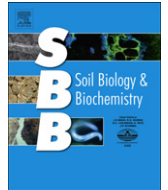




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A soil fauna index for assessing soil quality

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ABSTRACT

The characteristics of the faunal community in soil are closely related to soil quality. Using the soil faunal community as an indicator of soil quality is not cost-effective because of the complex taxonomic distinction and identification required, moreover; the power of the assessment is weak in relation to soil function. Recently, a functional method incorporating eco-morphological traits has been proposed, but it depends upon presence/absence data of soil arthropod community exclusively. To overcome the limitation, we designed a novel index using the diversity of the soil faunal community along with its functional traits, and the abundance of its members (Abundance-based Fauna Index, referred as FAI). The FAI method supports both the presence/absence data and its abundance. Using real and simulated data sets with eco-morphological and niche breadth traits, two taxonomic independent functional traits, we tested associations of FAI values with soil quality and found a good relationship. In addition to its usefulness for measuring soil quality, FAI may provide valuable information for linking functional traits of soil fauna and the belowground environmental condition.

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1. Introduction

Soil fauna are considered to be important components of the soil ecosystem for maintaining nutrient cycling and biological soil fertility (Davis, 1961; Edwards and Lofty, 1982; Hedlund and Öhrn, 2000; Wolters, 2000; Osler and Sommerkorn, 2007). Soil fauna are thought to be useful indicators of soil quality because they are sensitive to changes in land management and are involved in many soil functions (Stork and Eggleton, 1992; Buckerfield et al., 1997; Paoletti and Hassal, 1999; Yeates, 2003). As indicators of soil quality, the abundance and diversity of soil fauna integrate physical, chemical and microbiological properties of soil, and reflect general ecological change (Eijsackers, 1983; Ekschmitt et al., 2001; Menta et al., 2008; Paolo et al., 2010). It remains unclear, however, which soil fauna are the best indicators of soil quality, and what soil fauna data should be used to assess soil quality.

Recently, Parisi et al. (2005) and Parisi and Menta (2008) introduced a simplified eco-morphological index (EMI) based on the types of soil microarthropods present and which does not require species level identification. The EMI index was used to evaluate soil quality by generating another index, the Qualità Biologica del Suolo or QBS index. The QBS index is mainly based on the microarthropod groups present in a soil sample. Each microarthropod group in the soil sample receives an EMI score from 1 to 20, according to its adaptation to the soil environment. The QBS index is the sum of EMI scores. The underlying concept is that soil quality is positively correlated with the number of microarthropod groups that are well adapted to soil habitats. Thus, the QBS index is a measure of how well the soil fauna adapt to the particular soil. When applied to stable agricultural fields, such as maize fertilized by sewage sludge and farm yard manure, the QBS index generated repeatable results at the field and basin scale (Paolo et al., 2010).

The QBS index proposed by Parisi et al. (2005) is based on presence/absence data and does not include any measure of abundance. It follows that arthropod groups with the same EMIs are considered to have the same effect on the system when their true effects could differ substantially because of differences in abundance. In addition, application of both the EMI index and the

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QBS index is limited to soil arthropods. Where data for arthropods are lacking, the EMI index and the QBS index cannot be used to measure soil quality.

The aim of the current study was to develop a soil quality index that takes abundance into account and is not limited to microarthropods. The index described in this report, which we call the FAI, is based on taxonomic diversity and functional trait. To develop and evaluate the FAI, we used both simulated and real data sets from different geographical regions and selected two valuable taxonomic independent functional traits, the morphological adaptive differentiation and niche breadth. We also tested the FAI with null models and with data from soil communities with different species pools and species richness (see Villéger et al., 2008).

2. Soil faunal quality index based on taxonomic diversity and functional trait

According to Karlen et al. (1997), soil quality describes the capacity of a soil to sustain plant and animal productivity, to maintain or enhance water and air quality, and to support human health. The effect of soil on ecosystem functions and productivity was also considered central to the concept of soil quality in other reports (Knoepp et al., 2000; Andrews and Carroll, 2001; Nortcliff, 2002; Gil-Sotres et al., 2005). Soil quality is strongly related to soil organisms because soil organisms are responsible for decomposition, recycling of nutrients, and other important soil processes or functions.

