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The role of semi-natural and abandoned vegetation patches in sustaining lepidopteran diversity in an organic olive orchard

Stefano Scalercio[1], Nino Iannotta[1], Pietro Brandmayr[2]
[1]CRA – Istituto Sperimentale per l'Olivicoltura, Rende, Cosenza, Italy
[2]Dipartimento di Ecologia, Università della Calabria, Rende, Cosenza, Italy

Abstract

In an organic farm on the Ionian Coast of Calabria Region, southern Italy, Lepidoptera were monthly surveyed in order to contribute to the knowledge of the olive orchard butterflies and moths communities, and investigate the role assumed by patches at different seral stages in sustaining lepidopteran diversity and abundance. The sampling sessions were conducted in four contiguous stands representing a gradient of land use running from relatively undisturbed to highly modified vegetation cover. Diversity values, larval feeding preferences, adult dispersal abilities and biogeographical range of species assemblage were analysed to identify the main features of the community. Quantitative and qualitative similarities of species assemblages were computed. 1,371 individuals belonging to 195 species were collected. Although contiguous, species assemblages have attained lower similarity values than expected. The highest diversity values were recorded in semi-natural patches. Migrant species were more abundant in semi-natural and abandoned patches, and sedentary species were more abundant in olive orchard. The most represented species in the farm were those which are largely distributed through the Palaearctic; the farm also hosts species assemblages having strong larval feeding preferences for herbaceous plants. Species feeding on trees were very scarce. No significant correspondences were found between vegetation cover and distribution of feeding preferences. Although very important for the increase of agricultural landscape species richness, semi-natural and abandoned vegetation patches inhabit few habitat specialists, proving themselves stepping stones and/or corridors only, because of their reduced dimensions that enhance the border effect. Thanks to the favourable microclimate and the low pressure of human activities semi-natural and abandoned vegetation patches inhabit more species than crop areas, but many of these are highly mobile and widespread. The sheltering capacity of biotopes and behavioural features of species are probably the most important factors affecting composition and diversity of communities at the farm scale.

Key words: diversity, species assemblage, olive orchard, butterfly, moth, Calabria.

Introduction

The typical agricultural landscape in Calabria, southern Italy, is composed by several types of cultivation surrounded by, or enriched with, hedgerows and patches of semi-natural vegetation. Within agroecosystems, these landscape features are very important for dispersion of invertebrates, acting as corridors or stepping stones, furnishing protection in respect to agricultural practices or microclimatic refuge during periods of environmental stress, and providing alimentary sources (Burel, 1996; Rieux *et al.*, 1999; Dover and Sparks, 2000). Furthermore, they enhance biological control by increasing landscape heterogeneity and biodiversity (Marino and Landis, 1996; Altieri, 1999). Traditional farming systems, based mainly on practices like polycultures and crop rotation, and mosaic landscape structures, caused by both hard regional topography and little farm surfaces, facilitate sustainable agriculture (Paoletti, 1995). In the Calabrian agricultural landscape, many organic farms were established in the recent past. In particular, organic olive orchards are very numerous because of the favourable climate of the region and the ancient history of this cultivation starting in Calabria from the "Magna Graecia" period, twenty-seven centuries ago. Unfortunately, the available literature shows a significant lack of information about this agroecosystem. Some attempts were done towards the understanding of the relations between non target insect fauna and pesticides utilised in olive orchards (e.g. Cirio, 1997; Ruano *et al.*, 2004; Iannotta *et al.*, 2006), and some authors described the whole insect community of olive orchards at high taxonomic rank (e.g. Belcari and Dagnino, 1995; Brandmayr *et al.*, 1999; Ruiz and Montiel, 2000). Nothing is known about non target lepidopteran species in the olive ecosystem.

Life history traits of species are very important for identifying main ecological features of species assemblages and represent the starting point for any further analysis (Scalercio, 2006). In detail, we utilised (i) adult dispersal ability, about which few detailed data are available despite its importance in guiding species distribution of Lepidoptera (e.g. Balletto and Kudrna, 1985 for butterflies; Hausmann, 1990 for moths); (ii) biogeographical pattern, which provides insight into the ecology of a species (New, 1991); and (iii) larval feeding preferences, which are very important in determining spatial and seasonal distribution of Lepidoptera (Shapiro and Shapiro, 1973; Usher and Keiller, 1998; Kitching *et al.*, 2000).

In this study we tried to put in evidence the importance of a diversified agricultural landscape in a Mediterranean region in sustaining lepidopteran diversity. We assumed that lepidopteran species assemblages respond to landscape modifications in a plastic way, adapting themselves to environmental conditions by modifying ecological traits of its own species complex, and that the structure of species assemblages changes with diversity and architectural complexity of the vegetal cover because Lepidoptera spend their life eating plants, pollinating plants and staying on and/or underneath plants. In detail, the aims of the present study are to contribute to the knowledge of the olive orchard agroecosystem by examining butterflies and moths species assemblages, and to identify the role assumed by patches at different seral stages in sustaining lepidopteran diversity and abundance in an organic olive orchard.

Materials and methods

Study area

We conducted our study in the Azienda Archeo-Agrituristica Santa Maria del Mare Vetere, a farm organic from 1993 according to CEE 2092/91, situated in the municipality of Stalettì, Ionian Coast of Calabria, southern Italy (lat. 38° 45' 22" N; long. 16° 34' 4" E. figure 1). The farm has a very irregular topography. Geological substratum is mainly granitic, just few alluvial coins are present. The climate is typically Mediterranean, having a four months long dry and hot season. The maximum average temperature of the warmest month (August) is 31.3 °C and the average of minimum temperatures of the coldest month (January) is 8.2 °C. The landscape is dominated by olive orchards, but many remnants of wild vegetation are present, mainly in the deepest valleys and on the steepest slopes. Remnants represent different evolutionary stages of Mediterranean *maquis*, having forests composed by *Quercus* spp. [*Q. ilex* L., *Q. suber* L., *Q. virgiliana* (Ten.) Ten.] in old seres and evergreen shrubs (*Pistacia lentiscus* L., *Myrtus communis* L., *Cistus* spp.) in young seres.

