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The conservation and utilisation of biodiversity in agro-ecosystems

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Introduction

The intensification of arable agriculture over the last 50 years has been associated with substantial losses of biodiversity. There is a widespread belief among conservationists, the general public and politicians that low yielding organic agricultural systems are host to higher levels of biodiversity and more sustainable than high-yielding farming systems. Indeed, the organic division in the UK is 'currently booming with the largest ever wave of farm conversions underway and for many products consumer demand is growing faster than supply'. However, the organic industry has recently been the subject of a number of serious critiques of its methods. These all point to the lack of a scientific basis underpinning the organic farming method. The organic community defends its system by insisting that direct comparisons of organic and conventional crops are inappropriate and that only the whole system can be compared.

To date, information on declines in biodiversity in agroecosystems is concentrated on particular groups of organisms, particularly farmland birds and mammals, arable weeds, butterflies, moths and bumble bees. However, the distribution and abundance of these groups may not provide the data needed for a sustainable agriculture. If agroecologists, land managers and policy makers are to manage farmland biodiversity in the long term, organically or otherwise, then they also need to understand the ways in which species interact, since these interactions can have a profound impact on a community's response to species loss, stress and ecological restoration. This approach will be discussed in relation to two ongoing projects at the University of Bristol. The first compares biodiversity on organic and conventional farms at three trophic levels by constructing replicate farm-scale quantitative food webs. The second project constructs a single large food web for an organic farm. Once constructed, species will be removed from the model network to degrade the web, which will then be rebuilt, using Environmental Stewardship.

Project 1: Parasitoid webs in organic and conventional farming systems: structure, sustainability and exploitation

The increased biodiversity of natural enemies on organic farms is generally assumed to lead to effective and sustainable levels of pest protection. However, while this assumption is intuitively appealing, rather little is understood about the relationship between enemy diversity and the level of biological control. For example, a more diverse parasitoid complex is likely to contain more species of hyperparasitoid (parasitoids that attack other parasitoids) and these can reduce the efficacy of the primary parasitoids. Thus, while the diversity of natural enemies on a farm may provide a useful estimate of natural enemy efficacy, it remains a somewhat crude statistic.

If, however, the web of interactions between parasitoids and their hosts, both pest and non pest, could be characterised in agroecosystems, then it would be possible to rigorously compare the structure of the natural enemy community on organic and conventional farms. And if the web is amenable to manipulation, then explanatory patterns can be assessed by

field experiments, which remain the 'most elegant and least ambiguous way of quantifying species interactions'. The aims of this project are to:

- 1. To make such a whole system comparison to test the hypothesis that pest control is more effective and more sustainable on organic farms than conventional farms.
- 2. To improve and exploit the ability of the parasitoid species which provide the ecosystem service of pest control.

Farm scale food webs describing the interactions between plants, herbivores and parasitoids in both crop and natural habitats on farms, are being used as a means to test the first hypothesis. The webs have been constructed for ten pairs of organic and conventional farms. The food webs are still undergoing analysis. A large scale field experiment is currently being used on the 20 farms to test the efficacy of pest control in the two types of farming systems.

Project 2: Biodiversity in agro-ecosystems: a complex systems approach

Most data on declines in farmland biodiversity are for particular indicator groups, such as farmland birds, arable weeds or butterflies, describing for example their species richness or abundance. There is increasing disquiet, however, since this type of data may not provide the information needed for a wildlife-compatible agriculture and the conservation of ecosystem services, as these depend on interactions between species. This project will construct a farm-scale network of interactions, which contains indicator groups, such as the granivorous birds, arable plants and butterflies, together with the parasitoids, pollinators and seed dispersers that provide key ecosystem services, as well as pest species and the farmer. Once the web is complete, the aim is to use a complex systems approach to simulate primary species loss in the web and measure robustness in terms of the secondary extinctions that follow. Different types of extinction will be modelled, a random removal (the null model) and systematic removals, each of the latter representing known threats to biodiversity. Specifically the following predictions will be tested:

- 1) taxonomically and trophically remote species interact directly and indirectly via a network of interactions that links species to each other;
- plant and insect species form the bedrock of biodiversity in agro-ecosystems and the loss of these species will lead to a cascade of secondary extinctions that includes birds and mammals;
- 3) the rate of species loss from the network depends upon whether the species that form the primary extinctions are specialists, generalists, of high trophic rank, wide ranging, rare or habitat-specific species.

