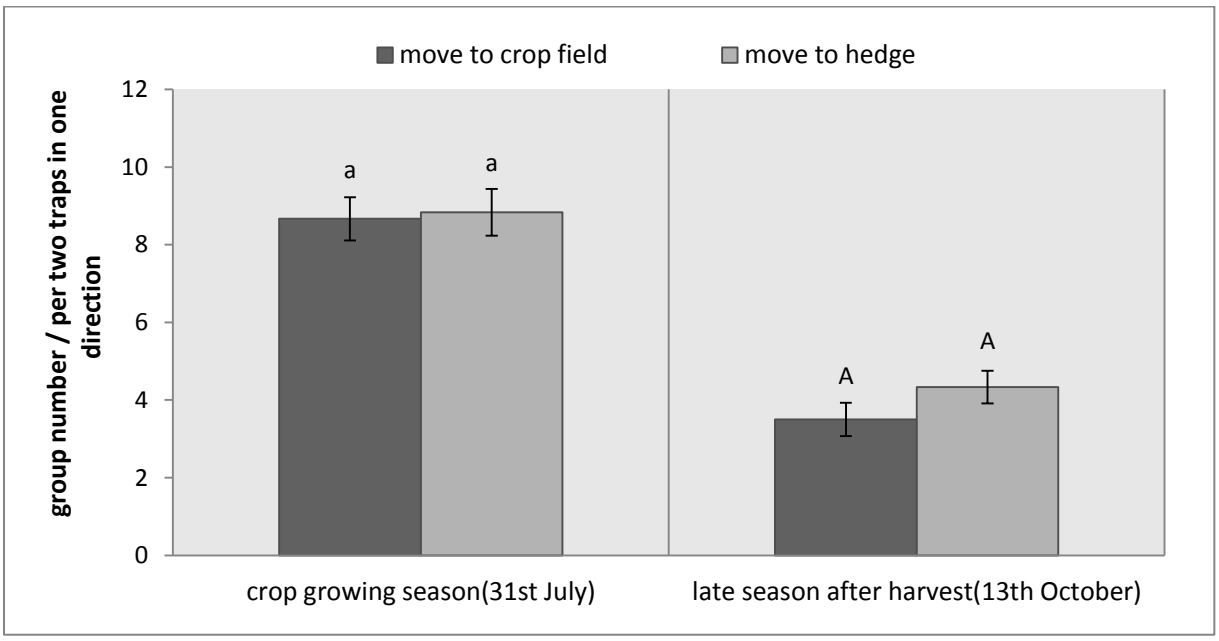

Figure 16 Group number of ground-dwelling natural enemies that moved to crop field and to hedge by bi-direction pitfall sampling in crop growing season and late season. Same letters above the bars indicate no significant difference (P>0.1) of enemy group number moving to crop field and hedge directions.

4 Discussion

4.1 Crop diversification on aphid density and natural enemy abundance

4.1.1 Crop diversification on aphid density

While there was a tendency for higher aphid densities at the field scale than on the strip and plant level, this difference was not statistically significant. In addition, there is no significant difference in the strip-plant comparison. There may be two reasons responsible for this result of this year. For one reason, it may result from that aphid population development is not synchronous in three treatments. The difference of aphid density among treatment may gradually diminish in the late season and disappear in end (Bukovinszky, 2004). It is also noticeable that wheat in large single cropping field was sowed more than 1 month earlier (Appendix ii). Hence, the aphid population dynamics should be taken into account next year, which means measuring the aphid density of targeted wheat plants in a certain time interval for many times (Bukovinszky, 2004). Besides, the abiotic factors including wind, temperature etc., may largely influenced the assessment results which commonly be challenging for filed assessments. In this study, visual assessment for aphid density actually was conducted for three times, however, the first two assessments were not successful due to sudden weather changes during the sampling day especially strong wind in the Netherlands. Another reason might be that Tukey contrast is a conservative analysis (Day & Quinn, 1989). The results of plant-field and strip-field comparisons were no significantly different, but the *p*-values were still close to 0.1 or less (Table 2). This means that more significant differences are expected to get, when more replicates and less interference factors (e.g. blocks, wind) are fulfilled for next year. The difference between strip-plant comparison was not significantly different (Table 2) and has least potential to be, according to the *p*-value close to 1. There is a suggestion that a high scale of crop diversification (both strip and plant scales) leads to lower aphid density than lower scale of crop diversification (field scale), while there is no difference in the strip-plant comparison. In addition, for all three scales of crop diversification, the mean aphid density was less than 5 aphids/tiller, which is below the economic injury level of 7 aphids/tiller (Larsson, 2005).

Therefore, as discussed above the effect of crop diversification on pest density is not clear based on only one time of visual assessment sampling of this year. The hypothesis on pest density is therefore rejected. However, an improved sampling method of multiple times measurement in a certain time interval next year with more replicates and less interference factors might lead to a reconsideration of this conclusion.

4.1.2 Crop diversification on natural enemy abundance

Natural enemy performance reflects the potential pest control effect of crop diversification. The result from different sampling methods showed that effect of crop diversification positively increases natural enemy abundance to different extent, which is in line with the “Enemy Hypothesis” (Pimentel, 1961; Root, 1973) and the majority of cases (Andow, 1991; Wilby, & Thomas, 2002; Altieri, & Nicholls, 2004; Bianchi et al., 2006; Hooks, & Johnson, 2003).

Firstly, the most diverse wheat-fababean intercropping had highest abundance of parasitized aphids, while there was no significant difference in wheat strip cropping and wheat single cropping. This difference may be explained by the higher floral resource availability in wheat-fababean intercropping than other two treatments because fababean plants were in bloom during the sampling period. As to

the benefit of flowering plant, one is that selected flowers can attract more parasitoids in terms of abundance and diversity (Heimpel, & Jervis 2005). Besides, the suitable floral resources including nectar (carbohydrate) and pollen (protein) resources provided by the flowering plants are of great important as energy and nutrient source (Heimpel, & Jervis, 2005; Bianchi, & Wäckers,2008) for parasitoids, and promote the success in terms of extended longevity, enhanced fecundity, increased the reproductive lifespan, accelerated egg maturation rate and more effectiveness of herbivore searching and parasitizing (Sheehan, 1986; Schmale et al., 2001; Lee et al., 2004; Wäckers, 2005; Winkler et al., 2006; Hogg et al., 2011; Rodriguez-Saona et al., 2012). Thus, the attraction of flower and floral resources can result in higher enemy efficacy in biological control agent of pest insects (van Rijn, & Sabelis, 2005; Bianchi, & Wäckers, 2008). From field observation that the seedling emergence of fababean was not high in wheat-fababean strip (data not shown), other flower plants at that period surrounding the sampled plots in the same treatment may be also responsible for parasitoid abundance. In addition to the flowering plant, the increased crop diversity can provide more varied and favorable habitats and shelters that may help natural enemy get rid of detrimental condition like excessive wind and extreme temperature, and predators like birds (Rodriguez-Saona et al., 2012). The adverse weather conditions have been demonstrated negatively influence the searching behaviour and population development of aphid parasitoids (Fink, & Völkl, 1995; Weisser et al., 1997). Therefore, the high parasitism rates at the plant scale (wheat-fababean intercropping) may be as a result of abundant flower resource and, favorable microclimate and shelters. The high parasitism rate of aphids does show better biological control effect of parasitoids in wheat-fababean intercropping. Although a parasitoid wasp may be able to parasite more than one aphid (Bianchi, & Wäckers, 2008), it results in different fraction of parasitism but from actually same number of parasitoids. Further experiments can use same age and amount of laboratory reared aphids to measure the parasitoids biological control effect on aphids in the real field with different scales of crop diversification.

Secondly, the positive relationship between natural enemy abundance and crop diversification from beat sampling demonstrates “the more diverse the better” in regard to crop diversification on natural enemy abundance. The natural enemy abundance showed a significant difference among three treatments (Figure 6 and Figure 7), which can be explained by more food and prey resource available in the most diverse intercropping. As most aphid predators are not monophagous, they rely on not only aphids but also other food resources (e.g. floral resource or other plant food) and/or various alternative preys to fulfil their lifespan and reproductive (Andow, 1991; Bianchi, & Wäckers, 2008; Rodriguez-Saona et al., 2012). For example, adults of many hoverfly species (syrphids) solely feed on pollen and nectar for life maintenance and reproduction but their larvae are aphidophagous and have been identified as vital biocontrol agents on aphids (Cowgill et al., 1993; Branquart, & Hemptinne, 2000; Scholz, & Poehling, 2000). Many hoverfly adults rely on pollen and nectar but lay egg in plants with aphids (Scholz, & Poehling, 2000). Nectar and pollen can also positively influence on omnivorous lacewing activity and reproduction, and thus suppress aphids population (Limburg, & Rosenheim, 2001; Robinson et al., 2008; Jonsson et al., 2009; Jacometti et al., 2010). Therefore, the floral resource from flowers may be the dominant for the abundance of hoverfly and lacewing. For more generalist predators like spiders and harvestmen, the main reason are more likely to be various prey and food available. The diet range includes living invertebrates (e.g. aphids and flies), dead animals (e.g. ants, beetles, earthworms, small rodents and birds), plant matter (e.g. grass stalks and fruit) and other non-animal material (e.g. the gills of fungi) (Henschel, 1994; Hvam, & Toft, 2008). Therefore, the more diverse cropping systems with various plants and herbivores is more likely to meet the

requirements and preferences of generalist enemies with a variety of alternative prey and food (Andow, 1991). Beat sampling was conducted when there were a variety of plants (Appendix ii and Appendix iii) and a number and variety of flowering ones (e.g. mustard, grasses, clovers, potato and buckwheat) at both wheat strip cropping and wheat-fababean intercropping in strip cropping system. The higher crop diversification with more abundant and diverse of plants and flowers, can provide more favorable food and prey resources for enemies, which is responsible for their abundance and efficiency. Even though the total natural enemy abundance was different between the strip and plant diversification treatments, there were no significant differences in the abundance for specific enemy groups and group richness. The accumulative effect of total enemies groups on pest control is not clear. Since not only the cooperative effect of pest prey but also intraguild predation or competition among these enemy groups might have an effect.