Four contiguous stands were surveyed from May 1998 to July 1999. They represent a gradient of land use running from a relatively undisturbed *Q. ilex* wood (QI), to an olive orchard periodically ploughed and organically managed (OO1). QI is a strip-like wood situated in a valley with occasional water floods, covering a surface of 520 m^2. An abandoned olive orchard (AB), covering a surface of 360 m^2, burned in 1986 and re-colonised by the wild vegetation was chosen as intermediate seral stage. Among other parameters, spatial attributes of a given area play an important role in determining lepidopteran diversity (Usher and Keiller, 1998). For this reason, AB and QI spatial attributes are comparable, while OO1 belongs to the landscape matrix. The shape of AB and QI were measured by a dimensionless parameter (R), defined as $R = 0.282P/A^{1/2}$, where P is the perimeter of the sampled site, A is the area and 0.282 is a factor which ensures that $R = 1$ for a circular wood. In order to test the efficacy of the experimental design, a second stand within the olive orchard was chosen (OO2) (table 1), where the trap worked in a different way.

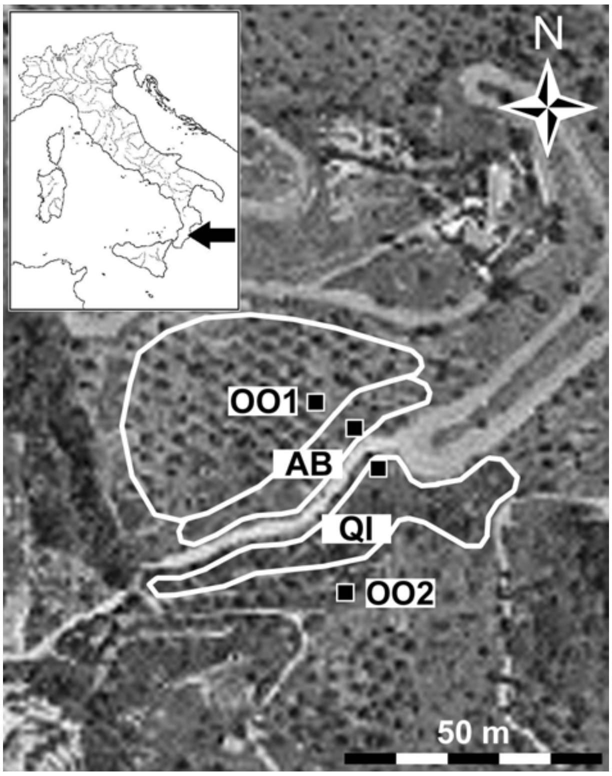

Figure 1. Location of study area. The position of the four bucket-light traps for moths sampling (black squares) and the three areas surveyed for butterflies monitoring (white lines) were superimposed to an aerial photograph of the study area.

Moths sampling

Moths were sampled by using bucket traps with 160W mercury-vapour lamp, powered by a portable electric generator. Four traps were used, one within each stand. Traps were turned-on at dusk and turned-off three hours later, optimising the sampling effort and minimising the collection of vagrant species. Anyway, it is well known that the highest numbers of species and individuals fly during the first quarter of the night. Before traps opening, a quick data collection was carried out around traps

Table 1. Main attributes of sampled sites. The shape of OO1 and OO2 was not measured because they belong to the landscape matrix. The shape index (R)is defined in the text.

Sampled sites	Altitude (m a.s.l.)	Shape (R)	Slope inclination (°)	Coverage by (%)			
				trees	shrubs	grasses	bare soil
QI	176	2.29	40	90	15	45	10
AB	181	2.32	25	5	35	95	5
OO1	185	-	5	70	5	5	90
OO2	180	-	5	70	5	5	90

registering species as singletons. Then, few chloroform drops were introduced into buckets to anesthetise the individuals trapped in. Specific determination was carried out in the field releasing individuals after counting. Just few specimens were collected and identified by morphological studies.

Fifteen sampling sessions were monthly carried out from May 1998 to July 1999 during standard environmental conditions: new moon, no or low wind speed (<1m/s), no rain, temperature near to the mean for the given month. Light traps were turned-on simultaneously avoiding unexpected differences in the abiotic environment. Summerville and Crist (2003) emphasized seasonal effects as an highly confounding factor on diversity and species composition. Nevertheless, in order to include seasonal effects in species richness data and species assemblages composition, the same sampling effort was carried out through all the seasons.

The traps were put in place with lamps at more or less 60 cm above the ground level. The height of the lamps has a direct influence on results by enlarging the trap attractive radius (Baker and Sadovy, 1978).There is no univocal result about the width of the area successfully sampled by a light trap, spanning from 700 m (Bowden, 1982) to 3 m (Baker and Sadovy, 1978) of radius depending on the kind of lamp light, the lamp position, the ambient light and the species behaviour. However, estimates based on field evidences reveal as the most likely effective a radius not wider than 50 m (Baker and Sadovy, 1978; Ricketts *et al.*, 2002). Whatever the attractive radius is, our data were reinforced by the simultaneous light-traps working and by the opportunely orientation and shading of traps. In order to test location and shading efficacy, the light-trap located in OO2 was not shaded, freely working in all directions. The distance between sampled sites was 15 metres for OO1-AB and for AB-QI, whilst the distance QI-OO2 was 40 metres. This sampling design could be affected by pseudoreplication (Hurlbert, 1984) and by interference between the traps working radius, but these issues were strongly reduced by the simultaneous traps working and by the very short duration of each sampling.

Butterfly sampling

Sample sites were monthly surveyed, from March 1998 to November 1998, always on sunny days and between 9:30 a.m. and 3:00 p.m. A zigzag line was followed during systematic walking surveys. Each survey lasted 10 minutes in order to limit the ingress of individuals into our sites during sampling and to minimise the double counting. No spot of the sample sites was covered more than once. A time-constrained method, yet used by other authors (e.g.: Blair and Launer, 1997), was here utilised instead of the standard butterfly counting method developed by Pollard (1977) because of the small surface of the sampled sites. At the beginning of each sampling, the numerical evaluation of the most mobile and visible species was carried out. Individuals observed at the site boundaries were not recorded. Specimens were identified in the field and released at the end of sampling. More difficult identifications were performed at the end of sampling with the aid of field guides.

Data analysis

Diversity was analysed utilising species number (S), Shannon's index (H'), here with $\log_2$, Fisher's alpha (α) and Simpson's index (D). The computing of moth species recorded out of light traps as singletons could lead to an overestimation of diversity indices, mainly α. In order to evaluate the overestimation, indices were calculated with and without singletons. Significant differences ($P<0.05$) among computed H' values were performed by using the Student's *t*-test. Running EstimateS5 (Colwell, 1997), we verified the sampling exhaustiveness (1) by building rarefaction curves of observed species after 50 randomisations of the sample, and (2) by calculating the total species number of sampled sites using ICE, an incidence-based coverage estimator of species number (S_{ICE}), and ACE, an abundance-based coverage estimator of species number (S_{ACE}).