The degraded webs generated by the complex systems analysis will be used to simulate the farm's restoration using Defra's new Environmental Stewardship schemes. Currently the network is under construction.

Conclusion

Food webs and other ecological networks have not yet been widely applied to the field of sustainable agriculture. Given the practical advances being made in network construction (for example, in eco-informatics), the theoretical advances (for example, complex systems approaches) and the ongoing threat of biodiversity loss, combined with ambitious agrienvironment schemes, now is a very exciting time to begin to use ecological networks as a practical tool for managing biodiversity on the large amount of land occupied by farmland, both nationally and globally.

Drivers of biodiversity in the cropping systems of the Rolling Pampas

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Local internal factors affecting community (alpha) biodiversity, such as individual and total biomass, density and productivity, are well understood, as well as how they can be affected by external factors causing disturbance and environmental stress. Soil-climate and land-use variation operating at the regional scale have been also recognised as drivers of biodiversity. Agricultural land-use is considered to negatively impact biodiversity, especially through clearance of pristine habitats for new planting, with the accompanying pressures of fragmentation of remaining habitats, pollution and disturbance. This is also the case for the intensification of existing agricultural systems, aimed at increasing yields per unit area (Sarr *et al.*, 2005).

The Rolling Pampa is the main cropland of Argentina, located between 34-36°S latitude and 58-62°W longitude. The representative soil is a Mollisol, of which Argiudol is the most common type. The gently rolling original landscape generated relatively homogeneous grassland, in which ecotones were infrequent (Soriano, 1991). It developed into an agricultural landscape during the ninetieth-twentieth centuries. The new cultural landscape created a mosaic that played a major role in moulding the existing plant communities, especially by affecting the overall species pool in the landscape (gamma diversity). Abandoned land, roads, corridors, wasteland and multiple crops and farming practices generated a large diversity of habitats (beta diversity). This structural complexity at the regional landscape level created conditions suitable for invasion processes, whereby the dynamics and composition of the weed community became insensitive to changes in agricultural practices, during most of the twentieth century. This reflected the regional species pool of Mediterranean weeds from Europe adapted to ploughing that were always present in croplands, regardless of what was cropped.

The heterogeneity of this mosaic has contributed, at the regional scale, to the continuous increase in species number that was registered for the spontaneous vegetation in croplands. This increase has occurred without loss of the dominant weeds and some functions (e.g. C_4 , C_3 , and production of secondary metabolites). Species richness of the original grassland growing in well-drained soils was *ca.* 222 species. It was dramatically impoverished to *ca.* 53 by 1926 (32 of the original flora plus 21 new) by early agricultural activities (Parodi 1926). This impoverishment in the flora was not unexpected, since the native grassland species habitat was lost by soil tilling.

Thereafter, weeds continually invaded the agricultural landscape. In 1960, the total number of species present in maize crops was 79, being 34 from the original grassland and 45 exotic (Leon & Suero, 1962). Now the total number of species present in maize crops is 99, 54 species from the original grassland and 45 exotic species. Species number increased during the 1926/1960 and 1960/1990 periods at the rates of 1.32 and 1.50 species per year respectively. The average annual rate of increase in species number since 1930 is 1.01. A great proportion of the floristic richness of the Rolling Pama has been restored through this process, even though the native perennial grasses have nearly disappeared.

Habitat loss for the native fauna produced local extinctions, but overall richness was especially increased by arthropods, birds (e.g. *Turdus rufiventris, Zenaida sp, Furnarius* sp.) and rodents (e.g. *Akodon azarae, Oligormys flavescens* and *Cavia apera*) that could exploit the new habitats created by human activities. Directed propagule dispersal by bird species played a major role in structuring communities in the agricultural landscape. This mechanism enhanced the occurrence of woodland succession processes, when trees were originally totally absent in the Pampas.