Thirdly, the whole-system pitfall sampling result in July demonstrated the similar relationship “the more diverse the better” as the beat sampling result with respect of crop diversification effect on natural enemy abundance, but the strip scale diversification had slightly and vague difference with plant scale and field scale diversification. More specifically, the plant scale diversification was always higher than field scale diversification in term of total and sole natural enemy abundance, while the performance of strip scale diversification was basically somewhere in between and usually showed no significant difference with neither plant scale nor field scale. As discussed above, it can be explained that high scale diversification has an advantage in the varieties of plants (Appendix ii and Appendix iii), and in number and variety of flowering plants (e.g. grasses, clovers). My detailed analysis on enemy distribution in strip elements, to some extent, confirmed the explanation. Except for hedge, the strip elements (i.e. mustard; the first and second grass-clover strip, and flower strip) where the plant scale diversification defeated the field scale diversification on natural enemy abundance, were blooming at that period. For example, the mustards were highly blooming among all strip elements, and natural enemy in mustard strip had the highest abundance among all strips within treatment comparison (Figure 10) and among treatments comparison (Figure 11). Because on the one hand, the flowering plants may attract various insects and provide many kinds of prey and non-prey food to natural enemies; on the other hand, the increased natural enemies can control density of those prey under the economic damage threshold and prevent these prey being pest (detrimental) for the crops. The hedges in three treatments have same plants species composition, thus the higher enemy abundance in the hedge in strip and plant scale diversification may dispersed and spilled from the adjacent strips in crop field (e.g. the first grass-clover strip) (Rusch et al., 2010). Very few ground-dwelling enemies were found in the potato strip in both within treatment comparison and among treatments comparison, which may result from the serious soil disturbance and less green cover of the potato strip. The potato strip had been tilled serious for loose soil, then four ridges within were made, and several times afterward re-ridged were conducted for weed control. Soil disturbance for potato cultivation may cause enemy drastic reduction. Because physical disturbance on soil caused by ploughing, negatively influence the abundance, activity and species diversity of ground-dwelling enemies in agro-ecosystem (Stinner, & House, 1990; Shearin et al., 2007; Pluess et al., 2008; Thorbek, & Bilde, 2004). Since the disadvantages and advantages for farm cultivation practices, it is vital to balance the integrated influence and conduct the practice moderately. Taking the potato cultivation for example, the re-ridge for potato strip was for weed control but negatively may hinder natural enemies. In addition to soil disturbance, afterwards the bare soil in potato strip may also lead to shortage of natural enemies. Ground-dwelling arthropod

density is higher in field with green cover than bare soil because green cover can provide a moister, shadier soil surface microclimate, as well as alternative prey or food resource (Stinner, & House, 1990; Andow, 1991; Dennis et al., 1994). Even though the wheat strip in three treatments showed no significant difference in sampled natural enemy density (Table 7), the biological control effect from natural enemy in the strip might still have advantage in a more diverse cropping systems. For one reason, the natural enemies can disperse from adjacent strips to the this strip (Rusch et al., 2010). For another reason, pitfalls were only put in the field for two days in whole-system sampling, and then extending the sampling period might make the difference more measurable (e.g. 2-week sampling period (Clough et al., 2005; Showler, & Greenberg, 2003)). As to the sole enemy abundance for natural enemy groups, the majority of enemy groups were positively related to crop diversification except for density of lady beetle (Figure 9). It may results from intra-guild predation in the high scale crop diversification (Lucas, 2005; Broatch et al., 2010). It is based on fact that high-level predators in food web (e.g. spider) do prey on lower-level ones (e.g. ladybeetle)(Wente, 2014) due to wide prey range, that lady beetles avoid foraging and ovipositing where the spider are present (Hodge,1999; Seagraves, 2009), and that spider is the most abundant enemy group in this year pitfall sampling (Figure 9). Although there were statistically more ladybeetles sampled in the field scale of crop diversification, the size of difference was small and the max density for all samples was no more than 5 per pitfall trap.

Although no significant block effect was tested during statistics analysis, some aspects related to block deserve attention for improving sampling efficiency. First, in the beat sampling, pooled natural enemy showed that higher amount of sampled natural enemy in block 2. Considering the experiment design that the plots/replicates with the same scale crop diversification treatment were highly closer to each other in block 2, while they were more separately in other blocks, it might come to that the size of plots/replicates may influence the measurable results. Second, in the pitfall sampling in July for ground-dwelling enemies, pooled natural enemy individuals showed a declining trend of enemy amount from block 1 to 3 in both treatments. Considering the characteristics of pitfall sampling and surface runoff caused by a slight gradient among blocks, the surface runoff, to some extent, may thrust pitfalls up and negatively influence the sampling efficiency. Thirdly, it was raining during the pitfall sampling in October and some pitfalls up floated. It might be the reason that the field surface was not even and flat which may lead to more flooding in the lower surface.

As discussed on natural enemy abundance, the accumulative effect of abundance of enemies may result in that the highest crop diversification has greatest potential of biological control effects. The key contributing factors to natural enemy abundance are: more favorable resources and microclimate, shelter available provided by plant diversity, flowering plants and green cover in the crop diversification process. However, some questions deserve attention for future exploration and research. First, due to the complexity of on diet range and preference of natural enemies, unclear is that how accumulative effect of many enemy groups of final biological control on specific target herbivore pests would be, additive or antagonistic? Second, how different are accumulative biological control effects on specific target herbivore pests in the strip and field scale diversification. This year data are elusive on the relation between aphid density at strip and plant scale. Third, based on abundant enemies available in these two treatments and the low aphid density, no statement can be made on the optimal scale of crop diversification. One can wonder if is it necessary to get the highest plant crop diversification and as result highest natural enemy abundance when the aphid density has been under the economic damage threshold in both the strip and plant diversification scale. Four, to

what extent does the biological control effect influence the crop yield? The hypothesis on natural enemy abundance is accepted with respect that the highest scales of crop diversification have highes natural enemies abundance in comparison with the field scale, however, the difference between the high diversity scales (the plant and strip scales) comparison is not clear this year. Further and more experiments based on this crop diversification design and field arrangement are expected to get clear answers.

4.2 Crop diversification on natural enemy conservation

The natural enemy conservation effect was not significantly different between the three diversification treatments. This is neither expected by my hypothesis nor does it fit with the results from other studies (Andow, 1991; Altieri, 1999; Landis, 2000; Khan et al., 2008). The key of natural enemy conservation by crop diversification lies in that polycultures provide a wider range of food resources for an extended period. More specially, scarce resources or habitats are left for natural enemies after the sole crop harvest in monocultures, while in polycultures after the one of the crop harvest, other crops or plants can also provide habitats and resources for natural enemies and thus conserve enemies better and longer time in the ecosystems. However, the situation is a different case in this study. All crops were harvest in September, all three treatments were sown with green manures. The green manure at field scale was sown 2 weeks earlier than those at strip and plant scales (Appendix vi). That earlier sowing of green manure at field scale might result in longer recovering time and more abundant resources available for natural enemies. It might balance out the effect of increased diversity of green manures in plant and strip scale and end up with no measured difference among treatments. From a sampling method perspective, pitfalls were only sampled in the field for two days when low temperature and heavy raining occurred (Appendix xv). Sampling efficiency of pitfall may be influenced by weather condition, because sampled objects may be less active and therefore have less chance to be trapped (Spence, & Niemelä, 1994; Umetsu et al., 2006; Allema, 2014). Then the difference among treatment may be even less measurable in such adverse weather condition. The conservation hypothesis is rejected but improved experiment design next year is expected to give clear answer.

4.3 Non-crop habitats on natural enemy movement

The effect of non-crop habitats in this study agrees with my hypothesis that they positively influence natural enemy abundance especially in late season. In the crop growing season, there was a relative balance state of ground-dwelling natural enemies that moved to hedge versus those to crop field. In late season, slightly more enemy moved to hedge than to the crop field (Figure 15). Interestingly, this is in agreement with the ground-dwelling natural enemy abundance in hedge-crop comparison in crop growing season and late season. More specifically, the natural enemy abundance in hedge and adjacent crop strips also was more or less in balance in crop growing season. But clearly more abundant enemies retained in hedge than crop field in late season (Figure 14). Therefore, the results of natural enemy movement and abundance are, to some extent, consistent and mutually supportive for positive function of non-crop habitats on natural enemy. In addition to the hedge, other non-crop habitats (the flower strip) showed advantages for natural enemy abundance, but no movement measurement were conducted this year. It is not difficult to explain the function of non-crop habitats. For one reason, as discussed before, soil disturbance negatively influence ground-dwelling enemies in ecosystems and thus crop harvest and sowing green cover may largely disturb the soil and natural enemies' habitats within crop field and impel them to disperse and emigrate (Olson, & Wäckers,

2007; Rusch et al., 2010). For another reason, stable and available resources such as alternate food, prey, and winter refuges in such non-crop habitats are important for natural enemy movement and conservation (Tscharntke et al., 2007). Natural enemies move to the undisturbed non-crop perennial habitats where less soil disturbance takes place and more stable resource are available in late season. Therefore, the hypothesis on non-crop habitat is accepted. Non-crop habitats act as winter refuges for natural enemies and may positively promote their activities on pest control next year.

5 Conclusion

This study suggest that the most diverse crop system has highest biological control potential. In this agro-system setting, the appropriate scale of crop diversification for the most effective bio-control effects is still in question. Undisturbed non-crop perennial habitats can support biological control effect by conserving natural enemies in the ecosystem especially after crop field harvest. Key factors that contribute to the biological control effect in the process of crop diversification, highly rely on spatially and temporally well-arranged favourable resources and conditions for natural enemies and suppress those for herbivore pest. The key factors are summarized as following: i) the number and variety of plants and flowers are important to promote natural enemies; ii) the spatial and temporal arrangement of these plants and flowers matter; iii) soil disturbance by farming practices like ploughing is likely to reduce natural enemy activity; iv) bare soil might be an adverse factor for natural enemies in the crop diversification, and living green manure can be alternative options; v) the non-crop habitats can conserve natural enemies as winter refuges with stable prey and food supply. Crop diversification for effective biological control effect is not simply increasing the variety of plants, rather the managements related to crop diversification are the key factors to promote natural enemy and to inhibit herbivore pests. For effective biological control provided by crop diversification, the following aspect have to be known: characteristics of involved plants, herbivore, and natural enemy; the relationships among them; and influencing factors on their performance. In conclusion, crop diversification is positively related to biological control potential from both bottom-up and top-down effects, while difference of the high scale of crop diversification (i.e. strip and plant scales in this study) still needs more studies to get clarified. Nevertheless, it is vital that farmers and ecologist figure out mixing crop to the appropriate scale rather than blindly pursue the more diverse the better. Non-crop habitats (e.g. hedge) can conserve natural enemies after crops harvest and may positively promote their pest control effect next year. It is recommended that those non-crop habitats are installed in cropping systems as beneficial habitats for natural enemies and for better pest control potential.