Here we assume that soil quality is correlated with faunal biodiversity and with function size of species (mean ability of species to perform certain function in soil). Accordingly, soil quality can be expressed as:

$$SQ = S \times P$$

where SQ is soil quality, S is the number of faunal species in the soil community (i.e. species richness), and P is apparent performance of soil fauna in soil functioning (using functional traits to estimate).

To constrain the SQ values to between 0 and 1, we used the soil with the highest soil quality (site "h") in the studied region as a reference value or as the denominator in the following equation:

$$FAI = SQ_o/SQ_h$$

where FAI is a faunal index that indicates soil quality, SQ_o is the SQ of the studied site, and SQ_h is the SQ of the site with the highest soil quality.

2.1. Formulation of soil faunal quality index

To formulate the FAI, we score the functional traits of each species of soil fauna to reflect the strength of each species that performs a special function in soil. Because soil resources are limited, the population size of any species is assumed to reach the carrying capacity (the number of individuals that can be supported) in a given soil environment (Butterfield, 2009). Thereby the apparent performance of soil fauna can be estimated through the product of the carrying capacity and the functional trait scores of soil fauna.

For species i , when its abundance d_i reaches to its maximum d_{imax} , its performance is assumed to be 1 (100%) for each trait of the species. Usually d_{imax} can be obtained using maximum abundance as a surrogate for species i among sites in the study region (i.e., the highest abundance of species found within the landscape or among samples depending on relevant experiment design and study objectives). The ratio of d_i to d_{imax} indicates the degree to which

species i exerts its maximum function or effect in the soil. The idea of using the ratio of d_i to d_{imax} as a relative measure had been suggested by Liao and Chen (1990) in an earlier study of the biodiversity of soil animal community. The mean performance of soil faunal community proposed here could be indicatively used as a measure of soil functioning. Assuming that the diversity of soil biology may match well with the diversity of soil fauna community, it can be measured through species richness and mean performance of soil fauna community.

Suppose the species richness of study site "o" is s_o and the species richness of site "h" is s_h , the number of lost species in site "o" would be as $s_h - s_o$; the lost species contribute 0 performance in site "o" relative to site "h", assuming that we have "n" number of functional trait values (t) with corresponding weight (w) for each species of a given site, then this index could be formulated as:

$$\begin{aligned} FAI &= \frac{SQ_o}{SQ_h} = \frac{s_o}{s_h} \times \frac{P_o}{P_h} \\ &= \frac{s_o}{s_h} \times \frac{\left(\sum_{i=1}^{s_o} \left(\frac{d_{io}}{d_{imax}} \times \sum_{k=1}^n (t_k w_k) \right) + (s_h - s_o) \times 0 \right)}{\left(\sum_{i=1}^{s_h} \left(\frac{d_{ih}}{d_{imax}} \times \sum_{k=1}^n (t_k w_k) \right) \right)} \Bigg/ s_h \\ &= \frac{s_o}{s_h} \times \frac{\sum_{i=1}^{s_o} \left(\frac{d_{io}}{d_{imax}} \times \sum_{k=1}^n (t_k w_k) \right)}{\sum_{i=1}^{s_h} \left(\frac{d_{ih}}{d_{imax}} \times \sum_{k=1}^n (t_k w_k) \right)} \end{aligned}$$

We standardized the trait values (range of 0 to 1) so that each trait parameter has the same weight for the estimation of functional performance regardless of the unit of any parameter. We agreed with Liao and Chen (1990) concepts, that the biomass can be used as another estimation of abundance of soil fauna. FAI can also be used for presence/absence data which is actually a particular case where each species has an abundance of 1. Considering that FAI is a relative measure based on functional trait scores, it is also suitable for broad taxonomic units following the concept of taxonomic sufficiency (Ellis, 1985) and Gray's proposal that aggregation of data into higher taxonomic groups would significantly reduce the degree of redundancy in species data (Gray, 1988).

2.2. Simplification of FAI

Recognizing the conceptual controversies of defining the high quality soil, Gil-Sotres et al. (2005) outlined two options for its assessment: (1) soils in equilibrium with all the components of the environment, i.e. a climax soil developed under climax vegetation; (2) soils capable of maintaining high productivity and causing minimal environmental distortion. Considering that a maximum quality soil is a reference which has to be assured exclusively in the study region, we placed here a pseudo site encompassing all species of the region (let S be equal to the number of species found from all study sites of the region) with maximal abundance for each species as an ideal reference site. The pseudo site has always the highest soil quality because its FAI value is 1. After introducing the pseudo site, the highest quality value is always available in the study region. For example, in the managed field experimental design, the highest quality value is the combination of managed and control sites.