Very recent agricultural practices (no-tillage cropping and soyabean transgenic cultivars resistant to glyphosate), together with market factors, have resulted in significant changes in diversity. Overall habitat heterogeneity (beta diversity) was again reduced and this impacted on biodiversity in the cropping fields. Alpha (local) diversity and functional richness are linearly related with gamma (regional) diversity, which showed an initial increase after the introduction of the new technology, but then decreased. Tillage systems and cultivars are the main agronomic variables affecting the occurrence of weeds. Arthropods associated with these communities are mainly generalists; recognised summer crop feeders and pollinators are not well represented. Moreover, absence of recently ploughed fields is affecting some bird guilds that in the past used readily accessible food resources.

In summary, the latest technological shift has compromised the existence of hedges, fences and roads that played a major role in the transformation of the original grassland landscape, sustained biodiversity by creating refuges for the native and exotic plant species, impeded species extinction and supported the development of threshold population sizes that allowed them to withstand environmental stochasticity within the agricultural landscape and allowed recolonisation of empty patches.

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Functional impacts of biodiversity: indigenous mice and insects reduce weed population growth rates in low-external-input cropping systems

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Herbicides are the most heavily used class of pesticide in American agriculture and pervade the production of agronomic crops. This is especially true in the Midwestern states, where farmers annually apply an estimated 68 million kg of herbicide active ingredients to 39 million ha of maize and soyabean. Herbicides have increased the productivity of agricultural labour, fostered the development of soil-conserving zero-tillage systems, and simplified the process of crop production. Nevertheless, many scientists, farmers and policy makers now seek alternatives to heavy reliance on herbicides, due to concerns over resistance evolution in weeds, environmental contamination and threats to human health. Information concerning the performance of alternative cropping systems and ecologically based weed management strategies is needed if substantial reductions in herbicide use are to be realised.

We conducted a multi-year, 9-ha field experiment near Boone, Iowa, to test the hypothesis that weeds could be suppressed as effectively in diversified, low-external-input (LEI) cropping systems as in less diverse systems that relied on conventional rates of herbicides. The experiment included a two year rotation system (maize/soyabean) that received herbicides and synthetic fertilisers at conventional rates, and a three year rotation (maize/soyabean/small grain + red clover) and a four year rotation (maize/soyabean/small grain + alfalfa/alfalfa) treated with less herbicide and fertiliser. Averaged over 2003-2006, herbicide inputs were 76% lower in the three year rotation (0.50 kg a.i. ha⁻¹ yr⁻¹) and 82% lower in the four year rotation (0.38 kg a.i. ha⁻¹ yr⁻¹) than in the two year rotation (2.09 kg a.i. ha⁻¹ yr⁻¹). Triticale was used as the small grain crop in 2003-2005; oat was used in 2006.

Particular attention was directed toward understanding the effects of contrasting rotation systems and attendant ecological processes on the population dynamics of two common annual weed species, velvetleaf (*Abutilon theophrasti*) and giant foxtail (*Setaria faberi*). In November 2002 we measured weed seed densities in the surface 20 cm of soil and then added a pulse of velvetleaf and giant foxtail seeds (470 + 1,876 viable seeds m⁻², respectively) to 7 m x 7 m areas of each experimental plot. Subsequently, during 2003-2006, we monitored densities of velvetleaf and giant foxtail seeds, seedlings, and reproductive adults, production of new seeds and losses of seeds to predators.

As compared with initial seed bank densities, velvetleaf seed densities in April 2006 were reduced 68% in the two year rotation, 31% in the three year rotation, and 51% in the four

year rotation. For giant foxtail, seed densities were reduced 97% in the two year rotation, 55% in the threeyear rotation, and 81% in the four year rotation between 2002 and 2006. These reductions in weed seed bank densities occurred despite cumulative additions, in the three year and four year rotations, of as many as 519 velvetleaf seeds m^{-2} and 6,983 giant foxtail seeds m^{-2} .