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Appendices

Appendix i. Arrangement of strip cropping systems and large wheat field

Appendix ii. Crop species/cultivars composition in three scales of crop diversification in spring

Strip	Sowing date	Non-mix treatment(strip scale)	Mix treatment(plant scale)
Flower strip	02-06-2014	#same# see Appendix iii	
Maize	22-05-2014	short season maize	long season maize relay cropping with clover
Wheat	26-05-2014	wheat	wheat-fababean intercropping
Grass-clover 2	26-05-2014	one Italian ryegrass one red clover	one Italian ryegrass one red clover two perennial ryegrass two white clover
Potato	20-05-2014	one cultivar: Raja	four cultivars: Raja, Connect, Carolus, Sarpo-mira
Mustard	20-05-2014	#same# Achilles	
Grass-clover 1	22-05-2014	#same as Grass-clover 2#	
Hedge	2004	#same# see Appendix iv	

Strip	Sowing date	Large field wheat single cropping(field scale)
Wheat	22-04-2014	wheat
Hedge	2004	see Appendix iv

Appendix iii. Flower species composition and quantity in flower strip

The flower seed mix includes annuals, 2 kg in total was sown on 2nd June

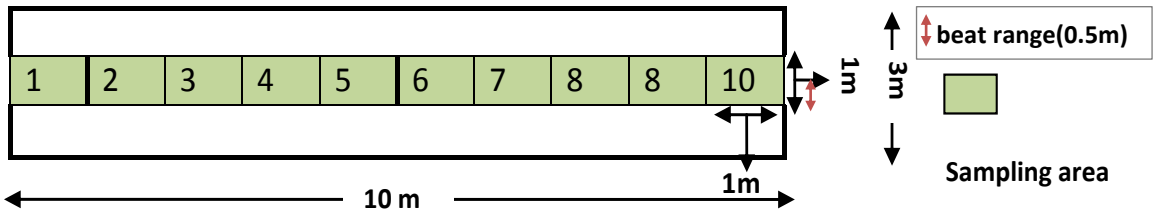
Flower species		Quantity/ 100g	Proportion
Buckwheat	*Fagopyrumesculentum*	6.0	30.0%
Yarrow	*Achilleamillefolium*	1.5	7.5%
Dill	*Anethumgraveolens*	1.5	7.5%
Common chicory	*Cichoriumintybus*	1.5	7.5%
Fennel	*Foeniculumvulgare*	1.5	7.5%
Wild parsnip	*Pastinaca sativa*	1.5	7.5%
Wild Angelica	*Angelica sylvestris*	0.8	3.8%
Cow parsley	*Anthriscussylvestris*	0.8	3.8%
Common Poppy	*Papaverrhoeas*	0.8	3.8%
Corn marigold	*Chrysanthemum segetum*	1.3	6.3%
Bishop's Flower	*Ammimajus*	1.5	7.5%
Cornflower	*Centaureacyanus*	1.5	7.5%

Appendix iv. Plant species composition and cultivation method of hedge

Low hedges D6 and D7 on March/April 2004	
Types:	blackthorn, dogwood ordinary, elderberry, field maple, privet, euonymus and dog rose
cultivation:	3 plants per meter (slightly offset from a line), 4 plants of each species in each case next to each other
Lage hagen D6 en D7 # original record from farmer #	
soorten:	sleedoorn, gewone kornoelje, vlier, spaanse aak, liguster, kardinaalsmuts en hondsroos
planten	3 planten per meter (iets verspringend uit een lijn), van elke soort telkens 4 planten naast elkaar

Note: translated by Google Translate

Appendix v. Sampling area in the central row of wheat strip

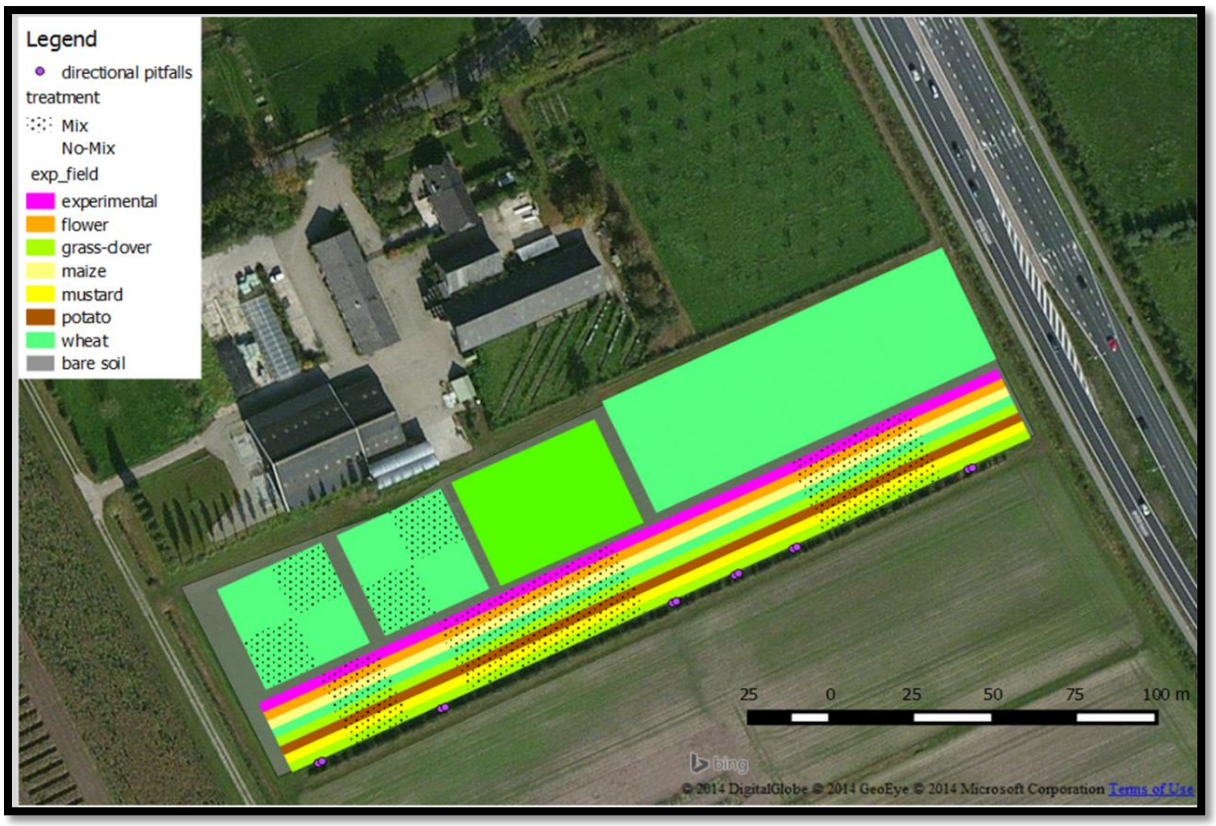


Appendix vii. Green manure sowing week and species composition in three treatments in 2014

Original crop	Crop harvest	Green manure sowing week	strip scale	plant scale
Flower strip	No harvest	\	#same# see Appendix iii	
Maize	Week 40	Week 31	undersowing 1 grass-1clover	grass-clover mix(5 species)
Wheat	Week 36	Week 38	Bristle oat	Bristle Oat, optima green
Grass-clover 2	Week 36	Week 38	Phacelia	green mix (8 species)
Potato	Week 36	Week 38	Italian ryegrass	grass-clover mix(3 species)
Mustard	Week 36	Week 38	Bristle oat	green mix (8 species)
Grass-clover 1	No harvest	\	#same as Grass-clover 2 in Appendix vii#	
Hedge	No harvest	\	#same# see Appendix iv	

Original crop	Crop harvest	Green manure sowing week	field scale (Large field wheat single cropping)
Wheat	Week 36	Week 36	Black radish, mustard and rye
Hedge	No harvest	\	see Appendix iv

Appendix vii. Bi-direction pitfall sampling location in the interface between hedge and crop field in non-mix treatment



Appendix viii. Bi-direction pitfall set that consists of four pitfalls and one screen

Appendix ix. R code for aphids density by visual assessment

```
########### Aphids density #############
rm(list = ls())
# visual observation of 10 plants per plot, data are expressed as aphids per plant
AH <- na.omit(read.csv("C:/Users/xie008/Desktop/aphid.csv"))
head(AH)
summary(AH)
attach (AH)

#define factors
treat=factor(AH$treatments)
treatment= factor(AH$treatments, levels=c("field", "strip", "plant"))
block<-as.factor(block)

# Install packages
require(MuMIn)    # for Multi Model Inference, dredge#
require(MASS)     # glm.nb model
require(multcomp) # for post-hoc test on differences between levels
library(pscl) # for zero-inflated nb

#making plots
hist(AH$aphids)
plot(AH$aphids~block)
boxplot(AH$aphids~treatment,ylab=list("Aphid density ( # / wheat
tiller)",cex=1.1),ylim=c(0, 20),font.lab=2,notch=TRUE)

#interaction of block and treatment effects on aphids density, no clear trend
interaction.plot(block,treatment, AH$aphids)

# Histogram
hist(AH$aphids)
# the count data trandfered to lod and sqrt, however the distributions are not
normal
# sqrtaphids <- sqrt(AH$aphids)
# hist(sqrtaphids)
# logaphids <- log(AH$aphids+1)
# hist(logaphids)

# Generalized Linear Models with different distributions are tested
# first try: simple multiple regression with Poisson distribution
M1 <- glm(AH$aphids ~ treatment+block, family = poisson)
summary(M1)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M1)
par(op)

# second try:simple multiple regression with quasipoisson distribution
M2 <- glm(AH$aphids ~ treatment+block, family = quasipoisson)
summary(M2)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M2)
par(op)

# thrid try:simple multiple regression with negative binomomial distribution
M3 <- glm.nb(AH$aphids ~ treatment+block, link = "log",na.action=na.fail)
summary(M3) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M3)
par(op)

# forth try:zero-inflated negative binomial model
M4 <- zeroinfl(AH$aphids ~ treatment+block, dist="negbin",data=AH)
summary(M4)

# Comparing AIC values: least value= AIC(M3)
```

```
AIC(M1)
AIC(M2)
AIC(M3)
AIC(M4)

# Based on negative binomial distribution, select best model
# Method 1: Automated model selection
MS1=dredge(M3)
subset(MS1,delta<4) #Subset of best models with a difference in AICc<4
subset(MS1,delta<100) #List of all models ranked by AICc
summary(MS1)

# Method 2: Manual model selection
drop1(M3,test="Chi")
M1a=update(M3, .~. -block)
drop1(M1a,test="Chi") # Optimal model

# From results from automated and manual model selection,block effect can be
excluded
# Best model: only treatments effect
MB <- glm.nb(AH$aphids ~ treatment, link = "log",na.action=na.fail)
summary(MB) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(MB)
par(op)
confint(MB)
summary(MB)

# post-hoc test:conservative pairwise comparisons with Tukey
comp1=glht(MB,linfct=mcp(treatment="Tukey"))
summary(comp1) # post-hoc test on differences between levels
confint(comp1)
```

Appendix x. R code for parasitized aphids by visual assessment

```
# Best model for fraction parasitism aphids
Mp <- glm(cbind(mummies,aphids) ~ treatment, family = binomial,na.action=na.fail)
summary(Mp)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(Mp)
par(op)

# post-hoc test:conservative pairwise comparisons with Tukey
comp2=glht(Mp,linfct=mcp(treatment="Tukey"))
summary(comp2) # post-hoc test on differences between levels
confint(comp2)

# Making tables and figure
(outputmean = t(tapply(AH$mummies,list(AH$treatments),mean)))
(outputSEM =
t(tapply(AH$mummies,list(AH$treatments),function(x)sqrt(var(x)/length(x)))))
(outputmean = t(tapply(fra,list(AH$treatments),mean)))
(outputSEM = t(tapply(fra,list(AH$treatments),function(x)sqrt(var(x)/length(x)))))

# figure: frpar~ treatment
frpar <- (AH$mummies/(AH$mummies+AH$aphids))
b<-ecdf(frpar)
plot(b,verticals = TRUE, do.points = FALSE)
dataf<-(subset(frpar, AH$treatment=="field" ))
datas<-(subset(frpar, AH$treatment== "strip" ))
datap<-(subset(frpar, AH$treatment== "plant" ))
f<-ecdf(dataf)
s<-ecdf(datas)
p<-ecdf(datap)
plot(f,verticals = TRUE, do.points = FALSE,col="red")
plot(s,verticals = TRUE, do.points = FALSE)
plot(p,verticals = TRUE, do.points = FALSE)
```

```
plot(f,verticals = TRUE, do.points = FALSE,col="red",
     ylab=list("Cumulative distribution",cex=1.1),xlab=list("Parasitism
fraction",cex=1.1),main="",xlim=c(0,1.0))
lines(s,verticals = TRUE, do.points = FALSE,col="green")
lines(p,verticals = TRUE, do.points = FALSE,col="blue")
legend(0.65,0.3,legend=(c(paste("field scale",sep=""),paste("strip
scale",sep=""),paste("plant scale",sep=""))),lty=1,col=c("green","red","blue"))
text(0.1,0.58,paste("b",sep=""),col="blue")
text(0.1,0.825,paste("a",sep=""),col="red")
text(0.1,0.87,paste("a",sep=""),col="green")
```

