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Assessment of the impact of trampling on soil Arthropoda in a Mediterranean habitat

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Abstract. The aim of this study was to assess the trampling impact on the soil biota, analysing the differences among the composition of soil microarthropod community collected in a holm oak wood crossed by a rather attended path in Genova (Italy). Totally, 27 soil samples (10×10×10 cm) were taken at fixed distances from the centre of the path. Statistical analysis of the recorded differences in the number and relative density of taxa as well as in the biological and biodiversity index values (QBS-ar, Shannon H', Simpson 1-D, and Equitability J indices) showed relevant trampling impact with growing disturbance effects with the proximity to the centre of the path.

Key words. Trampling impact, soil microarthropods, Mediterranean habitat, QBS-ar.

INTRODUCTION

In the framework of environmental monitoring, maintaining soil quality is very important in order to preserve biodiversity and to sustainable manage of renewable resources. Disturbances due to natural forces as well as to human activities can alter physical, chemical and biological characteristics of soils which can, in turn, impact long-term productivity. In particular, they can alter the microhabitats of soil arthropods, most of which are sedentary and unable to respond spatially and temporally to soil property changes. Microarthropods are very important because of their role in breaking down organic matter, regulating the recycling of nutrients, controlling the activity of microflora, developing soil structure and their high sensitiveness to disturbances. For these reasons, QBS-ar biotic index, based on the analysis of soil microarthropod communities, is one of more recent and more promising methods for studying soil quality (Blasi et al. 2013, Visioli et al. 2013, Menta et al. 2014). In particular, it can be useful to evaluate the effects of human impact in woods cut by roads or highly frequented paths. As previous studies outlined (Cluzeau et al. 1992, Cuendet 1992, Pižl & Schlaghamerský 2007), pedestrian activity affects soil characteristics (organic matter content, moisture, compaction) and the soil annelids populations in terms of density, biomass and community structure. In the present paper, we investigated the possible effects of human trampling on the abundance and richness of the soil microarthropods at different distances from the centre of a path, considering two different aims, the first pertaining to the environment and the second relative to the data treatment: (1) to assess the trampling impact on the soil biota, analysing the differences among the composition of soil arthorpods extracted from soil samples collected in a holm oak wood crossed by a rather relative path, and (2) to compare the numerical indication obtained by the QBS-ar application with other ecological indices.

MATERIALS AND METHODS

Study area

The research was carried out in a *Quercus ilex* wood at 100 m a. s. l. in the Genova Righi (Liguria, NW Italy, 44° 25' 33.7" N, 08° 56' 08.8" E). The site has the NE exposure and is located in the "Parco Urbano delle Mura" (City Park of Walls), which with its 876 hectares represents the largest "green lung" of the Genova city. The park provides the possibility of different excursions and, so, is over all interested by pedestrian traffic. The geological substrate of the site consists of flysch of the Mt. Antola (Upper Cretaceous), with different rock types arranged in the way of a typical turbidite fashion: marly limestone, slate, calcarenite and shale (Capponi & Crispini 2008).

Soil sampling and microarthropod extraction

In the study site, a total amount of 27 soil samples of 1 litre each (to a depth of 10 cm) were taken on the 29th of May 2012 after removing above ground plant cover and superficial litter. In particular, three samples were collected in each of the following 9 sampling points: path centre, upstream path edge, downstream path edge, 1m, 2 m and 5 m far from the upstream and downstream edges of the path, respectively. Microarthropods were extracted into 70% ethanol using Berlese-Tüllgren funnels (2.5 mm mesh size) for seven days. For each taxon the number of specimens was counted.

Soil biodiversity and biological quality indices

Soil quality was estimated using the QBS-ar index, based on the soil microarthropod community (Parisi et al. 2005, Gardi et al. 2008, Tabaglio et al. 2009, Menta et al. 2011). This index is based on the identification of soil arthropods to the order level and to the evaluation of their degree of adaptation to soil life conditions. The more an organism is adapted to soil life (being eyeless or small eyed, uncoloured, having short or specialized appendages, and so on) the higher is the value of the Eco-Morphological Index (EMI – from 1 to 20) given him. QBS-ar is the sum of EMI scores recorded for each taxon extracted by soil samples collected and it has an higher value when more adapted to soil microarthropods taxa are present, indicating that the soil where such animals lives are characterised by good biological quality. QBS-ar is applied considering the soil microarthropod community, separated in accordance with the biological form approach (sensu Sacchi & Testard 1971), with the aim of (1) evaluating the microarthropods' level of adaptation to life in the soil environment, and (2) overcoming the well-known difficulties of taxonomic analysis to species level for soil mesofauna.