Measured rates of velvetleaf and giant foxtail seedling emergence and literature values for rates of seed decay failed to explain the discrepancies between observed and expected seed densities. Substantial losses of velvetleaf and giant foxtail seeds to predators were detected, however. To determine rates of weed seed loss to predators during spring, summer and autumn, we placed velvetleaf and giant foxtail seeds on 6 cm x 8 cm sandpaper cards that were protected by narrow mesh wire screen or exposed to predators on the soil surface. Averaged over different crops, rotation systems and 27 sampling periods during May-November 2003 and April–November 2004, mean rates of seed removal were 33% per 48 hours for velvetleaf and 53% per 48 hours for giant foxtail. To determine rates of seed losses to predators during late autumn, winter and early spring, we placed velvetleaf and giant foxtail seeds in 60 cm x 60 cm wire mesh trays that were covered by wire mesh exclosure cages or 'sham' cages that allowed passage of seed predators through small doors. Averaged over crops and rotation systems, cumulative losses of seeds from November 2005 to March 2006 were 72% for velvetleaf and 62% for giant foxtail; seed losses to predators from November 2006 to April 2007 were 90% for velvetleaf and 84% for giant foxtail. Data obtained from pitfall traps and Sherman live traps indicated that field crickets, carabid beetles and prairie deer mice were the most important seed predators, with activity-densities of the different taxa exhibiting contrasting temporal patterns. Modelling analyses indicated that weed seed predation could account for the observed declines in soil seed banks and had particularly marked suppressive effects on weed dynamics in the LEI systems. Without seed predation, giant foxtail density in the LEI three year rotation would be expected to increase.

Measurements of weed biomass made in September and October of 2003-2006 in areas of the plots that were not intentionally infested with velvetleaf and giant foxtail indicated that weed productivity in maize and soyabean did not differ among rotation systems and was low (\leq 4.2 g m⁻²) in all years. Weed growth in small grain stubble was more variable than in other crop types and in 2003 reached the highest levels measured in the experiment (32.0 g m⁻²). In contrast, weed biomass in established alfalfa was low (\leq 3.2 g m⁻²) in all years and similar to levels measured in maize and soyabean.

Crop data taken to complement the weed studies indicted that maize and soyabean yields in the LEI 3-year and four year rotation systems matched (2003 and 2004) or exceeded (2005 and 2006) levels obtained from the conventionally managed two year rotation system. Labour requirements were higher for the LEI systems, but without government crop subsidy payments, net returns to land and management during 2003-2006 were greatest in the four year system (\$540 ha⁻¹ yr⁻¹), least in the three year system (\$475 ha⁻¹ yr⁻¹), and intermediate in the two year system (\$504 ha⁻¹ yr⁻¹). With subsidies, the economic advantage of the four year system was reduced, but not eliminated. We conclude that certain types of diversified LEI systems can be agronomically and economically competitive with less diverse, conventionally managed systems, and that ecological processes such as seed predation can contribute to effective weed management with less reliance on herbicides.

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Occurrence of mite species in tea plantations in Turkey

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Introduction

Tea (*Camellia sinensis* L.) is grown in the eastern Black Sea region of Turkey where 547,000 tonnes are produced from 76,700 ha. It is the most important source of income for 200,000 families (Anonymous, 2003). Mites are serious pests of tea world-wide. They damage the green tissues of leaves and cause yield reduction. Species belonging to the Tetranychidae, Tenuipalpidae, Tarsonemidae and Eriophyidae families cause economically important damage to tea in different parts of the world (Banerjee & Cranham, 1985; ChannaBasavanna, 1996).