Appendix xi. R code for above-ground natural enemy by beat sampling

```
##### Aboveground natural enemies by beating sampling ##########
#interaction of block and treatment effects on NE: clear treatment effect
interaction.plot(block,treatment,NE) #block effect appears esp in block 2#
# Generalized Linear Models with different distributions are tested:
# first try: simple multiple regression with Poisson distribution
M1 <- glm(NE ~ treatment + block, family = poisson,na.action=na.fail)
summary(M1) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M1)
par(op)
# second try:simple multiple regression with quasipoisson distribution
M2 <- glm(NE ~ treatment + block, family = quasipoisson)
summary(M2)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M2)
par(op)
# thrid try:simple multiple regression with negative binomomial distribution
M3 <- glm.nb(NE ~ treatment + block, link = "log",na.action=na.fail)
summary(M3) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M3)
par(op)
# comparing AIC values: least value= AIC(M1), it makes sense due to no many zeros
in this case
AIC(M1)
AIC(M2)
AIC(M3)
# Method 1: Automated model selection
MS1=dredge(M1)
subset(MS1,delta<4) #Subset of best models with a difference in AICc<4
subset(MS1,delta<100) #List of all models ranked by AICc
summary(MS1)
# Method 2: Manual model selection
drop1(M1,test="Chi")
M1a=update(M1, .~. -treatment:block)
drop1(M1a,test="Chi") # block effect(0.203043) not significant
M1b=update(M1a, .~. -block)
drop1(M1b,test="Chi") #Optimal model
# Best Model:  only treatments effects without block effect
MB = glm(NE~treatment,family=poisson,na.action=na.fail)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(MB)
par(op)
summary(MB)
confint(MB)
#Pairwise comparisons
comp=glht(MB,linfct=mcp(treatment="Tukey"))
summary(comp) #Significant differences between treatment levels
confint(comp)
############ NE groups############
# Making tables for NE
(outputmean = t(tapply(group,list(bt$treatment),mean)))
(outputSEM = t(tapply(group,list(bt$treatment),function(x)sqrt(var(x)/length(x)))))
hist(group)
```

```
plot(group~treatment)
# first try: simple multiple regression with Poisson distribution
M1 <- glm(bt$group ~ treatment, family = poisson)
summary(M1) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M1)
par(op)
# second try:simple multiple regression with quasipoisson distribution
M2 <- glm(bt$group ~ treatment, family = quasipoisson)
summary(M2)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M2)
par(op)
# thrid try:simple multiple regression with negative binomomial distribution
M3 <- glm.nb(bt$group ~ treatment, link = "log",na.action=na.fail)
summary(M3) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M3)
par(op)

# comparing AIC values: least value= AIC(M1)
AIC(M1)
AIC(M2)
AIC(M3)
#Pairwise comparisons #due to lack of samples???#
comp1=glht(M1,linfct=mcp(treatment="Tukey"))
summary(comp1) #Significant differences between treatment levels
confint(comp1)

########## test for specific enemy groups################
hist(hoverlarva) #a-b-b  p<0.05
Mh = glm(bt$hoverlarva~treatment,family=poisson,na.action=na.fail)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(Mh)
par(op)
summary(Mh)
confint(Mh)
comph=glht(Mh,linfct=mcp(treatment="Tukey"))
summary(comph)
hist(damselbug) #a-ab-b  p<0.05
Md = glm(bt$damselbug~treatment,family=poisson,na.action=na.fail)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(Md)
par(op)
summary(Md)
confint(Md)
compd=glht(Md,linfct=mcp(treatment="Tukey"))
summary(compd)

hist(spider) #a-ab-b  p<0.05
Ms = glm(bt$spider~treatment,family=poisson,na.action=na.fail)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(Ms)
par(op)
summary(Ms)
confint(Ms)
comps=glht(Ms,linfct=mcp(treatment="Tukey"))
summary(comps)
hist(bt$lacelarva) #a-ab-b  p<0.1
Ml = glm(bt$lacelarva~treatment,family=poisson,na.action=na.fail)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(Ml)
par(op)
summary(Ml)
confint(Ml)
compl=glht(Ml,linfct=mcp(treatment="Tukey"))
summary(compl)
######### make figure #######
```

```
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot1=plot(bt$hoverlarva~treatment,
     xlab="P<0.05",cex.lab=1.1,
     ylab="Hoverfly larva ( # / 5m^2)",cex.lab=1.1,ylim=c(0,10.5))
text(1,10,paste("a",sep="") )
text(2,10,paste("b",sep="") )
text(3,10,paste("b",sep="") )
plot2=plot(bt$damselbug~treatment,
xlab="P<0.05",cex.lab=1.1,
ylab="Damsel bug ( # / 5m^2)",cex.lab=1.1,ylim=c(0,10.5))
text(1,10,paste("a",sep="") )
text(2,10,paste("ab",sep="") )
text(3,10,paste("b",sep="") )
plot3=plot(spider~treatment,
     xlab="P<0.05",cex.lab=1.1,
     ylab="Spider ( # / 5m^2)",cex.lab=1.1,ylim=c(0,10.5))
text(1,10,paste("a",sep="") )
text(2,10,paste("ab",sep="") )
text(3,10,paste("b",sep="") )
plot4=plot(bt$lacelarva~treatment,
     xlab="P<0.1",cex.lab=1.1,
     ylab="Lacewing larva ( # / 5m^2)",cex.lab=1.1,ylim=c(0,10.5))
text(1,10,paste("a",sep="") )
text(2,10,paste("ab",sep="") )
text(3,10,paste("b",sep="") )
```