Species can be grouped in the following useful categories of dispersal ability: sedentary (SED): bad flyers spreading usually not more than few hundreds metres from the adult emergence site; spreader (SPR): species spreading usually not more than one or few kilometres from the adult emergence site; migratory (MIG): very good flyers spreading usually very far from the adult emergence site. While SED and MIG groups were composed by species with sufficiently known dispersal behaviour, the SPR group could be composed by species with a poorly known dispersal ability. In order to avoid mistakes while grouping species, further studies on their dispersal behaviour are required.

Biogeographical analysis was performed grouping species as follows: range larger than Palaearctic Region (BP1); range = Palaearctic (BP2); range = Euro-Mediterranean (BP3); range = Mediterranean (BP4). Species range was extrapolated from the above mentioned identification guides.

Larval feeding preferences were assessed assigning species to Summerville and Crist's (2003) feeding groups: (1) woody plants, trees and shrubs feeders (WP); (2) herb and graminoid feeders (HERB); (3) dead/decaying vegetation feeders (DET); (4) fungi/lichen/moss feeders (FLM); and (5) generalised feeders utilising at least two host categories (GEN). The 1.96% of individuals and the 6.12% of species have unknown feeding preferences. Although not perfectly correct, these species were in any case included in the group-level analysis determining feeding preferences according to the closest, mainly congeneric, species. In fact, in our opinion their exclusion *a priori* could be statistically more dangerous, because certainly incorrect, than their inclusion, because probably correct. In any case, the percentage of species and individuals with unknown alimentary behaviour has no statistical significance.

We calculated similarity among stands using (1) the qualitative Sørensen index, $S_s = 2c/(a+b)$, where c is the number of species found in both sites, and a and b are the number of species in sites A and B, respectively, and (2) the quantitative Renkonen index, $S_r = \Sigma\ p_{\min}\ (p_{ax}, p_{bx})$, where p_{ax} is the relative abundance of the species x in the site a, p_{bx} is the relative abundance of the same species in the site b and $p_{\min}$ is the lowest relative abundance value between them. Both S_s and S_r approach 1.0 value when species composition is identical between sites and 0.0 value when two sites have no species in common. The validity of similarity analysis was also examined by the cluster analysis, unweighted pair-group method using arithmetic average (UPGMA, percentage differences) based on the abundance matrix of moth assemblages, generated by the program STATISTICA Kernel release 5.5 (StatSoft, 1999).

All performed correlations were tested with Spearman rank correlations (C_s) because data were not normally distributed.

Results

Species assemblages

1,371 individuals belonging to 195 species were collected (table 2). 46 species occurred in all sampled sites, while 85 species occurred in only one of it. Species number is significantly related to abundance ($C_s = 0.9554$, $P<0.0001$, $n = 15$), so the same considerations that are made below on spatial distribution of diversity could be made on spatial distribution of abundance. The 19 most abundant species were necessary to attain the 50% of the sample and compose the head of the farm

Table 2. List of the abundances (summed over all trap nights and diurnal samples) of all species recorded from the four sampled sites. Species code number and nomenclature follow Karsholt and Razowski (1996). Butterflies were not sampled within OO2. For each species were reported: feeding preferences (F); dispersal ability (D); biogeographical pattern (B). Feeding preferences marked with ? were determined according to the closest, mainly congeneric, species.