Although Turkey is the world's fifth largest tea producer (Anonymous, 2003), minimal research has been done on tea mites. Düzgüneş (1963) recorded *Calacarus carinatus* (Green) Keifer and *Brevipalpus phoenicis* Geijskes on tea. Recently, Ozman-Sullivan *et al.* (2006) investigated mites on tea in Turkey, but no research has been done on their occurrence. Therefore, the aim of this study was to determine the occurrence of mites of tea plantations in Turkey

Materials and methods

Surveys of 115 tea plantations were done from sea level to maximum altitude (1000m) throughout the growing areas of the eastern Black Sea region in late spring of 2005 and 2006. Twenty five shoots of 20-25 cm length were collected from each plantation. The upper and lower leaf surfaces, petioles, buds, shoots and flowers were examined under a binocular microscope. All mites found were preserved in 70% ethyl-alcohol and later mounted in Hoyer's medium for identification using a phase contrast microscope.

Results and discussion

Phytophagous, predacious, mycophagous and saprophagous mite species were found on tea in this study (Table 1). Most species inhabited the undersurface of leaves. The most common species was the harmful mite *Calacarus carinatus* (80.00%), followed by harmful *Brevipalpus* spp. (*Brevipalpus obovatus* Donn. and *Brevipalpus phoenicis* (34.78%) and the predatory mites *Tydeus* spp. (2 unidentified species) (33.91%). The remaining species were uncommon. *Polyphagotarsonemus latus* (Banks), which is one of the most harmful mites, was found in only one plantation (0.87%) which was close to the Georgian border. The tetranychid mites *Oligonychus coffeae* (Neitner) and *Tetranychus kanzawai* Kishida, which are economically important in other countries (Banerjee & Cranham, 1985), were not found in this study.

Five species of eriophyoid mites have been reported from commercially important tea growing areas of different parts of the world. Two of these, *C. carinatus* and *Acaphylla theae* are economically important on tea in south-east Asian countries, especially in India (ChannaBasavanna, 1996). In the current study, *Calacarus carinatus* was the commonest species throughout tea growing areas in Turkey but *A. theae* was only found in only six orchards (5.20%) close to the Georgian border. Despite the fact that pesticides have not

been used to date in Turkish plantations, minimal mite damage was observed in the current study. However, the population densities of harmful mites should be regularly monitored to identify and manage any emerging threats.

Family	Species	Infested plantations	(%)
Eriophyidae	Calacarus carinatus*	92	80.00
	Acaphylla theae*	6	5.20
Tenuipalpidae	Brevipalpus spp.*	40	34.78
Tarsonemidae	Polyphagotarsonemus	1	0.87
	latus*		
	<i>Tarsonemus</i> sp.#	1	0.87
Tydeidae	<i>Tydeus</i> spp.+	39	33.91
Phytoseiidae	Amblyseius sp.+	12	10.43
Winterschmidtiidae	Czenspinskia	6	5.20
	transversostriata#		
Liacaridae and	2 unidentified	6	5.20
Oppidae	species#		

Table 1. Distributions of mite species in 115 tea plantations in Turkey (%).

*Harmful species, + predatory species, # mycophagous and saprophagous species

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Analysis of biodiversity of soil micro-organisms associated with *Sclerotium rolfsii* sclerotium debilitation under flooded field conditions, using PCR-DGGE and sequence data

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Introduction

Sclerotium rolfsii Sacc. is a soil-borne pathogen causing diseases on many crops species. The pathogen produces a large number of sclerotia that can persist in soil for several years, making the disease control difficult. The use of fungicides is limited not only by their high cost, but also by the increasing concern for the environment. Flooding infested fields was reported to lead to decrease in germinability of sclerotia of the fungus (Nakagawa *et al.*, 1994), due probably to colonisation by bacteria-like organisms. rDNA sequences of bacteria isolated from *S. rolfsii* sclerotia showed that about 90% of the isolates were *Pantoea agglomerans* (Okabe *et al.*, 2003). No culture-independent studies for the assessment of bacteria associated with debilitation of sclerotia of S. *rolfsii* have been published to date. The current research aimed to study diversity of bacterial populations found with sclerotia under flooding, using rDNA-PCR DGGE and sequence data.