After introducing the ideal reference site, the FAI could be simplified as:

$$FAI = \frac{s_o}{S} \times \frac{\sum_{i=1}^{s_o} \left(\frac{d_{io}}{d_{imax}} \times \sum_{k=1}^n (t_k w_k) \right)}{T} \quad (1)$$

Where FAI is the proportion of the highest soil quality for site o , S is the number of species of all sites in study region. T is the sum of all functional trait scores for S species following

$$T = \sum_{i=1}^S \left(\sum_{k=1}^n (t_k W_k) \right)$$

To clarify the calculation of FAI, we present a case study using hypothetical abundances data of 4 sites having six species (Table 1). The power of indication is obvious when FAI is employed, for example, although there is a high diversity of soil fauna in the third site, where its FAI value is the smallest. Its soil environment is not suitable for population development because species abundance was minimum (Table 1). For multiple-trait approaches, individual traits should not be considered in isolation because pairs of traits are often coordinated (Westoby and Wrigh, 2006), but the functional traits have to be independent of each other, and their interaction should be used as a new trait. What functional traits should be included are not arbitrary but are assigned as proposed by Petchy and Gaston (2006). Their scores, such as the values of the morphological, physiological and life history characteristics, have to be matched well with the strength of a species which performs a special function. For single trait value or the combined score of all traits, their scores are assigned to each species to meet a set of criteria such as EMI as an estimation of adaptation trait for soil environment, and Liao's occurrence ratio (ratio of the number of sites with species "i" to the total number of study sites) as an estimation of niche breadth trait when one emphasizes the role of eurytopic species (Liao et al., 1997). In the EMI case, some taxa display a range of EMI values (e.g., for collembola and coleoptera) based on the Parisi et al. (2005) methods, and these taxa are separated into several groups with a single EMI value for each of them.

When EMI is adopted, then the FAI:

$$F_{EMI} = \frac{S_o}{S} \times \frac{\sum_{i=1}^{S_o} \left(\frac{d_{io}}{d_{imax}} \times EMI_i \right)}{\sum_{i=1}^S (EMI_i)}$$

When the occurrence is adopted, the FAI would be as:

$$F_C = \frac{S_o}{S} \times \frac{\sum_{i=1}^{S_o} \left(\frac{d_{io}}{d_{imax}} \times C_i \right)}{\sum_{i=1}^S (C_i)}$$

Here C_i is the number of sites with the i th number of species or taxa.

Table 1

Calculation of FAI based on equation (eq. (1)) using hypothetical abundance data for a six species region pool and 4 local communities. The d_{imax} value is from the maximum among 4 communities marked using bold character of the number. T is the sum of all functional trait scores for these six species.

	Sp1	Sp2	Sp3	Sp4	Sp5	Sp6	T
Trait value	0.82	0.74	0.63	0.55	0.24	0.02	3.00
d_{imax}	150	180	70	4	70	120	
d_i							S_o/S
Site1	150	0	70	0	0	0	2/6
Site2	0	5	0	4	0	110	3/6
Site3	0	1	0	1	2	1	4/6
Site4	90	180	20	0	70	120	5/6
d_i/d_{imax}							FAI
Site1	1.00	0.00	1.00	0.00	0.00	0.00	0.16
Site2	0.00	0.03	0.00	1.00	0.00	0.92	0.10
Site3	0.00	0.01	0.00	0.25	0.03	0.01	0.03
Site4	0.60	1.00	0.29	0.00	1.00	1.00	0.46

In a given study region, because S or T is a constant, when the index value will not be constrained to a range of 0–1, the corresponding FAI can be simplified as:

$$FAI' = S_o \times \sum_{i=1}^{S_o} \left(\frac{d_{io}}{d_{imax}} \times \sum_{k=1}^n (t_k W_k) \right)$$

$$F'_{EMI} = S_o \times \sum_{i=1}^{S_o} \left(\frac{d_{io}}{d_{imax}} \times EMI_i \right)$$

$$F'_C = S_o \times \sum_{i=1}^{S_o} \left(\frac{d_{io}}{d_{imax}} \times C_i \right)$$