Family and species	Sampled sites				F	D	B
	QI	AB	OO1	OO2			
Sesiidae							
4019 *Tinthia tineiformis*	0	0	4	0	HERB	SED	BP4
4086 *Bembecia uroceriformis*	1	0	0	0	HERB	SED	BP3
Cossidae							
4156 *Parahypopta caestrum*	3	1	1	4	WP	SED	BP3
4166 *Dyspessa ulula*	1	0	0	0	HERB	SED	BP2
4176 *Zeuzera pyrina*	0	1	1	1	WP	SPR	BP1
Lasiocampidae							
6749 *Lasiocampa trifolii*	1	1	0	1	GEN	SPR	BP2
Sphingidae							
6853 *Hyles euphorbiae*	0	2	0	0	HERB	MIG	BP2
Hesperiidae							
6882 *Carcharodus alceae*	0	1	1	-	HERB	SPR	BP2
6925 *Thymelicus acteon*	1	2	2	-	HERB	SPR	BP3
6932 *Gegenes pumilio*	0	4	2	-	HERB	SPR	BP1
Papilionidae							
6958 *Iphiclides podalirius*	4	3	0	-	WP	SPR	BP2
6960 *Papilio machaon*	2	7	2	-	HERB	MIG	BP2
Pieridae							
6966 *Leptidea sinapis*	3	0	0	-	HERB	SED	BP2
6973 *Anthocaris cardamines*	2	1	0	-	HERB	SPR	BP2
6985 *Euchloe ausonia*	0	2	2	-	HERB	SPR	BP1
6995 *Pieris brassicae*	5	10	11	-	HERB	MIG	BP1
6997 *Pieris mannii*	1	0	0	-	HERB	SED	BP2
6998 *Pieris rapae*	18	19	18	-	HERB	MIG	BP1
7000 *Pieris napi*	0	1	0	-	HERB	SPR	BP1
7005 *Pieris edusa*	0	2	3	-	HERB	SPR	BP2
7015 *Colias croceus*	5	2	3	-	HERB	MIG	BP2
Lycaenidae							
7034 *Lycaena phlaeas*	0	1	0	-	HERB	SPR	BP1
7073 *Lampides boeticus*	0	2	1	-	GEN	MIG	BP1
7097 *Celastrina argiolus*	8	0	0	-	WP	SED	BP1
7163 *Polyommatus icarus*	2	13	27	-	HERB	SPR	BP2
Nymphalidae							
7243 *Vanessa atalanta*	0	0	3	-	HERB	MIG	BP1
7245 *Vanessa cardui*	1	4	3	-	HERB	MIG	BP1
7270 *Melitaea cinxia*	0	1	0	-	HERB	SPR	BP2
7307 *Pararge aegeria*	1	0	0	-	HERB	SED	BP2
7309 *Lasiommata megera*	1	3	13	-	HERB	SPR	BP2
7334 *Coenonympha pamphilus*	1	1	2	-	HERB	SPR	BP2
7341 *Pyronia cecilia*	5	11	6	-	HERB	SED	BP4
7350 *Maniola jurtina*	1	0	0	-	HERB	SED	BP2
7434 *Hipparchia blachieri*	0	0	2	-	HERB	SPR	BP4
7441 *Hipparchia statilinus*	0	3	3	-	HERB	SPR	BP3
7145 *Aricia agestis*	0	0	1	-	HERB	SPR	BP2
Drepanidae							
7481 *Thyatira batis*	1	0	0	0	WP	SPR	BP2
7504 *Watsonalla uncinula*	2	2	1	1	WP	SPR	BP3
Geometridae							
7583 *Rhoptria asperaria*	2	0	0	0	WP	SPR	BP3
7689 *Apochima flabellaria*	1	0	0	0	HERB	SPR	BP1
7694 *Agriopis bajaria*	1	0	1	0	WP	SPR	BP2
7724 *Menophra abruptaria*	3	1	1	0	WP	SPR	BP4
7725 *Menophra japygiaria*	1	0	0	0	HERB	SPR	BP4
7733 *Synopsia sociaria*	1	2	1	1	GEN	SPR	BP2
7754 *Peribatodes rhomboidaria*	4	6	0	4	GEN	SPR	BP2
7770 *Selidosema ambustaria*	2	1	1	0	GEN?	SED	BP4
7794 *Ascotis selenaria*	1	0	0	0	GEN	SPR	BP2
7837 *Campaea honoraria*	0	0	0	1	WP	SPR	BP3
7850 *Gnophos sartata*	2	0	0	1	GEN	SED	BP4
7916 *Siona lineata*	0	0	0	1	GEN	SED	BP2
7926 *Semiaspilates ochrearia*	2	1	0	1	HERB	SPR	BP4
7933 *Dyscia sicanaria*	0	0	0	2	HERB?	SED	BP2
7966 *Pseudoterpna coronillaria*	2	1	0	0	GEN	SPR	BP4
7984 *Chlorissa etruscaria*	3	4	1	2	HERB	SPR	BP2
7987 *Microloxia herbaria*	1	0	0	0	HERB	SPR	BP2
8017 *Cyclophora puppillaria*	8	3	1	5	WP	MIG	BP2
8023 *Cyclophora suppunctaria*	0	2	0	0	WP	SPR	BP3
8027 *Timandra comae*	0	0	0	1	HERB	SPR	BP2
8048 *Scopula submutata*	1	0	0	0	HERB	SED	BP4
8052 *Scopula vigilata*	3	1	2	6	HERB	SED	BP4
8059 *Scopula marginepunctata*	5	6	2	3	HERB	MIG	BP2
8062 *Scopula imitaria*	3	4	3	7	GEN	MIG	BP4
8073 *Scopula minorata*	0	0	0	2	HERB	MIG	BP1
8092.1 *Idaea leipnitzi*	1	0	0	0	HERB?	SED	BP4
8094 *Idea consanguinaria*	1	0	0	0	HERB	SPR	BP4
8099 *Idaea ochrata*	0	0	0	2	HERB	SED	BP2
8107 *Idaea rusticata*	1	0	0	0	GEN	SPR	BP2
8110 *Idaea filicata*	27	10	5	20	GEN	SPR	BP3
8113 *Idaea efflorata*	0	1	0	0	HERB?	SED	BP4
8115 *Idaea attenuaria*	0	0	0	1	HERB?	SED	BP4
8129 *Idaea elongaria*	1	2	0	1	HERB	SPR	BP2
8131 *Idaea obsoletaria*	18	6	2	10	HERB	SPR	BP2
8155 *Idaea seriata*	11	5	2	4	DET	MIG	BP3
8161 *Idaea dimidiata*	1	0	0	0	GEN	SPR	BP1
						Continued	