Appendix xii. R code for ground-dwelling enemies by whole-system pitfall sampling in July

```
rm(list = ls())
# NE data in pitfall sampling expressed as NE amount per plot (one pitfall per
strip)
NEpit<- read.csv("C:/Users/xie008/Desktop/NE pitfall -1.csv")
attach(NEpit)
head(NEpit)

# install packages
install.packages(c("MuMIn","MASS","lme4"),dependencies=F)
require(MASS)      # glm.bn model
require(MuMIn)     # for Multi Model Inference, dredge#
require(multcomp) # for post-hoc test on differences between levels
library(lme4)

# define factors and order
treat=factor(NEpit$treatment)
treatment= factor(treat, levels=c("field", "strip", "plant"))
block<-as.factor(block)
strip<-as.factor(strip)
strips=factor(strip, levels=c("Hedge", "Grass1",
"Mustard","Potato","Grass2","Wheat","Maize","Flower"))
distance=factor(NEpit$distance)

#NE= NEindividual= total amount of all individuals of one pitfall trap
NE=NEindividual

# Making histgram and plot
hist(NE)
plot(NE~treatment)
plot(NE~block)
plot(NE~strip)

#interaction of block and treatment effects on NE,clear treatment effect
interaction.plot(block,treatment, NE) #block effect appears esp in block 2&3

# Making tables
strips=factor(strip, levels=c("Hedge", "Grass1",
"Mustard","Potato","Grass2","Wheat","Maize","Flower"))
(outputmean = t(tapply(NE,list(strips,treatment),mean)))
(outputSEM  =  t(tapply(NE,list(strips,treatment),function(x)sqrt(var(x)/length(x)))))
```

```
(outputmean = t(tapply(NE ,list(distance,treatment),mean)))
(outputSEM =
t(tapply(NE ,list(distance,treatment),function(x)sqrt(var(x)/length(x)))))

# Generalized Linear Models with different distributions are tested:
# first try:multiple regression with Poisson distribution
M1 <- glm(NE ~ treatment+block, family = poisson,na.action=na.fail)
summary(M1) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M1)
par(op)

# second try: multiple regression with quasipoisson distribution
M2 <- glm(NE ~ treatment+block, family = quasipoisson)
summary(M2)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M2)
par(op)

# thrid try: multiple regression with negative binomial distribution
M3 <- glm.nb(NE ~ treatment+block, link = "log",na.action=na.fail)
summary(M3) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M3)
par(op)

# comparing AIC values: least value= AIC(M3)
AIC(M1)
AIC(M2)
AIC(M3)

# selec best model based on nagative binomial dstribution
# Method 1: Automated model selection
MS1=dredge(M3)
subset(MS1,delta<4) #Subset of best models with a difference in AICc<4
subset(MS1,delta<100) #List of all models ranked by AICc
summary(MS1)
anova(M3,test="LRT") # treatment(0.0002099 ***);block(0.1546204)

# Method 2: Manual model selection
drop1(M3,test="Chi")
M1a=update(M3, .~. -block) #
drop1(M1a,test="Chi") #Optimal model


# Best Model:  only treatments effects without block effect
MB = glm.nb(NE ~ treatment, link = "log",na.action=na.fail)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(MB)
par(op)
summary(MB)
confint(MB)

#Pairwise comparisons
comp1=glht(MB,linfct=mcp(treatment="Tukey"))
summary(comp1) #Significant differences between treatment levels
confint(comp1)

######## NE groups:natural enemy richness###########

hist(NEgroup)
plot(NEgroup~treatment)
(outputmean = t(tapply(NEgroup,list(treatment),mean)))
(outputSEM = t(tapply(NEgroup,list(treatment),function(x)sqrt(var(x)/length(x)))))

# first try: simple multiple regression with Poisson distribution
M1 <- glm(NEgroup ~ treatment, family = poisson)
```

```
summary(M1) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M1)
par(op)

# second try:simple multiple regression with quasipoisson distribution
M2 <- glm(NEgroup ~ treatment, family = quasipoisson)
summary(M2)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M2)
par(op)

# thrid try:simple multiple regression with negative binomomial distribution
M3 <- glm.nb(NEgroup ~ treatment, link = "log",na.action=na.fail)
summary(M3) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M3)
par(op)

# comparing AIC values: least value= AIC(M1)
AIC(M1)
AIC(M2)
AIC(M3)

#Pairwise comparisons
comp1=glht(M1,linfct=mcp(treatment="Tukey"))
summary(comp1) #Significant differences between treatment levels
confint(comp1)

############# test for specific enemy groups############
plot(spider~treatment)
plot(rovebeetle~treatment)
plot(Poe.cupreus~treatment)
plot(ladybeetle~treatment)

hist(spider) #a-ab-b p<0.05
MB1 = glm.nb(spider~ treatment, link = "log",na.action=na.fail)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(MB1)
par(op)
summary(MB1)
confint(MB1)

compB1=glht(MB1,linfct=mcp(treatment="Tukey"))
summary(compB1)


hist(rovebeetle) #a-b-b p<0.01
MB3 = glm.nb(rovebeetle~ treatment, link = "log",na.action=na.fail)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(MB3)
par(op)
summary(MB3)
confint(MB3)

compB3=glht(MB3,linfct=mcp(treatment="Tukey"))
summary(compB3)

hist(Poe.cupreus) #a-ab-b p<0.1 (P=0.0775 .)
MB4 = glm.nb(Poe.cupreus~ treatment, link = "log",na.action=na.fail)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(MB4)
par(op)
summary(MB4)
confint(MB4)

compB4=glht(MB4,linfct=mcp(treatment="Tukey"))
summary(compB4)
```

```
hist(ladybeetle) # a-b-b p<0.1
MB2 = glm.nb(ladybeetle~ treatment, link = "log",na.action=na.fail)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(MB2)
par(op)
summary(MB2)
confint(MB2)

compB2=glht(MB2,linfct=mcp(treatment="Tukey"))
summary(compB2)

# make figure for the four enemy groups
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot1=plot(spider~treatment,
           xlab="P<0.05",cex.lab=1.1,
           ylab="Spider ( # / trap)",cex.lab=1.1,ylim=c(0,25))
text(1,23,paste("a",sep="") )
text(2,23,paste("ab",sep="") )
text(3,23,paste("b",sep="") )


plot2=plot(rovebeetle~treatment,
           xlab="P<0.01",cex.lab=1.1,
           ylab="Rove beetle ( # / trap)",cex.lab=1.1,ylim=c(0,25))
text(1,23,paste("a",sep="") )
text(2,23,paste("b",sep="") )
text(3,23,paste("b",sep="") )

plot3=plot(Poe.cupreus~treatment,
           xlab="P<0.1",cex.lab=1.1,
           ylab="Poecilus cupreus ( # / trap)",cex.lab=1.1,ylim=c(0,25))
text(1,23,paste("a",sep="") )
text(2,23,paste("ab",sep="") )
text(3,23,paste("b",sep="") )

plot4=plot(ladybeetle~treatment,
           xlab="P<0.1",cex.lab=1.1,
           ylab="Lady beetle ( # / trap)",cex.lab=1.1,ylim=c(0,25))
text(1,23,paste("a",sep="") )
text(2,23,paste("b",sep="") )
text(3,23,paste("b",sep="") )

######### test NE in different strips within treatment#########
# subset
dataf<-(subset(NEpit, NEpit$treatment=="field" ))
datas<-(subset(NEpit, NEpit$treatment== "strip" ))
datap<-(subset(NEpit, NEpit$treatment== "plant" ))
#stripsyst<-(subset(NEpit, NEpit$treatment!= "field" ))

# Making plot
plot(dataf$NEindividual~dataf$strip)
plot(datas$NEindividual~datas$strip)
plot(datap$NEindividual~datap$strip)
(outputmean = t(tapply(datap$NEindividual,list(datap$strip),mean)))
(outputSEM =
t(tapply(datap$NEindividual,list(datap$strip),function(x)sqrt(var(x)/length(x)))))

# field level:data=dataf
# first try: simple multiple regression with Poisson distribution
M1 <- glm(NEindividual ~ strip, family = poisson,data=dataf)
summary(M1) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M1)
par(op)

# second try:simple multiple regression with quasipoisson distribution
M2 <- glm(NEindividual ~ strip, family = quasipoisson,data=dataf)
```

```
summary(M2)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M2)
par(op)

# thrid try:simple multiple regression with negative binomial distribution
M3 <- glm.nb(NEindividual ~ strip, link = "log",na.action=na.fail,data=dataf)
summary(M3) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M3)
par(op)

# comparing AIC values: least value= AIC(M1)
AIC(M1)
AIC(M2)
AIC(M3)

#Pairwise comparisons #Wheat - Hedge P= 0.111 at field scale
summary(M1)
confint(M1)


# strip level:data=datas
# first try: simple multiple regression with Poisson distribution
M1 <- glm(NEindividual ~ strip, family = poisson,data=datas)
summary(M1) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M1)
par(op)

# second try:simple multiple regression with quasipoisson distribution
M2 <- glm(NEindividual ~ strip, family = quasipoisson,data=datas)
summary(M2)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M2)
par(op)

# thrid try:simple multiple regression with negative binomial distribution
M3 <- glm.nb(NEindividual ~ strip, link = "log",na.action=na.fail,data=datas)
summary(M3) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M3)
par(op)

# comparing AIC values: least value= AIC(M3)
AIC(M1)
AIC(M2)
AIC(M3)

#Pairwise comparisons #
comp1=glht(M3,linfct=mcp(strip="Tukey"))
summary(comp1) #Significant differences between strips
confint(comp1)

# plant level:data=datap
# first try: simple multiple regression with Poisson distribution
M1 <- glm(NEindividual ~ strip, family = poisson,data=datap)
summary(M1) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M1)
par(op)

# second try:simple multiple regression with quasipoisson distribution
M2 <- glm(NEindividual ~ strip, family = quasipoisson,data=datap)
summary(M2)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M2)
par(op)
```

```
# thrid try:simple multiple regression with negative binomial distribution
M3 <- glm.nb(NEindividual ~ strip, link = "log",na.action=na.fail,data=datap)
summary(M3) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M3)
par(op)

# comparing AIC values: least value= AIC(M3)
AIC(M1)
AIC(M2)
AIC(M3)

#Pairwise comparisons #
comp1=glht(M3,linfct=mcp(strip="Tukey"))
summary(comp1) #Significant differences between strips
confint(comp1)

########## test NE in same strip among three treatments##########

#Hedge:distance=1
dataH = NEpit[which(NEpit$distance == "1"),]
#Grass1:distance=2
dataG1 = NEpit[which(NEpit$distance == "2"),]
#Mustard:distance=3
dataMu = NEpit[which(NEpit$distance == "3"),]
#Potato:distance=4
dataP = NEpit[which(NEpit$distance == "4"),]
#Grass2:distance=5
dataG2 = NEpit[which(NEpit$distance == "5"),]
#Wheat:distance=6
dataW = NEpit[which(NEpit$distance == "6"),]
#Maize:distance=7
dataMa = NEpit[which(NEpit$distance == "7"),]
#Flower:distance=8
dataF = NEpit[which(NEpit$distance == "8"),]

#dataH
# first try: simple multiple regression with Poisson distribution
M1 <- glm(NEindividual ~ treatment, family = poisson,data=dataH)
summary(M1) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M1)
par(op)

# second try:simple multiple regression with quasipoisson distribution
M2 <- glm(NEindividual ~ treatment, family = quasipoisson,data=dataH)
summary(M2)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M2)
par(op)

# thrid try:simple multiple regression with negative binomial distribution
M3 <- glm.nb(NEindividual ~ treatment, link = "log",na.action=na.fail,data=dataH)
summary(M3) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M3)
par(op)

# comparing AIC values: least value= AIC(M1)
AIC(M1)
AIC(M2)
AIC(M3)

#Pairwise comparisons # a-b-b p<0.01
comp1=glht(M1,linfct=mcp(treatment="Tukey"))
summary(comp1)
confint(comp1)
```

```
#dataG1
# first try: simple multiple regression with Poisson distribution
M1 <- glm(NEindividual ~ treatment, family = poisson,data=dataG1)
summary(M1) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M1)
par(op)

# second try:simple multiple regression with quasipoisson distribution
M2 <- glm(NEindividual ~ treatment, family = quasipoisson,data=dataG1)
summary(M2)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M2)
par(op)

# thrid try:simple multiple regression with negative binomial distribution
M3 <- glm.nb(NEindividual ~ treatment, link = "log",na.action=na.fail,data=dataG1)
summary(M3) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M3)
par(op)

# comparing AIC values: least value= AIC(M1)
AIC(M1)
AIC(M2)
AIC(M3)

#Pairwise comparisons # a-b-b p<0.01
comp1=glht(M1,linfct=mcp(treatment="Tukey"))
summary(comp1)
confint(comp1)

#dataMu
# first try: simple multiple regression with Poisson distribution
M1 <- glm(NEindividual ~ treatment, family = poisson,data=dataMu)
summary(M1) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M1)
par(op)

# second try:simple multiple regression with quasipoisson distribution
M2 <- glm(NEindividual ~ treatment, family = quasipoisson,data=dataMu)
summary(M2)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M2)
par(op)

# thrid try:simple multiple regression with negative binomial distribution
M3 <- glm.nb(NEindividual ~ treatment, link = "log",na.action=na.fail,data=dataMu)
summary(M3) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M3)
par(op)

# comparing AIC values: least value= AIC(M3)
AIC(M1)
AIC(M2)
AIC(M3)

#Pairwise comparisons # a-ab-b p<0.01
comp1=glht(M3,linfct=mcp(treatment="Tukey"))
summary(comp1)
confint(comp1)

#dataP
# first try: simple multiple regression with Poisson distribution
M1 <- glm(NEindividual ~ treatment, family = poisson,data=dataP)
```

```
summary(M1) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M1)
par(op)

# second try:simple multiple regression with quasipoisson distribution
M2 <- glm(NEindividual ~ treatment, family = quasipoisson,data=dataP)
summary(M2)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M2)
par(op)

# thrid try:simple multiple regression with negative binomial distribution
M3 <- glm.nb(NEindividual ~ treatment, link = "log",na.action=na.fail,data=dataP)
summary(M3) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M3)
par(op)

# comparing AIC values: least value= AIC(M1)
AIC(M1)
AIC(M2)
AIC(M3)

#Pairwise comparisons # a-b-b p<0.05
comp1=glht(M1,linfct=mcp(treatment="Tukey"))
summary(comp1) #
confint(comp1)

#dataG2
# first try: simple multiple regression with Poisson distribution
M1 <- glm(NEindividual ~ treatment, family = poisson,data=dataG2)
summary(M1) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M1)
par(op)

# second try:simple multiple regression with quasipoisson distribution
M2 <- glm(NEindividual ~ treatment, family = quasipoisson,data=dataG2)
summary(M2)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M2)
par(op)

# thrid try:simple multiple regression with negative binomial distribution
M3 <- glm.nb(NEindividual ~ treatment, link = "log",na.action=na.fail,data=dataG2)
summary(M3) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M3)
par(op)

# comparing AIC values: least value= AIC(M3)
AIC(M1)
AIC(M2)
AIC(M3)

#Pairwise comparisons # a-b-b p<0.01
comp1=glht(M3,linfct=mcp(treatment="Tukey"))
summary(comp1)
confint(comp1)

#dataW
# first try: simple multiple regression with Poisson distribution
M1 <- glm(NEindividual ~ treatment, family = poisson,data=dataW)
summary(M1) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M1)
par(op)
```

```
# second try:simple multiple regression with quasipoisson distribution
M2 <- glm(NEindividual ~ treatment, family = quasipoisson,data=dataW)
summary(M2)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M2)
par(op)

# thrid try:simple multiple regression with negative binomial distribution
M3 <- glm.nb(NEindividual ~ treatment, link = "log",na.action=na.fail,data=dataW)
summary(M3) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M3)
par(op)

# comparing AIC values: least value= AIC(M1)
AIC(M1)
AIC(M2)
AIC(M3)

#Pairwise comparisons # no significant difference
comp1=glht(M1,linfct=mcp(treatment="Tukey"))
summary(comp1) #
confint(comp1)

#dataMa
# first try: simple multiple regression with Poisson distribution
M1 <- glm(NEindividual ~ treatment, family = poisson,data=dataMa)
summary(M1) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M1)
par(op)

# second try:simple multiple regression with quasipoisson distribution
M2 <- glm(NEindividual ~ treatment, family = quasipoisson,data=dataMa)
summary(M2)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M2)
par(op)

# thrid try:simple multiple regression with negative binomial distribution
M3 <- glm.nb(NEindividual ~ treatment, link = "log",na.action=na.fail,data=dataMa)
summary(M3) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M3)
par(op)

# comparing AIC values: least value= AIC(M1)
AIC(M1)
AIC(M2)
AIC(M3)

#Pairwise comparisons # no significant difference
comp1=glht(M1,linfct=mcp(treatment="Tukey"))
summary(comp1)
confint(comp1)

#dataF
# first try: simple multiple regression with Poisson distribution
M1 <- glm(NEindividual ~ treatment, family = poisson,data=dataF)
summary(M1) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M1)
par(op)

# second try:simple multiple regression with quasipoisson distribution
M2 <- glm(NEindividual ~ treatment, family = quasipoisson,data=dataF)
summary(M2)
```

```
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M2)
par(op)

# thrid try:simple multiple regression with negative binomial distribution
M3 <- glm.nb(NEindividual ~ treatment, link = "log",na.action=na.fail,data=dataF)
summary(M3) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M3)
par(op)

# comparing AIC values: least value= AIC(M1)
AIC(M1)
AIC(M2)
AIC(M3)

#Pairwise comparisons # a-ab-b p<0.1 (p=0.0657)
comp1=glht(M1,linfct=mcp(treatment="Tukey"))
summary(comp1)
confint(comp1)
```