3. Assessing the validity of the FAI

The proposed FAI is flexible. First we measure the similarity of species diversity in soil relative to the reference site. When one places all species of the reference site into a new site, the S_o/S reflects the "probability" that the number of species can be maintained in the specific soil by soil resource. Then we measure the similarity of functional score in soil fauna community. The functional similarity reflects the "probability" of a soil fauna community to play a full role in the new site when putting all species of the reference site into the new site. Thus their product is an estimate of the capability of that soil to maintain a high diversity and function. The index value is constrained to a range of 0–1, reflecting the contribution of each species in proportion to its relative population size. Moreover, the present index allows that the reference site is alterable considering the integrated information of all sample sites. For example, when comprehensive surveys of all land use and vegetation types on a given soil have not been fully done, the reference site is based on the combination of the series of sites sampled. The FAI values provide ranking of these sampled sites and deviations from the reference site on soil quality.

3.1. Criteria fulfilled

Some researchers have proposed that soil quality indices should include: (1) sensitivity to variations of soil management; (2) good correlation with the beneficial soil functions; (3) helpfulness in revealing ecosystem processes; and (4) be cheap and easy to measure (Trasar-Cepeda et al., 1998; Andrews et al., 2003; Parisi et al., 2005). Our index meets almost all criteria required for soil quality assessment after thoroughly selecting appropriate soil faunal community and function traits. We propose that FAI is a relative measure that reveals how a specific soil performs when compared with the best soil in the same region. FAI also meets the criteria proposed by Parisi et al. (2005). First, FAI is related to species abundance because the increase of 1 unit of the abundance parameter for species "i" will always lead to an increase of $(t_i \times S_o) / (d_{imax} \times ST)$ for this index value. Second, it is also related with species richness because when a species enters in a new site, the increase of 1 unit for species richness will lead to an increase of lower limit of FAI/s for the FAI value of the site. So any alteration in species abundance or richness can be detected by this index. Third, the FAI approach can be generalized to any classification level and be compatible with broad taxonomic units as well as single taxon method depending on personal preference. The broad taxonomic unit method is low cost for end-user and easy to measure. As Lawton et al. (1998) pointed out, the proportion of 'morpho-species' that cannot be assigned to named species and the number of 'scientist-hours' required to process samples both increase dramatically for smaller-bodied taxa.

3.2. Test and justification of FAI

3.2.1. Association between FAI and QBS

In order to test whether the FAI reveals soil quality or not, we used QBS index as a reference and measured the strength of the association between them based on the artificially generated communities. The number of species in the common species pool was fixed to 30 ($G = 30$). Twenty species richness values were considered from 6 to 25 in generated communities. The sampling distribution for the EMI scores and species abundance were generated using a uniform distribution, and the EMI score for each species was in a range of 20. The occurrence (the number of communities with species i in the study region) was also obtained based on the presence or absence of an artificial community for each species. Twenty replicates per species richness level were generated using R software (R Development Core Team, 2009) for each case. All indices were further computed for 400 data sets. Pearson's coefficients of correlation between each FAI and QBS index were then further tested.

Simulation results clearly showed that F_{EMI} and QBS index are strongly and positively correlated (Fig. 1I.a and II.a). As expected, it is more likely to obtain a higher FAI value with higher ratio of d_i to $d_{i_{max}}$ in the community. When using presence/absence data sets (Fig. 1I), the FAI came to a maximal ratio of 1, and the values are always higher than abundance data sets (Fig. 1II). In presence/absence data case, the correlation coefficients of FAI with QBS were higher than in abundance data case. This was not an artifact because QBS is a measure based on the presence/absence data set. Our analysis quickly reveals the peculiarities of QBS to the detriment of assessment precision (Fig. 2). The variance of abundance explained by the QBS was very low (<11%) in comparison to FAI where >50% of the abundance variation were explained (when EMI was employed). Moreover, in low quality soil, QBS only showed a marginal correlation with abundance when $5 < s_0 < 12$ (Fig. 2). When the shifts of species richness occur in a narrow range, QBS

index became weak because the changes of soil fauna community mainly occur in species abundance. When soil fauna are classified into broad taxonomic units, changes of broad taxa number always occur at a lower probability than that of species number (Yan et al., 2009a,b). Thus, when the changes occur in a narrow range, QBS index value leads to a non-significant assessment. The QBS index for the exposure of correspondences between soil fauna community and soil quality is not preferred when abundance data are available. In such an instance, FAI is more suitable than the QBS index due to the sensitivity of assessment and its application potential. For our artificially generated indices, a strong association between EMI and Liao's occurrence was found (Fig. 1I.C for presence/absence data; Fig. 1II.C for abundance data), indicating that each of two functional traits can be used independently to compute the FAI value.