Family and species	Sampled sites				F	D	B
	QI	AB	OO1	OO2			
8167 *Idaea subsericeata*	4	1	2	2	GEN	SPR	BP2
8173 *Idaea infirmaria*	0	1	0	0	HERB	SPR	BP4
8176 *Idaea distinctaria*	2	5	3	1	HERB	SED	BP4
8180 *Idaea ostrinaria*	0	1	0	0	HERB	SED	BP4
8186 *Idaea degeneraria*	6	3	3	5	GEN	MIG	BP2
8207 *Rhodostrophia calabra*	0	1	1	1	GEN	SED	BP3
8211 *Rhodometra sacraria*	2	1	1	3	HERB	MIG	BP1
8257 *Xanthorhoe disjunctaria*	1	2	1	1	HERB?	SED	BP4
8279 *Epirrhoe galiata*	0	1	1	1	HERB	SPR	BP2
8289 *Camptogramma bilineata*	0	0	1	0	HERB	SED	BP2
8299 *Metopoceras omar*	0	0	0	2	HERB?	SED	BP2
8321 *Nebula salicata*	6	3	3	2	HERB	SPR	BP3
8403 *Horisme radicaria*	1	1	0	1	HERB	SPR	BP3
8509 *Eupithecia centaureata*	2	3	1	0	HERB	SPR	BP2
8513 *Eupithecia breviculata*	0	1	0	0	HERB	SED	BP3
8547 *Eupithecia semigraphata*	0	0	0	1	HERB	SED	BP3
8558 *Eupithecia gemellata*	4	0	8	1	HERB	SED	BP3
8573 *Eupithecia innotata*	1	4	0	0	GEN	SED	BP2
8599 *Gymnoscelis rufifasciata*	6	6	3	2	GEN	MIG	BP2
Notodontidae							
8698 *Clostera curtula*	0	1	0	0	WP	SPR	BP2
8732 *Pterostoma palpina*	1	0	0	0	WP	SPR	BP2
8750 *Phalera bucephala*	0	1	0	0	WP	SPR	BP2
8754 *Peridea anceps*	0	0	0	2	WP	SPR	BP2
8760 *Harpya milhauseri*	0	0	0	1	WP	SPR	BP2
Noctuidae							
8787 *Acronicta rumicis*	0	0	1	1	GEN	MIG	BP1
8803 *Cryphia ochsi*	2	1	0	0	FLM	SPR	BP3
8818 *Cryphia muralis*	1	1	0	0	FLM	SPR	BP3
8841 *Nodaria nodosalis*	1	0	0	0	HERB	SPR	BP1
8857 *Zanclognatha zelleralis*	1	1	0	0	GEN	SED	BP2
8882 *Catocala promissa*	1	0	0	0	WP	SPR	BP3
8888 *Catocala nymphagoga*	0	3	1	0	WP	MIG	BP3
8902 *Ophiusa tirhaca*	1	0	0	0	WP	MIG	BP1
8904 *Dysgonia algira*	5	3	2	2	GEN	MIG	BP3
8909 *Prodotis stolida*	1	2	2	2	GEN	SPR	BP1
8934 *Lygephila craccae*	1	2	0	0	HERB	SPR	BP2
8959 *Aedia leucomelas*	3	0	0	0	HERB	MIG	BP2
8965 *Tyta luctuosa*	3	3	3	3	HERB	SPR	BP2
8979 *Zethes insularis*	1	1	0	0	WP?	SED	BP4
8997 *Hypena obsitalis*	0	0	0	1	HERB	SPR	BP3
9001 *Hypena lividalis*	2	2	0	3	HERB	MIG	BP1
9008 *Rivula sericealis*	0	0	1	0	HERB	SPR	BP2
9020 *Zebeeba falsalis*	6	1	0	4	WP	SED	BP4
9023 *Eutelia adulatrix*	2	1	1	2	WP	SPR	BP2
9051 *Macdunnoughia confusa*	0	0	1	0	HERB	MIG	BP2
9056 *Autographa gamma*	1	1	0	2	HERB	MIG	BP2
9081 *Trichoplusia ni*	3	1	1	1	HERB	MIG	BP1
9085 *Ctenoplusia accentifera*	1	0	0	0	HERB	MIG	BP1
9094 *Abrostola agnorista*	0	0	0	1	HERB?	SPR	BP3
9097 *Emmelia trabealis*	0	0	1	0	HERB	SPR	BP2
9100 *Acontia lucida*	2	0	0	0	HERB	SPR	BP1
9106 *Pseudozarba bipartita*	2	2	0	1	HERB?	SED	BP4
9114 *Protodeltote pygarga*	0	1	0	0	HERB	SPR	BP2
9135 *Eublemma viridula*	0	1	0	1	HERB	SPR	BP3
9140 *Eublemma ostrina*	2	1	0	5	HERB	SPR	BP2
9142 *Eublemma parva*	5	3	1	7	HERB	SPR	BP1
9147 *Eublemma purpurina*	0	0	1	0	HERB	SPR	BP2
9165 *Metachrostis velox*	1	2	1	1	WP	SPR	BP4
9251 *Omphalophana antirrhini*	1	0	2	3	HERB	SED	BP3
9253 *Omphalophana anatolica*	0	0	0	2	HERB?	SED	BP2
9340 *Aegle vespertalis*	1	0	0	1	HERB	SPR	BP4
9350 *Sinthymia fixa*	20	11	20	40	HERB	SED	BP4
9364 *Heliothis viriplaca*	1	1	0	1	HERB	MIG	BP2
9367 *Heliothis peltigera*	3	0	0	0	HERB	MIG	BP2
9370 *Helicoverpa armigera*	3	4	0	0	HERB	MIG	BP1
9409 *Stilbia faillae*	0	0	0	1	GEN?	SED	BP4
9436 *Paradrina flavirena*	13	8	2	5	HERB	SPR	BP3
9454 *Hoplodrina ambigua*	9	6	0	0	GEN	MIG	BP2
9458 *Atypha pulmonaris*	1	0	0	0	HERB	SPR	BP2
9460 *Spodoptera exigua*	12	6	3	3	HERB	MIG	BP1
9462 *Spodoptera littoralis*	1	0	0	0	HERB	MIG	BP1
9465 *Sesamia cretica*	0	1	0	0	HERB	MIG	BP1
9518 *Cloantha hyperici*	0	1	0	0	HERB	SPR	BP3
9520 *Callopistria juventina*	2	0	0	0	HERB	SPR	BP2
9522 *Methorasa latreillei*	0	0	1	0	HERB	SPR	BP3
9528 *Ipimorpha subtusa*	1	0	0	0	WP	SPR	BP2
9537 *Parastichtis ypsillon*	0	1	0	0	WP	SPR	BP2
9565 *Agrochola lychnidis*	3	2	2	1	GEN	MIG	BP3
9647 *Aporophila australis*	0	1	0	0	HERB	SPR	BP4
9651 *Aporophila nigra*	0	1	0	1	HERB	SPR	BP3
9692 *Dryobota labecula*	1	0	0	0	WP	SPR	BP3
9716 *Trigonophora flammea*	0	1	0	0	GEN	SPR	BP3
9744 *Mniotype solieri*	1	0	0	0	HERB	MIG	BP3
9789 *Mesapamea secalis*	0	1	0	0	HERB	MIG	BP2
9797 *Eremobia ochroleuca*	1	0	0	0	HERB	SPR	BP3
9895 *Discestra trifolii*	0	0	0	3	HERB	MIG	BP1
9917 *Lacanobia oleracea*	1	0	0	0	GEN	MIG	BP2
9928 *Aetheria bicolorata*	1	0	1	2	HERB	SPR	BP2
9935 *Hadena luteago*	1	0	0	1	HERB	SPR	BP2
10002 *Mythimna albipuncta*	3	1	0	0	HERB	MIG	BP2
10003 *Mythimna vitellina*	1	0	0	0	HERB	MIG	BP2
10015 *Mythimna putrescens*	1	2	1	2	HERB	SPR	BP2
10018 *Mythimna languida*	2	1	0	0	HERB	MIG	BP1
10019 *Mythimna congrua*	1	0	0	0	HERB	SPR	BP3
10022 *Mythimna l-album*	21	5	2	5	HERB	MIG	BP1
10029 *Mythimna scirpi*	2	3	0	5	HERB	MIG	BP3
10031 *Mythimna prominens*	4	4	1	2	HERB	SPR	BP1
10033 *Mythimna riparia*	1	0	0	1	HERB	MIG	BP3
10035 *Mythimna unipuncta*	2	0	0	1	HERB	MIG	BP1
10078 *Hada calberlai*	11	6	0	5	HERB	SPR	BP4
10082 *Axylia putris*	1	0	1	2	HERB	SPR	BP2
10087 *Ochropleura leucogaster*	3	2	0	0	GEN	MIG	BP4
10096 *Noctua pronuba*	4	3	0	0	GEN	MIG	BP2
10099 *Noctua comes*	3	3	1	0	HERB	MIG	BP3
10102 *Noctua janthina*	2	3	0	0	HERB	MIG	BP3
10105 *Noctua interjecta*	1	1	0	0	HERB	MIG	BP3
10199 *Xestia c-nigrum*	1	0	0	0	HERB	MIG	BP1
10226 *Cerastis faceta*	2	0	1	2	WP	SPR	BP4
10238 *Peridroma saucia*	7	5	0	2	HERB	MIG	BP1
10336 *Agrotis crassa*	0	0	0	1	HERB	MIG	BP2
10343 *Agrotis puta*	0	1	0	1	HERB	SPR	BP2
10346 *Agrotis ipsilon*	2	0	0	1	HERB	MIG	BP1
10348 *Agrotis exclamationis*	1	0	0	0	HERB	MIG	BP2
10351 *Agrotis segetum*	1	1	1	0	HERB	MIG	BP1
Lymantriidae							
10380 *Ocneria rubea*	0	1	0	0	WP	SPR	BP3
Nolidae							
10437 *Nola chlamitulalis*	0	0	0	1	HERB	SPR	BP2
10451 *Pseudoips prasinana*	1	1	0	0	WP	SPR	BP3
Arctiidae							
10493 *Eilema caniola*	18	8	5	11	FLM	MIG	BP3
10522 *Dysauxes famula*	30	22	11	39	HERB	SPR	BP3
10550 *Phragmatobia fuliginosa*	6	8	3	4	GEN	MIG	BP1
10555 *Cymbalophora pudica*	2	1	1	2	HERB	SPR	BP4
10600 *Arctia villica*	2	2	3	6	HERB	SPR	BP2