The biodiversity of the soil microarthropod communities was evaluated considering the number of observed taxa (NT), Shannon diversity index (H'), Simpson index (1-D) and Equitability index (J). These diversity measures were calculated using the number of specimens observed in each sample identified at the taxonomical level as mentioned above.

Statistical analysis

On data about taxa abundance, the following statistical analysis were performed: Non-metric multidimensional scaling (MSD; Bray-Curtis similarity) just to visualize on a plot the differences among soil samples, One-way ANOSIM, and Similarity Percentage (SIMPER) for assessing which taxa are primarily responsible for previously observed differences between groups of samples (Bray-Curtis distance/similarity measure).

Since there were not significant differences among the nine sampling points separately considered, edges, upstream and downstream samples were combined, respectively. Cumulative data of the samples collected from each of the four transept parts (centre, edges, upstream and downstream) were used to calculate the main diversity indices. Kruskall-Wallis test for equal medians was performed for taxa numbers, individual numbers, QBS-ar values, Simpson Index (1-D), Shannon diversity index (H') and Equitability (J). In case of statistical significance of differences, Mann-Whitney post hoc test was carried out. Software PAST (PAleontological STatistics ver. 2.16) (Hammer et al. 2001) was used to perform all the statistics mentioned above.

RESULTS

A total of 22 taxonomic groups, belonging to Chelicerata, Crustacea, Myriapoda and Hexapoda were identified from the 27 soil samples collected (Table 1). Acari and Collembola were the most abundant groups in all four parts of the transect crossing. The number of taxa significantly increased from the centre of the path to downstream and upstream (Fig. 1). QBS-ar and Shannon index showed the same trend. Differently, total number of individuals, Simpson and Equitability indices didn't show differences among the four parts of the transect (Fig. 1).

Taxa density per sampling point are shown in Table 1. The centre of the path was characterized by a lower number of taxa and by the absence of taxa well adapted to soil and more vulnerable such as Symphyla, Diplura, the taxa of Diplopoda (Polydesmida, Julida, Polyxenida) and Chilopoda (Geophilomorpha). Moving toward the upstream and downstream wood, the number of

Table 1. Taxa density (ind. m^{-2}) ± Standard Deviation per sampling point in transect crossing Righi's path (down. – downstream, up. – upstream).

taxa	5 m down.	2 m down.	1 m down.	down. edge	centre	up. edge	1 m up.	2 m up.	5 m up.
Acarina	2654±1157	2887±1105	722±334	2102±1312	2994±2351	3758±510	5605±2078	4692±4012	2335±1223
Collembola	1741±1328	1401±497	955±362	467±297	382±321	1656±389	6582±3556	6539±3270	786±378
Protura	106±106	64±64	±	–	21±21	±	42±21	149±93	7±12
Thysanoptera	297±209	467±340	276±245	467±321	1189±1157	1295±418	1550±977	913±658	460±639
Coleoptera	234±174	–	–	21±21	–	42±42	127±97	149±77	21±21
Coleoptera (larvae)	85±80	–	–	––	21±21	21±21	21±21	361±185	28±18
Diptera	–	21±21	–	––	21±21	42±21	–	–	7±12
Diptera (larvae)	85±56	85±85	–	42±42	998±966	361±139	403±118	106±56	545±488
Geophilomorpha	191±97	127±74	64±37	85±42	–	170±106	127±64	361±77	127±74
Polydesmida	106±98	21±21	–	–	–	85±85	–	510±478	–
Julida	85±56	149±118	21±21	21±21	–	828±446	340±93	786±480	191±133
Symphyla	616±332	573±478	106±21	21±21	–	382±321	361±245	510±314	–
Hymenoptera	701±481	212±56	234±112	106±42	–	149±56	361±170	382±321	616±494
Oniscidea	255±250	64±37	42±21	212±212	–	–	42±21	127±74	42±21
Diplura	–	21±21	21±21	21±21	–	–	21±21	21±21	–
Blattoidea	–	–	–	191±191	–	–	–	–	21±21
Homoptera	–	–	–	21±21	–	–	–	–	42±42
Pseudoscorpionida	–	21±21	–	–	–	–	42±21	64±37	–
Psocoptera	–	–	–	–	–	–	21±21	–	–
Polyxenida	–	–	21±21	–	–	–	–	–	21±21
Heteroptera	–	–	–	–	–	–	–	42±42	–
other Holometabola larvae	–	–	–	–	–	–	–	21±21	–
Araneae	–	21±21	–	–	–	–	–	–	64±64
Scolopendromorpha	–	–	–	–	–	–	–	–	42±42