Using real soil community data from the several cases reported by some authors (Gardi et al., 2002; Parisi et al., 2005; Paolo et al., 2010), the association between FAI and QBS was consistently observed along with trends resulting from using the model data (Fig. 3).

3.2.2. Case study

In this section we applied the theoretical results to real soil communities, and used our collected data from Huitong Experimental Station of Forest Ecology, Chinese Academy of Sciences (latitude $26^{\circ}40' - 27^{\circ}09'N$ and longitude $109^{\circ}26' - 110^{\circ}08'E$). Data were collected from seven carefully designed experimental sites (named as "A, B, C, D, E, F, G") with different land use histories. Soil sampling was carried out in September 2006 (It is the best time to collect soil samples for most of taxa in the region because their abundance values are close to their annual means) following the data collection protocol of the Chinese Ecosystem Research Network (CERN, <http://www.cern.ac.cn>). We followed the Parisi et al. (2005) ideas and tested the association between land use intensity gradients and FAI. For each study site, soil sampling was

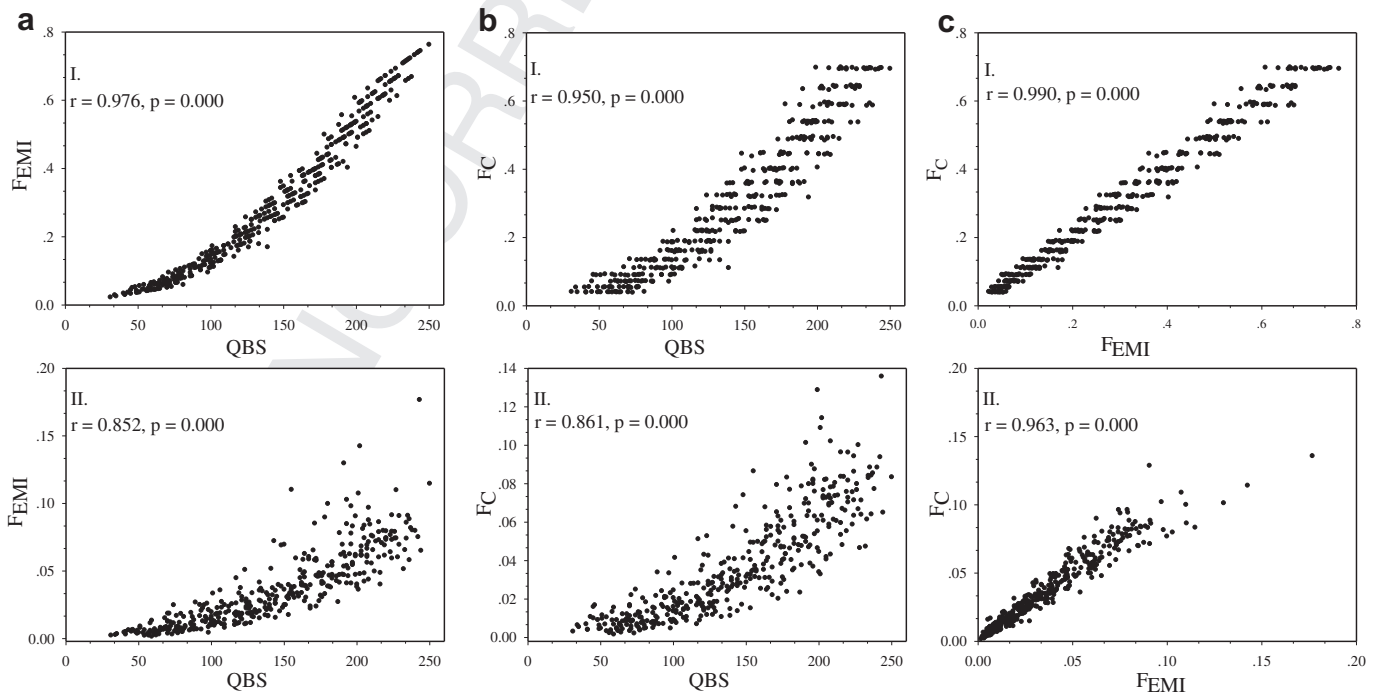


Fig. 1. Relationships developed by simulated data set between F_{EMI} and QBS (a), F_C and QBS (b), F_C and F_{EMI} (c). Figure I is for presence/absence data sets used for index values, whereas Figure II is for abundance data sets used in computation.