species assemblage. *Dysauxes famula* (7.4% of individuals in the 100% of surveyed sites), and *Synthymia fixa* (6.6%, 100%) are the most abundant and widespread species. The former is polyphagous, very abundant in coastal areas of southern Italy, the latter is monophagous linked by trophic larval relations to *Psoralea bituminosa* L., an abundant plant in areas with intermediate environmental perturbations. Both species are thermophilous, favoured by the climate. 66 species were collected as singletons or out of the traps.

Noctuidae (S = 89; N = 508) and Geometridae (S = 55; N = 380) are the most species-rich and abundant families among moths, as often worldwide occurs. Geometridae were relatively more abundant within the olive orchard (OO1) and the abandoned vegetation patch (AB). Butterfly families, instead, are uniformly distributed in terms of species richness and abundance in the organic olive orchard (OO1) and in the abandoned and burned olive orchard (AB), showing a decrement in the Quercus ilex wood (QI).

Venn diagrams show the repartition of species among the three uniformly sampled stands (figure 2). The highest number of exclusive species was recorded within QI, the lowest within OO1. Six species, all moths, were exclusively recorded for the couple QI-OO1, ten species, six of which butterflies, were exclusively recorded for the couple AB-OO1, and even 32 species were exclusively recorded for the couple QI-AB.

Species assemblages attained low similarity values comprised between 0.46 and 0.68 (table 3). When butterflies and moths were grossly considered, qualitative (S_s) and quantitative (S_r) similarity indices show very similar patterns (table 3a). QI-AB is always the most similar comparison pair, and QI-OO1 is always the less similar one. Similarity values, mainly the qualitative ones, remain lower than expected. Although a relevant number of species is shared between AB and OO1, these stands were quite different from a quantitative viewpoint. When only moths were considered, S_r showed a different pattern, the comparison pair QI-OO1 being more similar than AB-OO1 (table 3b). The light trap located within OO2 (freely working in all directions) collected a species assemblage more similar to other stands than to OO1 on the quantitative front only, showing on the other hand, a OO1-like qualitative similarity pattern. The cluster analysis grouped grossly the sampled olive orchards (figure 3).

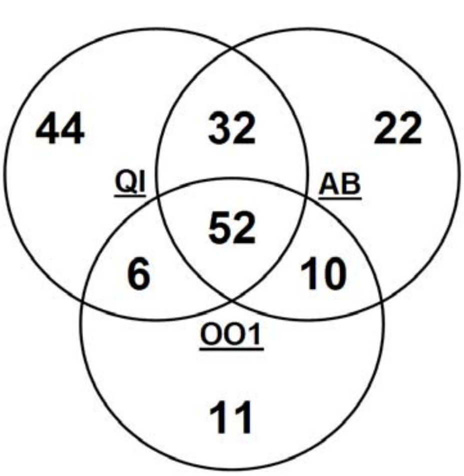

Figure 2. Venn diagrams showing the number of exclusive and shared species among uniformly sampled stands.

Table 3. Similarity among sampled species assemblages. a): with butterflies; b): without butterflies. Similarity values above 1's diagonal are quantitative (S_r), similarity values below 1's diagonal are qualitative (S_s).

a)

stands	QI	AB	OO1
QI	1	0.63	0.46
AB	0.67	1	0.58
OO1	0.54	0.66	1

b)

stands	QI	AB	OO1	OO2
QI	1	0.68	0.63	0.60
AB	0.68	1	0.57	0.56
OO1	0.54	0.59	1	0.63
OO2	0.61	0.63	0.63	1

Diversity

Rarefaction curves of observed species richness at the last sample still had a relatively high inclination, proving the performed sampling effort not exhaustive (figure 4). A relatively high number of species should be recorded producing a slightly higher sampling effort as confirmed by ICE (S_{ICE} = 276) and ACE (S_{ACE} = 246), which shows the percentage of recorded species comprised between the 64.9% and the 72.8% of the total, respectively. In detail, farm data show butterflies more exhaustively sampled (79,2±9,4% Standard Deviation, SD) than moths (67,8±11,3% SD). Halving the sampling effort, more or less the 2/3 of final species richness should be recorded (figure 3). This observation led

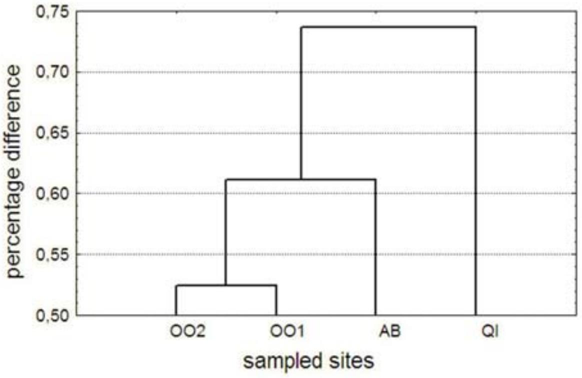

Figure 3. Dendrogram of sampled sites classified by the cluster analysis (UPGMA, percentage differences), based on the abundance matrix of species assemblages.