Materials and methods

Sclerotium rolfsii strain 63 (MAFF 306493, Kagawa, Japan) was sub-cultured on PDA and soil was inoculated using the method of Nakagawa *et al.* (1994). Organic matter was incorporated into the soil at 6000 kg ha⁻¹ and sclerotia were bagged and buried. After 30-day flooding, sclerotia were recovered from soil and plated on water agar to assess sclerotial viability, while soybean seeds were planted to record stand plants 30 days after planting. Bacterial 16S rDNA was extracted from the sclerotia using the FastDNA Spin Kit for soil (Qbiogene, Inc, Irvine, USA). The DNA was PCR-amplified using the bacterial universal primers GC-338f and 907r (Lane, 1991). DGGE was performed using the D Code System (BioRad, Tokyo, Japan) and PCR products (200 ng) were loaded in 8% (w/v) polyacrylamide gels in TAE buffer. Electrophoresis was carried out at 60°C at 65V for 18h. Gels were then stained with SYBER Green I for 30 min and analysed with Molecular Imager FX (Bio-Rad). DGGE band profiles were analysed and Shannon diversity index was calculated. Objective bands were excised and closest relatives to the sequences of the bands were determined using the BLAST search program.

Results and discussions

Sclerotia recovered from flooded plots showed percentage germination lower than that from unflooded plots. Under these conditions, frequency of sclerotia colonised by bacteria was the highest for wheat bran, followed by rice straw amendments. The trend was similar for healthy plants (%) recorded 30 days after planting (Table 1). The DGGE band patterns showed the highest diversity for flooded samples amended with wheat bran or rice straw.

	(%)	(%) Sclerotia	(%) Stand	Shannon
Treatments	Germinated sclerotia ^b	colonized by bacteria ^b	plants	diversity index
Control			44.61 b	
Control + Rs			69.61 c	
Control + Wb			30.39 a	
Unflooded + No	96.67 b	3.33 a	44.12 b	1.73 a
Unflooded + Rs	93.33 b	15.23 ab	46.57 b	1.74 a
Unflooded + Wb	86.67 ab	57.00 d	17.65 a	2.01 b
30-day flooded + No	80.00 ab	10.00 a	66.67 c	1.57 a
30-day flooded + Rs	76.67 ab	26.67 b	78.92 cd	2.36 c
30-day flooded + Wb	63.33 a	41.34 c	91.67 d	2.27 bc

 Table 1 % germinated sclerotia of Sclerotium rolfsii, %sclerotia colonised by bacteria and

 %stand plants^a following different soil treatments

^aSoyabean was sown and stand plants were recorded 30 days after planting. Control was not treated. No, Rs and Wb mean no organic matter applied, rice straw and wheat bran, respectively. ^bThese assessments were performed on water agar. Within columns, means with different letters significantly differ (P = 0.05) according to the General Linear Model.

The constructed dendrogram separated flooded from unflooded and amended from unamended plots. Identified sequences showed bacteria clones from flooded plots to belong to Clostridia groups, known as anaerobic bacteria (Momma *et al.*, 2007), whereas all clones from unflooded plots belong to Betaproteobacteria and Actinobacteria. These results are consistent with early reports indicating that members of clostridial cluster I belong to the dominant populations colonising and degrading rice straw in anaerobic paddy soils (Weber *et al.*, 2001). In the current study, flooded soil amended with wheat bran and rice straw showed the lowest germination of sclerotia and disease incidence, but the highest diversity of bacteria associated with sclerotia. Thus, debilitation of sclerotia under flooding might be associated with this large number of bacteria belonging to Clostridia groups that negatively influenced the survival of the pathogen sclerotia and improve plant health. Clostridia are considered to play a major role in biological soil deinfestations, consisting of flooding and wheat bran amendment (Momma *et al.* 2007).

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The benefits of medicinal and aromatic plants rotations before tomato crops on biodiversity of soil fauna

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Introduction

Crop rotations are fundamental to sustainable cropping systems. A well-designed crop rotation creates diversity and improves soil conditions and soil fertility, as well as generating biodiversity of the soil fauna. Medicinal and aromatic plants have chemical constituents active in curing aliments or providing flavour and fragrances. Medicinal plants possess active ingredients used mainly in preventing or curing aliments. They may have other properties which permit them to be used as botanical insecticides. We investigated a two-phase experiment using pre-planted aromatic plants to reduce insect pests in a following tomato crop.