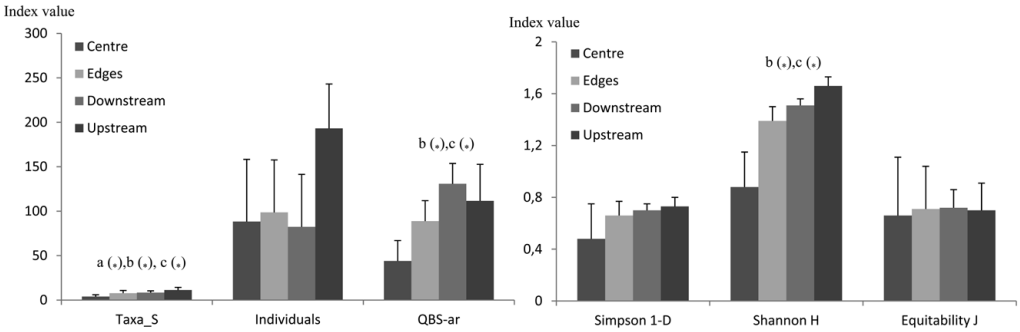

Fig. 1. Indices values (columns) and standard deviations (bars) calculated to assess the trampling impact on soil arthropod communities in four parts of a transect crossing Righi's path. The letters show significant differences: a – Centre vs Downstream, b – Centre vs Upstream, c – Downstream vs Upstream. Significant differences level: * – $p<0.05$.

taxa increased and some groups typical of natural and undegraded soils, such as Myriapoda and Pseudoscorpiones, appeared. As showed in Table 2, SIMPER evidenced eight taxa responsible for more than 95% of the differences between all significantly different couples analysed: Acari, Collembola, Thysanoptera, Symphyla, Geophilomorpha, larvae of Diptera, Oniscidea, and adults of Coleoptera.

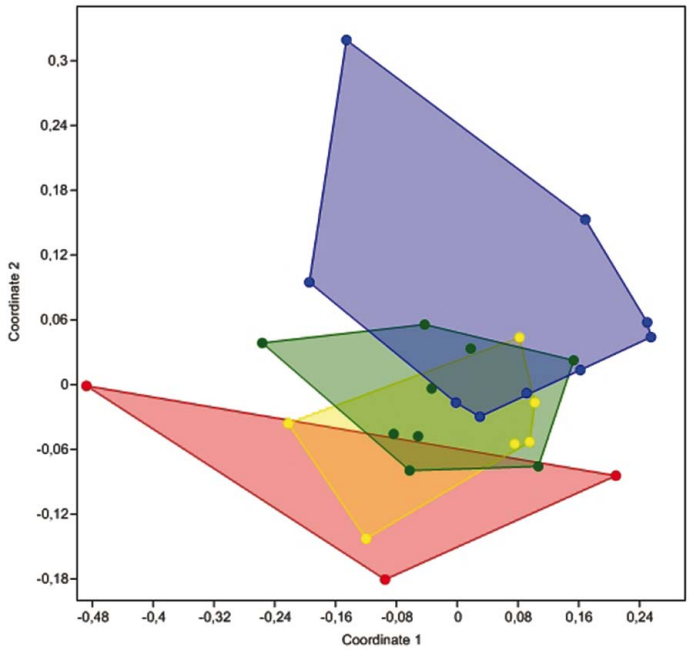

Fig. 2. Non-metric MDS convex hulls: red = centre, yellow = edges, green = downstream, blue = upstream.