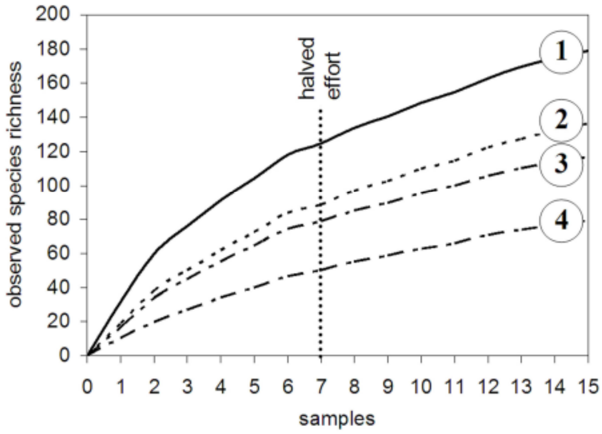

Figure 4. Rarefaction curves of observed species richness made by running EstimateS (Colwell, 1997). Halving the sampling effort more or less the 2/3 of final species richness should be recorded: the whole Farm (1), 69.7±10.5% Standard Deviation, SD, QI (2), 65.1±12.2% SD, AB (3), 67.4±11.3% SD, and OO1 (4), 63.4±12.3% SD. Data collected within OO2 were not included within the Farm data.

us to affirm that although not exhaustive, our sampling effort was able to sample the 'head' of a given species assemblage, missing just species belonging to the 'tail' of it. After the seventh sample, curves of uniformly sampled sites are quite parallel showing similar trends which support the reliability of our data for comparison analysis.

The highest species richness was recorded in QI, while the lowest species richness was recorded in OO1 (table 4). These stands are representative of the late- and the early-successional stages respectively. The highest species richness of butterflies was attained in AB and OO1, the intermediate- and the early-successional stage respectively. A very similar pattern was recorded by using other diversity indexes, *H'* showing just a small increase in AB, and *D* showing AB the most diverse stand. As sensitive to sample dimension, *S* and *H'* attain the highest values in the whole farm, while *α* and *D*, not so sensitive to sample dimension, are higher in QI than in the whole farm. OO2's diversity values were always comprised between OO1's and AB's diversity values. Without singletons no diversity pattern changed.

The analysis of significant differences (Student *t*-test) among computed *H'* have shown a highly significant decrease of diversity ($P<0.01$) only in OO1 when singletons are included in the analysis, becoming weaker ($P<0.05$) when singletons are not included. Butterflies have never shown significant differences of *H'* (table 4).

Mobility

More than an half of species inhabiting the surveyed farm belongs to the spreader group (table 5), one third belongs to the migrant group, while less than 20% belongs to the sedentary group. Quantitative data showed an evident increase in migrant species. In fact, at the head of the farm community, the 57.9% are migrant, the 31.6% are spreader and only the 10.5%, i.e. *S. fixa* and *P. cecilia*, are sedentary species. Mobility groups were uniformly ranked within all sampled sites, attaining everywhere SPR the highest percentage and SED the lowest percentage (table 5). Spreader species were more or less uniformly distributed among surveyed sites and percentwise were always represented by fewer individuals than species. MIG species seem to concentrate their populations in less perturbed patches, showing low percentages within olive orchards. In QI the highest percentage of sedentary species was collected, while AB inhabits the lowest percentage of them (table 5). Intermediate SED species percentage were attained by OO1, showing a significant increase of individuals.

Finally, from a qualitative viewpoint, species assemblages have shown no significant differences in the distribution of mobility groups, being uniformly distributed along the successional gradient, but from a quantitative viewpoint, migrant species were more abundant in seminatural and abandoned patches, and sedentary species were more abundant in olive orchards.

Biogeography

Biogeographical groups proved poorly discriminating, showing very similar patterns through the farm. Species largely distributed in the Palaearctic (BP2) were the

Table 4. Diversity values attained by each sampled butterfly (B) and moth (M) assemblage: species richness (*S*), Shannon's index (*H'*), Fisher's alpha (*α*) and Simpson's index (*D*) with (+) and without (−) singletons. Butterflies were not sampled (n.s.) within OO2. Data collected within OO2 were not included within the Farm data.

Stands		*S*		*H'*		*α*		*D*	
		B	M	B	M	B	M	B	M
QI	+	17	117	3.31	6.03	7.3	56.5	0.867	0.977
	−	9	64	2.77	5.41	3.2	22.6	0.828	0.969
AB	+	21	95	3.74	6.04	8.5	54.6	0.907	0.981
	−	15	49	3.45	5.31	5.2	19.8	0.894	0.972
OO1	+	18	61	3.40	5.32	6.3	41.8	0.872	0.964
	−	15	27	3.26	4.33	4.9	11.8	0.864	0.937
OO2	+	n.s.	87	n.s.	5.45	n.s.	40.9	n.s.	0.955
	−	n.s.	49	n.s.	4.85	n.s.	17.7	n.s.	0.942
Farm	+	29	149	3.91	6.20	8.4	54.1	0.902	0.977
	−	22	93	3.69	5.52	5.8	28.3	0.896	0.974

Table 5. Percentage of species (S) and individuals (N) belonging to mobility (M), biogeographical (B) and larval feeding preferences (A) groups within each sampled site. Groups were arranged according to the decreasing percentage of species belonging to a given groups. Data collected within OO2, not comparable to other because of the lack of butterflies in the sample, were not included within the Farm data.

		QI		AB		OO1		OO2		Farm	
		S	N	S	N	S	N	S	N	S	N
M	SPR	47.0	42.0	52.6	45.2	51.9	46.5	48.3	49.0	51.9	44.1
	MIG	35.1	42.8	33.6	42.1	32.9	32.8	29.9	26.2	31.1	40.3
	SED	17.9	15.2	13.8	12.7	15.2	20.7	21.8	24.8	16.9	15.6
B	BP2	40.3	28.7	37.1	32.2	38.0	35.3	37.9	26.2	40.1	31.3
	BP3	21.6	30.8	25.0	26.8	22.8	22.0	25.3	35.4	22.6	27.5
	BP1	20.1	24.1	19.8	24.9	22.8	23.7	18.4	13.6	20.3	24.2
	BP4	17.9	16.5	18.1	16.1	16.5	19.1	18.4	24.8	16.9	16.9
A	HERB	64.2	62.7	62.9	68.6	67.1	80.5	65.5	68.5	66.6	68.7
	GEN	17.9	20.0	19.0	19.8	17.7	12.4	19.5	18.5	15.8	18.2
	WP	14.9	10.5	14.5	7.3	12.7	4.1	12.6	7.9	15.3	8.0
	FLM	2.2	4.4	2.6	2.8	1.3	2.1	1.2	3.6	1.7	3.4
	DET	0.7	2.3	0.9	1.4	1.3	0.8	1.2	1.3	0.6	1.7

most represented (table 5), but their abundance decreased in respect to their richness, mainly in QI. Mediterranean species (BP4) were the less represented and abundant. Among them, just *S. fixa* (n = 91), *P. cecilia* (n = 22), *Hada calberlai* (n = 22) and *Scopula imitaria* (n = 17), belong to the head of the farm community. BP4 was well represented in OO1 and OO2, where the highest percentage of individual belonging to this group was collected.