Appendix xiii. R code for ground-dwelling enemies by whole-system pitfall sampling in October

```
# NE data in pitfall sampling expressed as NE amount per pitfall (each plot
including 8 strips/8 pitfalls)
rm(list = ls())
#data reading
NEpit<- na.omit(read.csv("C:/Users/xie008/Desktop/NE pitfall-2.csv"))
attach(NEpit)
head(NEpit)

# install packages
install.packages(c("MuMIn","MASS","lme4"),dependencies=F)
require(MASS)     # glm.bn model
require(MuMIn)    # for Multi Model Inference, dredge#
require(multcomp) # for post-hoc test on differences between levels
library(lme4)
require(nlme)

# define factors and order
treat=factor(NEpit$treatment)
treatment= factor(treat, levels=c("field", "strip", "plant"))
block<-as.factor(block)
strip<-as.factor(strip)
strips=factor(strip, levels=c("Hedge", "Grass1",
"Mustard","Potato","Grass2","Wheat","Maize","Flower"))
distance=factor(NEpit$distance)

# NE= total amount of all individuals
NE=spider+rovebeetle+      Caralarvae+   Poe.cupreus   +Cli.collaris+Pse.rufipes+
       Pte..melanarius+    Pte.vernalis+Cli.fossor+   Har..affinis+Ama.lunicollis+
       Ama.aenea+    Ama.fulva+    Lor..pilicornis+    Ago..muelleri+      Cal..Mela
       +Ama.fam+     rovelarva+    harvestmen+   earwig+       centipede

# Making plots
hist(NE)
hist(spider)
hist(Caralarvae)
hist(rovebeetle)
hist(harvestmen)

plot(NE~treatment)
plot(NE~block)
plot(NE~strips,ylab=" Natural enemy amount per pitfall" ,ylim=c(0, 20))
interaction.plot(block,treatment,NE) # abnormal in block 2 maybe the flooded
pitfalls#
```

```
# Making tables
(outputmean = t(tapply(NE,list(treatment),mean)))
(outputSEM = t(tapply(NE,list(treatment),function(x)sqrt(var(x)/length(x)))))

(outputmean = t(tapply(NE,list(strips,treatment),mean)))
(outputSEM =  t(tapply(NE,list(strips,treatment),function(x)sqrt(var(x)/length(x)))))

(outputmean = t(tapply(NE ,list(distance,treatment),mean)))
(outputSEM =
t(tapply(NE ,list(distance,treatment),function(x)sqrt(var(x)/length(x)))))


# first try: simple multiple regression with Poisson distribution
M1 <- glm(NE ~ treatment+block, family = poisson,na.action=na.fail)
summary(M1)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M1)
par(op)

# second try:simple multiple regression with quasiPoisson distribution
M2 <- glm(NE ~ treatment+block, family = quasipoisson,na.action=na.fail)
summary(M2)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M2)
par(op)

# thrid try:simple multiple regression with negative binomomial distribution:AIC:
605.84
M3 <- glm.nb(NE ~ treatment+block, link = "log",na.action=na.fail)
summary(M3)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M3)
par(op)

# comparing AIC values: least value= AIC(M3)
AIC(M1)
AIC(M2)
AIC(M3)

# Method 1: Automated model selection
MS1=dredge(M3)
subset(MS1,delta<4) #Subset of best models with a difference in AICc<4
subset(MS1,delta<100) #List of all models ranked by AICc
summary(MS1)
anova(M3,test="LRT") # treatment(0.18480);block(0.02988 *) but the block due to the
flooded pitfalls in plot8#

# Best Model:  only treatments effects without block effect
MB = glm.nb(NE ~ treatment, link = "log",na.action=na.fail)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(MB)
par(op)
summary(MB)
confint(MB)

#Pairwise comparisons
comp1=glht(MB,linfct=mcp(treatment="Tukey"))
summary(comp1) #Significant differences between treatment levels

####### NE groups:natural enemy richness ###############

hist(NEgroup)
plot(NEgroup~treatment)
(outputmean = t(tapply(NEgroup,list(treatment),mean)))
(outputSEM = t(tapply(NEgroup,list(treatment),function(x)sqrt(var(x)/length(x)))))

# first try: simple multiple regression with Poisson distribution
M1 <- glm(NEgroup ~ treatment, family = poisson)
```

```
summary(M1) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M1)
par(op)

# second try:simple multiple regression with quasipoisson distribution
M2 <- glm(NEgroup ~ treatment, family = quasipoisson)
summary(M2)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M2)
par(op)

# thrid try:simple multiple regression with negative binomomial distribution
M3 <- glm.nb(NEgroup ~ treatment, link = "log",na.action=na.fail)
summary(M3) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M3)
par(op)

# comparing AIC values: least value= AIC(M1)
AIC(M1)
AIC(M2)
AIC(M3)

#Pairwise comparisons
comp1=glht(M1,linfct=mcp(treatment="Tukey"))
summary(comp1) #Significant differences between treatment levels
confint(comp1)


########## test for specific enemy groups##########
plot(spider~treatment)
plot(Caralarvae~treatment)
plot(rovebeetle~treatment)
plot(harvestmen~treatment)

hist(spider) # not significant
MB1 = glm.nb(spider~ treatment, link = "log",na.action=na.fail)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(MB1)
par(op)
summary(MB1)

compB1=glht(MB1,linfct=mcp(treatment="Tukey"))
summary(compB1)

hist(Caralarvae)  #strip - field == P= 0.0978 .
MB2 = glm.nb(Caralarvae~ treatment, link = "log",na.action=na.fail)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(MB2)
par(op)
summary(MB2)

compB2=glht(MB2,linfct=mcp(treatment="Tukey"))
summary(compB2)

hist(rovebeetle)
MB3 = glm.nb(rovebeetle~ treatment, link = "log",na.action=na.fail)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(MB3)
par(op)
summary(MB3)

compB3=glht(MB3,linfct=mcp(treatment="Tukey"))
summary(compB3)

hist(harvestmen)
MB4 = glm.nb(harvestmen~ treatment, link = "log",na.action=na.fail)
```

```
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(MB4)
par(op)
summary(MB4)
confint(MB4)

compB4=glht(MB4,linfct=mcp(treatment="Tukey"))
summary(compB4)
# however no signifcant difference from above enemy group results (P>0.05)

########## test NE in different strips within treatment##########

# NEindividual= total amount of all individuals
NE=NEpit$NEindividual

# subset
dataf<-(subset(NEpit, NEpit$treatment=="field" ))
datas<-(subset(NEpit, NEpit$treatment=="strip" ))
datap<-(subset(NEpit, NEpit$treatment=="plant" ))
#datasp<-(subset(NEpit, NEpit$treatment!= "field" ))

# Making plot
op <- par(mfrow = c(1, 2), mar = c(3, 4, 5, 0.5))
plot(dataf$NEindividual~dataf$strip)


# field level:data=dataf
# first try: simple multiple regression with Poisson distribution
M1 <- glm(NEindividual ~ strip, family = poisson,data=dataf)
summary(M1) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M1)
par(op)

# second try:simple multiple regression with quasipoisson distribution
M2 <- glm(NEindividual ~ strip, family = quasipoisson,data=dataf)
summary(M2)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M2)
par(op)

# thrid try:simple multiple regression with negative binomial distribution
M3 <- glm.nb(NEindividual ~ strip, link = "log",na.action=na.fail,data=dataf)
summary(M3) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M3)
par(op)

# comparing AIC values: least value= AIC(M3)
AIC(M1)
AIC(M2)
AIC(M3)

#Pairwise comparisons #Wheat - Hedge 0.000674 *** at field scale
summary(M3)
confint(M3)

# strip level:data=datas
# first try: simple multiple regression with Poisson distribution
M1 <- glm(NEindividual ~ strip, family = poisson,data=datas)
summary(M1) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M1)
par(op)

# second try:simple multiple regression with quasipoisson distribution
M2 <- glm(NEindividual ~ strip, family = quasipoisson,data=datas)
summary(M2)
```

```
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M2)
par(op)

# thrid try:simple multiple regression with negative binomial distribution
M3 <- glm.nb(NEindividual ~ strip, link = "log",na.action=na.fail,data=datas)
summary(M3) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M3)
par(op)

# comparing AIC values: least value= AIC(M3)
AIC(M1)
AIC(M2)
AIC(M3)

#Pairwise comparisons #
comp1=glht(M3,linfct=mcp(strip="Tukey"))
summary(comp1) #Significant differences between strips
confint(comp1)

# plant level:data=datap
# first try: simple multiple regression with Poisson distribution
M1 <- glm(NEindividual ~ strip, family = poisson,data=datap)
summary(M1) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M1)
par(op)

# second try:simple multiple regression with quasipoisson distribution
M2 <- glm(NEindividual ~ strip, family = quasipoisson,data=datap)
summary(M2)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M2)
par(op)

# thrid try:simple multiple regression with negative binomial distribution
M3 <- glm.nb(NEindividual ~ strip, link = "log",na.action=na.fail,data=datap)
summary(M3) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M3)
par(op)

# comparing AIC values: least value= AIC(M1)
AIC(M1)
AIC(M2)
AIC(M3)

#Pairwise comparisons #
comp1=glht(M1,linfct=mcp(strip="Tukey"))
summary(comp1) #Significant differences between strips
confint(comp1)

########### test NE in same strip among three treatments##########

#Hedge:distance=1
dataH = NEpit[which(NEpit$distance == "1"),]
#Grass1:distance=2
dataG1 = NEpit[which(NEpit$distance == "2"),]
#Mustard:distance=3
dataMu = NEpit[which(NEpit$distance == "3"),]
#Potato:distance=4
dataP = NEpit[which(NEpit$distance == "4"),]
#Grass2:distance=5
dataG2 = NEpit[which(NEpit$distance == "5"),]
#Wheat:distance=6
dataW = NEpit[which(NEpit$distance == "6"),]
#Maize:distance=7
```

```
dataMa = NEpit[which(NEpit$distance == "7"),]
#Flower:distance=8
dataF = NEpit[which(NEpit$distance == "8"),]

#dataH
# first try: simple multiple regression with Poisson distribution
M1 <- glm(NEindividual ~ treatment, family = poisson,data=dataH)
summary(M1) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M1)
par(op)

# second try:simple multiple regression with quasipoisson distribution
M2 <- glm(NEindividual ~ treatment, family = quasipoisson,data=dataH)
summary(M2)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M2)
par(op)

# thrid try:simple multiple regression with negative binomial distribution
M3 <- glm.nb(NEindividual ~ treatment, link = "log",na.action=na.fail,data=dataH)
summary(M3) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M3)
par(op)

# comparing AIC values: least value= AIC(M3)
AIC(M1)
AIC(M2)
AIC(M3)

#Pairwise comparisons # not significant
comp1=glht(M3,linfct=mcp(treatment="Tukey"))
summary(comp1)
confint(comp1)

#dataG1
# first try: simple multiple regression with Poisson distribution
M1 <- glm(NEindividual ~ treatment, family = poisson,data=dataG1)
summary(M1) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M1)
par(op)

# second try:simple multiple regression with quasipoisson distribution
M2 <- glm(NEindividual ~ treatment, family = quasipoisson,data=dataG1)
summary(M2)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M2)
par(op)

# thrid try:simple multiple regression with negative binomial distribution
M3 <- glm.nb(NEindividual ~ treatment, link = "log",na.action=na.fail,data=dataG1)
summary(M3) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M3)
par(op)

# comparing AIC values: least value= AIC(M1)
AIC(M1)
AIC(M2)
AIC(M3)

#Pairwise comparisons # b-a-ab p<0.05
comp1=glht(M1,linfct=mcp(treatment="Tukey"))
summary(comp1)
confint(comp1)
```

```
#dataMu
# first try: simple multiple regression with Poisson distribution
M1 <- glm(NEindividual ~ treatment, family = poisson,data=dataMu)
summary(M1) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M1)
par(op)

# second try:simple multiple regression with quasipoisson distribution
M2 <- glm(NEindividual ~ treatment, family = quasipoisson,data=dataMu)
summary(M2)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M2)
par(op)

# thrid try:simple multiple regression with negative binomial distribution
M3 <- glm.nb(NEindividual ~ treatment, link = "log",na.action=na.fail,data=dataMu)
summary(M3) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M3)
par(op)

# comparing AIC values: least value= AIC(M3)
AIC(M1)
AIC(M2)
AIC(M3)

#Pairwise comparisons # not significant
comp1=glht(M1,linfct=mcp(treatment="Tukey"))
summary(comp1)
confint(comp1)

#dataP
# first try: simple multiple regression with Poisson distribution
M1 <- glm(NEindividual ~ treatment, family = poisson,data=dataP)
summary(M1) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M1)
par(op)

# second try:simple multiple regression with quasipoisson distribution
M2 <- glm(NEindividual ~ treatment, family = quasipoisson,data=dataP)
summary(M2)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M2)
par(op)

# thrid try:simple multiple regression with negative binomial distribution
M3 <- glm.nb(NEindividual ~ treatment, link = "log",na.action=na.fail,data=dataP)
summary(M3) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M3)
par(op)

# comparing AIC values: least value= AIC(M1)
AIC(M1)
AIC(M2)
AIC(M3)

#Pairwise comparisons # not significant
comp1=glht(M1,linfct=mcp(treatment="Tukey"))
summary(comp1) #
confint(comp1)

#dataG2
# first try: simple multiple regression with Poisson distribution
M1 <- glm(NEindividual ~ treatment, family = poisson,data=dataG2)
summary(M1) # Model Fit and coefficients
```

```
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M1)
par(op)

# second try:simple multiple regression with quasipoisson distribution
M2 <- glm(NEindividual ~ treatment, family = quasipoisson,data=dataG2)
summary(M2)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M2)
par(op)

# thrid try:simple multiple regression with negative binomial distribution
M3 <- glm.nb(NEindividual ~ treatment, link = "log",na.action=na.fail,data=dataG2)
summary(M3) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M3)
par(op)

# comparing AIC values: least value= AIC(M1)
AIC(M1)
AIC(M2)
AIC(M3)

#Pairwise comparisons # # not significant
comp1=glht(M1,linfct=mcp(treatment="Tukey"))
summary(comp1)
confint(comp1)

#dataW
# first try: simple multiple regression with Poisson distribution
M1 <- glm(NEindividual ~ treatment, family = poisson,data=dataW)
summary(M1) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M1)
par(op)

# second try:simple multiple regression with quasipoisson distribution
M2 <- glm(NEindividual ~ treatment, family = quasipoisson,data=dataW)
summary(M2)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M2)
par(op)

# thrid try:simple multiple regression with negative binomial distribution
M3 <- glm.nb(NEindividual ~ treatment, link = "log",na.action=na.fail,data=dataW)
summary(M3) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M3)
par(op)

# comparing AIC values: least value= AIC(M1)
AIC(M1)
AIC(M2)
AIC(M3)

#Pairwise comparisons # b-a-ab p<0.05
comp1=glht(M1,linfct=mcp(treatment="Tukey"))
summary(comp1) #
confint(comp1)

#dataMa
# first try: simple multiple regression with Poisson distribution
M1 <- glm(NEindividual ~ treatment, family = poisson,data=dataMa)
summary(M1) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M1)
par(op)
```

```
# second try:simple multiple regression with quasipoisson distribution
M2 <- glm(NEindividual ~ treatment, family = quasipoisson,data=dataMa)
summary(M2)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M2)
par(op)

# thrid try:simple multiple regression with negative binomial distribution
M3 <- glm.nb(NEindividual ~ treatment, link = "log",na.action=na.fail,data=dataMa)
summary(M3) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M3)
par(op)

# comparing AIC values: least value= AIC(M1)
AIC(M1)
AIC(M2)
AIC(M3)

#Pairwise comparisons # no significant difference
comp1=glht(M1,linfct=mcp(treatment="Tukey"))
summary(comp1)
confint(comp1)

#dataF
# first try: simple multiple regression with Poisson distribution
M1 <- glm(NEindividual ~ treatment, family = poisson,data=dataF)
summary(M1) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M1)
par(op)

# second try:simple multiple regression with quasipoisson distribution
M2 <- glm(NEindividual ~ treatment, family = quasipoisson,data=dataF)
summary(M2)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M2)
par(op)

# thrid try:simple multiple regression with negative binomial distribution
M3 <- glm.nb(NEindividual ~ treatment, link = "log",na.action=na.fail,data=dataF)
summary(M3) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M3)
par(op)

# comparing AIC values: least value= AIC(M1)
AIC(M1)
AIC(M2)
AIC(M3)

#Pairwise comparisons # # no significant difference
comp1=glht(M1,linfct=mcp(treatment="Tukey"))
summary(comp1)
confint(comp1)
```