The results mentioned above are well summarized by non-metric MDS output (Fig. 2) which shows that the arthropod communities from centre, upstream and downstream seem to be quite distinct, while samples collected along the path edges overlap the centre group on one side and the downstream and upstream on the other.

DISCUSSION

The decline of the number of taxa, diversity index (H') and QBS-ar values moving towards the centre of the path can be explained as an effect of the trampling on the soil microarthropod communities. Edging away from the centre of the path, some taxa missing at the centre appear: Oniscidea, Hymenoptera, Symphyla, millipedes of the orders Julida and Polyxenida, centipedes of the order Geophilomorpha and Protura. Some of these taxa, such as Protura and Symphyla, have notable functional traits, as they are considered typical of undisturbed habitats (Blasi et al. 2013); however, they were not present in the 5 m upstream sample, proving thus the hypothesis of the edge effect disturbance. Overall, no sample reached a QBS-ar value higher than 150. Since stable forest ecosystems are characterised by high QBS-ar scores (>200), these results should be considered indicative of important regressive impacts (Blasi et al. 2013). Some authors suggest that richness might be better measured in functional terms rather than as a number of taxonomic units (Martinez 1996). In fact, the loss of keystone species belonging to soil macroinvertebrate communities could severely affect an ecosystem in many ways: it influences the ability of the soil to process energy and nutrients which can change the distribution and abundance of other organisms, like plants, micro and macro invertebrates and vertebrates (Haskell 2000). Therefore, an analysis based only on QBS-ar index is not enough deepened to describe trampling effects on soil communities; in fact, it uses presence/absence data just at the order level, not including any measure of abundance and it concerns only microarthropods (Lee et al. 2009).

Table 2. SIMPER analysis: main taxa responsible of the 95% of the dissimilarities recorded for the 3 couples of sampling sites of transect crossing Righi's path, resulting significantly different according to One-way ANOSIM. AD – numerical contribution of each taxon to overall dissimilarity, Co% – % contribution of each taxon to overall dissimilarity cumulative % [Cu%] – sum of % contribution of the taxon and those of taxa above him in the table.

centre *vs* downstream overall average dissimilarity 73.68				centre *vs* upstream overall average dissimilarity 79.68				downstream *vs* upstream overall average dissimilarity 63.32			
taxa	AD	Co%	Cu%	taxa	AD	Co%	Cu%	taxa	AD	Co%	Cu%
Acarina	26.14	35.48	35.48	Acarina	25.74	32.30	32.30	Collembola	19.81	31.28	31.28
Collembola	15.40	20.91	56.39	Collembola	20.64	25.90	58.20	Acarina	19.73	31.16	62.44
Thysanoptera	9.01	12.22	68.61	Thysanoptera	8.41	10.56	68.76	Thysanoptera	4.72	7.45	69.89
Symphyla	5.72	7.76	76.37	Diptera (larvae)	5.15	6.47	75.22	Symphyla	3.63	5.73	75.62
Diptera (larvae)	5.54	7.51	83.88	Hymenoptera	4.30	5.39	80.62	Hymenoptera	3.36	5.31	80.92
Hymenoptera	4.25	5.76	89.65	Julida	3.57	4.47	85.09	Julida	2.56	4.05	84.97
Geophilomorpha	2.11	2.87	92.52	Geophilomorpha	3.40	4.27	89.36	Diptera (larvae)	1.53	2.42	87.39
Oniscidea	1.25	1.70	94.21	Coleoptera	1.83	2.29	91.65	Coleoptera	1.52	3.00	89.78
Coleoptera	1.06	1.44	95.65	Oniscidea	1.51	1.90	93.54	Geophilomorpha	1.51	2.39	92.17
				Symphyla	1.04	1.30	94.85	Oniscidea	1.13	1.79	93.96
				Coleoptera (larvae)	1.00	1.26	96.10	Polydesmida	0.96	1.52	95.48

In order to solve these problems, we suggest to integrate such kind of study, when possible, with an index based also on taxonomic diversity and functional traits, as Lee et al. (2009) have done to evaluate human trampling and litter removal effects in a subtropical hardwood forest, identifying soil arthropods to the family level and recording their numerical abundance in soil samples.

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