Larval feeding preferences

The farm hosts a community with strong larval feeding preferences for herbaceous plants (table 5). The head of the farm community includes more or less exclusively herb and generalist feeders. The only exceptions are the FML *Eilema caniola* (n = 42), the DET *Idaea seriata* (n = 22), and the WP *Cyclophora puppillaria* (n = 17), all these species having an high dispersal ability. All sampled stands showed patterns very similar to this, AB and OO1 only loosing woody plant feeders within the head of their assemblages. The most abundant WP feeder was *Cyclophora puppillaria*, which ranks sixteenth. *C. puppillaria*, together with *Parahypopta caestrum* (n = 9), linked to *Asparagus* spp., are the only WP feeders wherever present. Only woody plant feeders in all stands, and generalist feeders in OO1 and OO2, were more abundant as number of species than as individuals. QI had some peculiarities: (1) inhabits a lower percentage of individuals than species with herbaceous feeding preferences, and (2) shows the smallest decrease of the WP feeders abundance. Within AB intermediate percentage values of feeding groups were often recorded.

Only the analysis of quantitative data provides differences among surveyed assemblages, because vegetation cover was unable to decisively influence feeding preferences of species. In other words, no significant correspondences was found between vegetation cover and feeding preferences of species.

Discussion

Lepidoptera diversity is known to be affected by landscape attributes acting in many ways depending on the observation scale (Dover, 1996; Usher and Keiller, 1998; Weibull *et al.*, 2000; Krauss *et al.*, 2003; Summerville and Crist, 2003; Summerville *et al.*, 2003). Our results demonstrate Lepidoptera distribution patterns depending at a very small scale (from 10 to 100 metres) and in a very fragmented landscape (with patches smaller than 1 ha) mainly on architecture and diversity of habitats, both simplified by human activities. The vegetation cover of semi-natural and abandoned patches itself is unable to favour specialist species because of the small area occupied (Usher and Keiller, 1998). The highest species richness found in the small woodlot was favoured by its spatial attributes, and may be well explained by species supplementation (Summerville and Crist, 2003), which permits the coexistence of species with different ecological needs. In our study butterflies diversity peaked at the moderately disturbed site, as stated by Blair and Launer (1997), whilst moths diversity is higher where human activities are lower, both attaining their lowest diversity values at the highly disturbed site. Behavioural features of species determine the different distribution of butterflies, which prefer herbaceous environments rich of adult alimentary sources, and moths, which lightly prefer woody habitats (Ricketts *et al.*, 2002). The decrease of similarity shown by stands with very different vegetation architecture may be due to the different ecology and behaviour of butterflies and moths in a relevant part.

High dispersal ability of lepidopteran species is known to be increased by environmental perturbations (Shapiro and Shapiro, 1973; Usher and Keiller, 1998; Kitching *et al.*, 2000). Available literature is in contrast with our data which showed this attribute higher in well preserved vegetation patches. The distribution of Geometridae, indicated as good bioindicator because of their prevalence in woody habitats and their low dispersal ability (Usher and Keiller, 1998; Kitching *et al.*, 2000; Hausmann, 2002), seems to confirm this anomalous fact.

Matrix species, generally with high dispersal ability in human-modified landscapes (Shapiro and Shapiro, 1973), may easily penetrate little semi-natural and/or abandoned patches indifferently living within both agricultural matrix and small woodlands fragment (Daily and Ehrlich, 1996; Ricketts *et al.*, 2001). This is confirmed by the high percentage of herbaceous plant feeders in the surveyed woodlot. These species concentrated their populations within the surveyed woodlot because they found here the shelter against unfavourable climatic conditions, mainly during the summer. In Mediterranean areas, migrant and mesophilous species prefer to spend the daytime in woods of evergreen plants, which have important sheltering capacity (Rieux *et al.*, 1999). Shelter is known to be important for Lepidoptera (Dover, 1996; Dover *et al.*, 1997; Dover and Sparks, 2000; Clausen *et al.*, 2001) at least from the following viewpoints: (1) physical, by providing with shade, lower temperature and higher moisture than in open habitats during the summer, and by modifying wind speed; (2) chemical, by providing areas with no pesticides and low pressure of agronomic practices; and (3) behavioural, by providing many resting and mating places for adults.

In other words, semi-natural and abandoned vegetation patches, when very small as in our study, could act as stepping stones and/or corridors favouring Mediterranean landscape permeability to mesophilous and widespread species.

Some authors affirmed that community composition mainly vary across broad spatial scale, whilst dominance and evenness vary also at fine spatial scale (Summerville and Crist, 2003). The utilisation of light traps with a small attractive radius, switched off three hours after the sunset, allows us to reveal similarity values lower than expected for contiguous stands. The distribution of ecological features showed surveyed assemblages more similar than similarity analysis *per se*, underlining not so strong ecological boundaries among surveyed patches. In any case, when significant differences among sites were detected starting from diversity values, species composition and ecological features, the latter were probably the best for detecting and evaluating environmental changes (Summerville *et al.*, 2003).

Conclusion

Although very important for the increasing of agricultural landscape diversity, semi-natural and abandoned vegetation patches host few habitat specialists, acting mainly as stepping stones and/or corridors. In fact, they host more species than the agricultural matrix thanks to the favourable microclimate and the low pressure of human activities, but many of them are highly mobile and widespread species.

Micro-distribution patterns of species should be an important working issue in the management of agricultural landscapes at the farm scale. Sheltering capacity of a given biotope and behavioural features of species are probably the most important factors affecting community composition and diversity distribution at this scale. Surveys based on capture-recapture methods should be an important implementation on the knowledge of micro-scale factors leading to a given species assemblage.

Weibull *et al.* (2000) found that no difference in butterfly diversity is due to the farming system. Probably, results similar to those presented here should be obtained in a conventional olive orchard with the same small-scale heterogeneity but, to date, the effects of farming systems on moth diversity are unknown.

In order to use lepidopteran communities as bioindicators, more studies focused on biology and behaviour of species are in need. The improvement of the knowledge could refine researches and reinforce descriptive capability of this taxonomic group. In our opinion, ecological features of a taxon could be considered as the best “indicator”, even more than the taxon itself.

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Authors' addresses: Stefano SCALERCIO (corresponding author, stefano.scalercio@entecra.it), Nino IANNOTTA, CRA Istituto Sperimentale per l'Olivicoltura, c.da Li Rocchi-Vermicelli, I-87036 Rende (CS), Italy; Pietro BRANDMAYR, Dipartimento di Ecologia, Università della Calabria, Via P. Bucci, I-87036 Arcavacata di Rende (CS), Italy.

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