Methods

The present experiment was carried out over a period of eight months, extending from November 2004 to June 2005 at Fayoum, upper Egypt. Five medicinal and aromatic plants were cultivated: marjoram (*Marjorana hortensis* Moench), flax (*Linum usitatissimum* L.), tooth pick-plant or khella (*Ammi visnaga* (L.)), chamomile (*Marticaria recutita* L. = *Chamomilla recutita* (L.)) and daisy (*Chrysanthemum vulgare* (L.)) and the sixth plot was left fallow without cultivation as control. These medicinal and aromatic plants were followed by transplanted tomato (*Lycopersicum esculentum*). Individual plots were 9m by 9m and treatments were replicated four times, giving a total of 24 plots in a randomised complete block design. We compared soil fauna populations (as activity density) in the different plots during the phase with the aromatic plants with those after planting tomatoes using pitfall traps. Traps were set for 24 hours once a week in both phases of the experiment. The aim of this study was to evaluate the effect of the different rotational treatments, by investigating the functional (trophic) group structure of the soil fauna: herbivores, carnivores, detritivores, parasites, pollen grain transmitters and disease vectors. Data were subjected to Correspondence Analysis.

Results

The main groups found were flies, ants, true spiders, Collembola and aphids. Soil fauna associated with the control plot in the first period was the most widely separated from those of other plots. As a result of the Correspondence Analysis, soil fauna associated with all medicinal and aromatic plants, except with flax, were clustered together. Soil fauna associated with flax were grouped with soil fauna associated with all tomato plots.

Rotation of tomato plant after medicinal and aromatic plants can play an essential role in breaking the life cycle of herbivores in tomato, and can provide the basis for effective non-chemical pest control.

Our results indicated that each of the two different cropping phases could affect the population of the mesofauna. The results revealed that planting the two aromatic plants, marjoram and daisy, affect to a great extent the composition of soil fauna; these plants were suitable for reducing the numbers of different pests. The marjoram was characterised by very low number of all species of soil fauna compared with the other plots. While the khella showed the highest activity-density of the soil fauna community. Moreover, most plots of tomato recorded more soil fauna than those of aromatic plants. We concluded that the soil organisms of rotary cultivated plots are more abundant with tomato than with aromatic plants. Others have indicated that crop rotations will improve the biological activity of soil.

Amongst the different functional groups, number of herbivores was highest in the aromatic plant plots. This was due to the large numbers of the root-feeding *Delia* sp., the robber fly *Eumerus* sp. and aphids, particularly in khella, chamomile and fallow plots. The surplus amount of litter and weeds in the fallow plot of the first period contributed to this effect. This result was concurs with work of others who state that various agricultural pests such as larval Diptera establish in the soil and feed on the roots of crops. On the other hand, the detritivores were less abundant due to the chemical contents of the aromatic plants. In contrast, there was a decrease in the number of herbivores during the second period with tomato. Medicinal and aromatic plants have chemicals within them that repel and even kill pests. Moreover, many of these plants have important industrial applications, as insecticides or insect repellent. Interestingly, the abundances of predators collected from tomato plots were double that compared with the corresponding number in aromatic plants.

Conclusion

The effect of medicinal and aromatic plants on activity density of soil fauna can be related to their continuously secreted oils. These oils, of course, are volatile and quickly dissipated. Our results indicated that each of the two different cropping phases could affect the population of the mesofauna. The result revealed that, planting the two aromatic plants marjoram and daisies affect to a great extent the composition of soil fauna taxa; these species were suitable for reducing the numbers of different pests. The marjoram was characterised by very low number of all species of soil fauna compared with the other plots. The khella showed the highest activity-density of soil fauna community. Moreover, most plots of tomato recorded more soil fauna than that of aromatic plants.

We conclude that the soil organisms of rotary cultivated plots are more abundant with tomato than with aromatic plants. We can say that the rotary cultivation plots had more soil animals than the medicinal and aromatic plants. These results indicate that crop rotation will improve the biological activity of soil.