Appendix xiv. R code for natural enemy movement by bi-direction pitfall sampling

```
#1-Natural enemies movement with bidirectional pitfall sampling in July in crop
growing season#
# data are expressed as the pooled NE numbers in two pitfalls in one direction of
one samling site
rm(list = ls())
move1<- read.csv("C:/Users/xie008/Desktop/NE movemnet 1.csv")
head(move1)
summary(move1)
```

```
# install packages
require(MASS)  #glm.nb model
require(MuMIn)    # for Multi Model Inference
require(multcomp) # for post-hoc test on differences between levels

#define factor
direction <-as.factor(move1$direction)

# sum NE individuals and enemies groups exist in a pooled sample
NEmove1=move1$individual
# individual <-
move1$spider+move1$rovebeetle+move1$Caralarvae+move1$Poe.cupreus+move1$Pse.rufipes+
move1$Pte..melanarius+move1$Pte.vernalis+move1$Cal.melanocephalus+move1$Cli.fossor+
move1$Cli.collaris+move1$Har..affinis+move1$Ago.muelleri+move1$Ama.aenea+move1$Ama.
fulva+move1$Ama.familiaris+move1$Ama.lunicollis+move1$Lor..pilicornis+move1$earwig+
move1$centipede+move1$weevil+move1$mite#

hist(NEmove1)
hist(move1$group)
hist(spider)
hist(Poe.cupreus)
hist(rovebeetle)
hist(Pse.rufipes)

# make plot
boxplot(NEmove1~direction, main="Natural enemy movement ",ylab="NE individuals per
bidirection pifall set",ylim=c(0, 90))
boxplot(move1$group~move1$direction,main="Natural enemy groups ",ylab="NE
group",ylim=c(4, 15))

# select distribution and fitted model:
# first try: simple multiple regression with Poisson distribution
M1 <- glm(NEmove1 ~ direction, family = poisson,na.action=na.fail)
summary(M1) # Model Fit and coefficients
anova(M1,test="LRT") #Effect Significance (Likelihood Ratio Statistics)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M1)
par(op)

# second try:simple multiple regression with quasiPoisson distribution
M2 <- glm(NEmove1 ~ direction, family = quasipoisson,na.action=na.fail)
summary(M2)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M2)
par(op)

# thrid try:simple multiple regression with negative binomomial distribution:AIC:
605.84
M3 <- glm.nb(NEmove1 ~ direction, link = "log",na.action=na.fail)
summary(M3)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M3)
par(op)

# comparing AIC values: least value= AIC(M3)
AIC(M1)
AIC(M2)
AIC(M3)

confint(M3)
summary(M3)

#Pairwise comparisons # p>0.1   (0.184)
comp1=glht(M3,linfct=mcp(direction="Tukey"))
summary(comp1) #Significant differences between all factor levels

# groups
Mg1<- glm(move1$group ~ direction, family = poisson,na.action=na.fail)
```

```
summary(Mg1)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(Mg1)
par(op)
Mg2<- glm.nb(move1$group ~ direction, link = "log",na.action=na.fail)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(Mg2)
par(op)
summary(Mg2)

# comparing AIC values: least value= AIC(Mg1)
AIC(Mg1)
AIC(Mg2)
#Pairwise comparisons  # p>0.1 (# 0.922)
comp1=glht(Mg1,linfct=mcp(direction="Tukey"))
summary(comp1) #Significant differences between all factor levels

# Making tables
(outputmean = t(tapply(NEmove1,list(direction),mean)))
(outputSEM = t(tapply(NEmove1,list(direction),function(x)sqrt(var(x)/length(x)))))

# Making tables
(outputmean = t(tapply(move1$group,list(direction),mean)))
(outputSEM =
t(tapply(move1$group,list(direction),function(x)sqrt(var(x)/length(x)))))

####### test for specific enemy groups###########
hist(Poe.cupreus)
hist(rovebeetle)
hist(Pse.rufipes)

plot(move1$spider~move1$direction)
plot(move1$Poe.cupreus~move1$direction)
plot(move1$rovebeetle~move1$direction)
plot(move1$Pse.rufipes~move1$direction)

hist(spider) # no sig.
MB1 = glm.nb(move1$spider~move1$direction, link = "log",na.action=na.fail)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(MB1)
par(op)
summary(MB1)
confint(MB1)

hist(Poe.cupreus) # no sig.
MB4 = glm.nb(move1$Poe.cupreus~move1$direction, link = "log",na.action=na.fail)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(MB4)
par(op)
summary(MB2)
confint(MB2)

hist(rovebeetle) # no sig.
MB3 = glm.nb(move1$rovebeetle~move1$direction, link = "log",na.action=na.fail)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(MB3)
par(op)
summary(MB3)
confint(MB3)

hist(Pse.rufipes) # # no sig.
MB2 = glm.nb(move1$Pse.rufipes~move1$direction, link = "log",na.action=na.fail)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(MB2)
par(op)
summary(MB4)
confint(MB4)
```

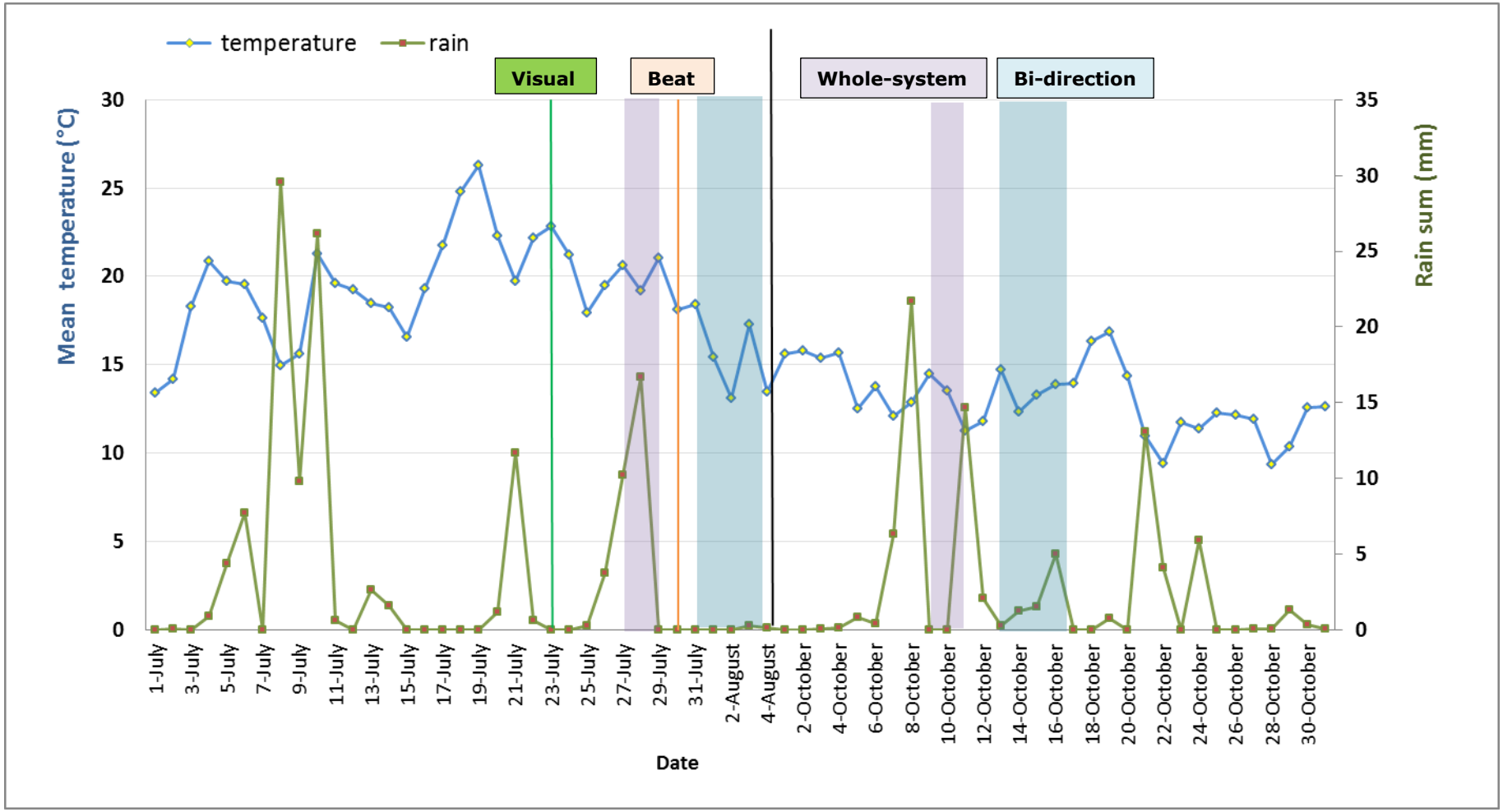
```
# Natural enemies movement with bidirectional pitfall sampling On October in late
season
# data are expressed as the pooled NE numbers in two pitfalls in one direction of
one samling site
rm(list = ls())

move2<- read.csv("C:/Users/xie008/Desktop/NE movement 2.csv")
head(move2)
summary(move2)

install.packages(c("MuMIn","MASS","lme4"),dependencies=F)
require(MASS)
require(nlme)
require(MuMIn)    # for Multi Model Inference
require(multcomp) # for post-hoc test on differences between levels

#define factor
direction <-as.factor(move2$direction)

# NE= total amount of all individuals
NEmove2 <-move2$individual

hist(NEmove2,nclass=20)
hist(move2$group)

# plot
boxplot(NEmove2~direction,main="Natural enemy movement after harvest ",ylab="NE
individuals per bidirection pifall set",ylim=c(0, 20))
boxplot(move2$group~direction)

# select distribution and fitted model:
# first try: simple multiple regression with Poisson distribution
M1 <- glm(NEmove2~direction, family = poisson,na.action=na.fail)
summary(M1) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M1)
par(op)

# second try:simple multiple regression with quasiPoisson distribution
M2 <- glm(NEmove2 ~ direction, family = quasipoisson,na.action=na.fail)
summary(M2)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M2)
par(op)

# thrid try:simple multiple regression with negative binomomial distribution:AIC:
605.84
M3 <- glm.nb(NEmove2 ~ direction, link = "log",na.action=na.fail)
summary(M3)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M3)
par(op)

# comparing AIC values: least value= AIC(M1)
AIC(M1)
AIC(M2)
AIC(M3)

summary(M1)
confint(M1)


# Making tables
(outputmean = t(tapply(NEmove2,list(direction),mean)))
(outputSEM = t(tapply(NEmove2,list(direction),function(x)sqrt(var(x)/length(x)))))

# groups
Mg1<- glm(move2$group ~ direction, family = poisson,na.action=na.fail)
```

```
summary(Mg1)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(Mg1)
par(op)
Mg2<- glm.nb(move2$group ~ direction, link = "log",na.action=na.fail)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(Mg2)
par(op)
summary(Mg2)

# comparing AIC values: least value= AIC(Mg1)
AIC(Mg1)
AIC(Mg2)
#Pairwise comparisons
comp1=glht(Mg1,linfct=mcp(direction="Tukey"))
summary(comp1) #Significant differences between all factor levels
# Making tables
(outputmean = t(tapply(move2$group,list(direction),mean)))
(outputSEM =
t(tapply(move2$group,list(direction),function(x)sqrt(var(x)/length(x)))))


#2- Natural enemies movement with bidirectional pitfall sampling in non-mix strip
in October
# data are expressed as the pooled NE numbers in two pitfalls in one direction of
one sampling site
rm(list = ls())
move2<- read.csv("C:/Users/xie008/Desktop/NE movement 2.csv")
head(move2)
summary(move2)
install.packages(c("MuMIn","MASS","lme4"),dependencies=F)
require(MASS)
require(nlme)
require(MuMIn)    # for Multi Model Inference
require(multcomp) # for post-hoc test on differences between levels
#define factor
direction <-as.factor(move2$direction)
# NE= total amount of all individuals
NEmove2 <-move2$individual
hist(NEmove2,nclass=20)
hist(move2$group)

# plot
boxplot(NEmove2~direction,main="Natural enemy movement after harvest ",ylab="NE
individuals per bidirection pifall set",ylim=c(0, 20))
boxplot(move2$group~direction)
# select distribution and fitted model:
# first try: simple multiple regression with Poisson distribution
M1 <- glm(NEmove2~direction, family = poisson,na.action=na.fail)
summary(M1) # Model Fit and coefficients
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M1)
par(op)
# second try:simple multiple regression with quasiPoisson distribution
M2 <- glm(NEmove2 ~ direction, family = quasipoisson,na.action=na.fail)
summary(M2)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M2)
par(op)
# thrid try:simple multiple regression with negative binomomial distribution:AIC:
605.84
M3 <- glm.nb(NEmove2 ~ direction, link = "log",na.action=na.fail)
summary(M3)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(M3)
par(op)
# comparing AIC values: least value= AIC(M1)
AIC(M1)
```

```
AIC(M2)
AIC(M3)
summary(M1)
confint(M1)
# Making tables
(outputmean = t(tapply(NEmove2,list(direction),mean)))
(outputSEM = t(tapply(NEmove2,list(direction),function(x)sqrt(var(x)/length(x)))))
# groups
Mg1<- glm(move2$group ~ direction, family = poisson,na.action=na.fail)
summary(Mg1)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(Mg1)
par(op)
Mg2<- glm.nb(move2$group ~ direction, link = "log",na.action=na.fail)
op <- par(mfrow = c(2, 2), mar = c(5, 4, 1, 1))
plot(Mg2)
par(op)
summary(Mg2)
# comparing AIC values: least value= AIC(Mg1)
AIC(Mg1)
AIC(Mg2)
#Pairwise comparisons
comp1=glht(Mg1,linfct=mcp(direction="Tukey"))
summary(comp1) #Significant differences between all factor levels
# Making tables
(outputmean= t(tapply(move2$group,list(direction),mean)))
(outputSEM=t(tapply(move2$group,list(direction),function(x)sqrt(var(x)/length(x)))))
```

Appendix xv. weather condition of sampling periods

Weather information from Weather station De Veenkampen that is located to the west of Wageningen, the Netherlands and is a fully automated weather station.



#Visual: Visual assessment; Beat: Beat sampling;
Whole-system: Whole-system pitfall trap sampling; Bi-direction: Bi-direction pitfall trap sampling#
Data Source: http://www.met.wau.nl/veenkampen/data/

END