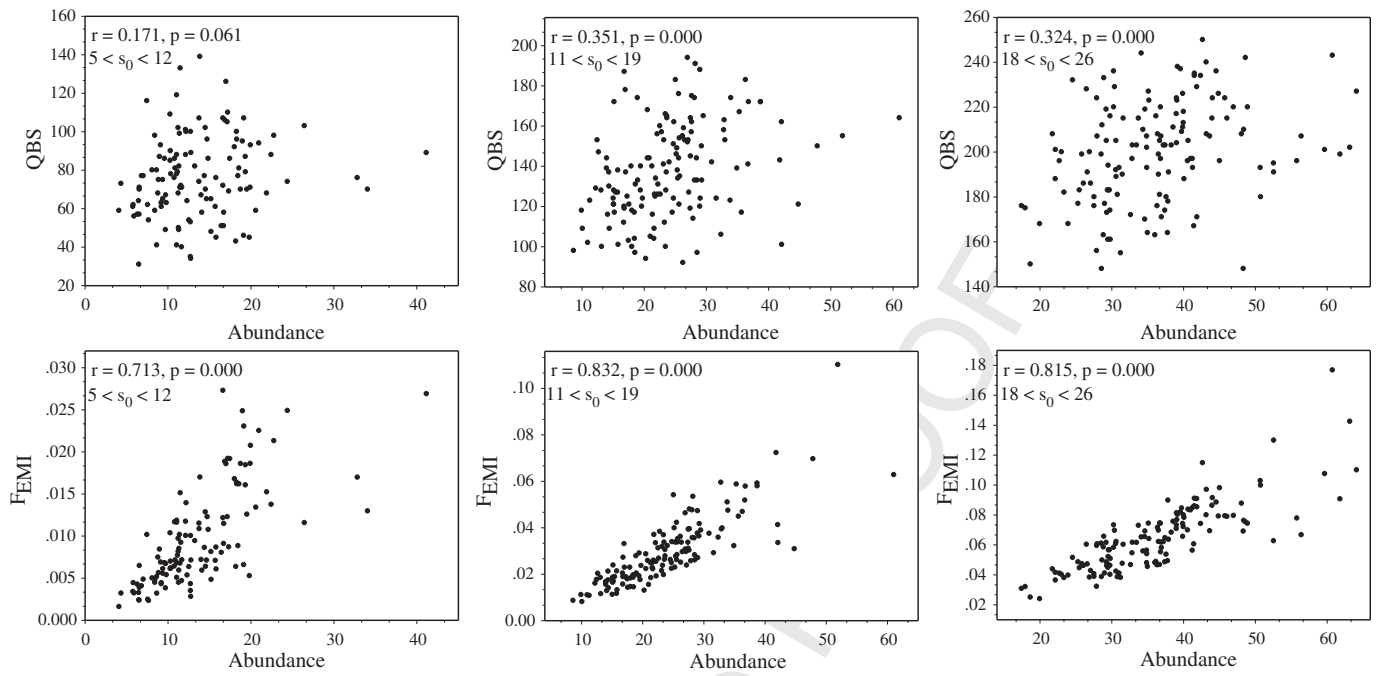


Fig. 2. Relationships of species abundance with QBS index and F_{EMI} index. The term s_0 is referred to the number of species, and s_0 is limited to a range of 25 taxa (because 25 taxa is enough in QBS method which using broad taxonomic units).

carried out in five representative plots based on homogeneous vegetation. A number of soil samples were taken randomly from different places of one site. Hence, the total number of observations was 35 (equal to the number of sites multiplied by the number of plots of each site). Each plot was sampled at soil depths of 0–5 cm, 5–10 cm and 10–15 cm, respectively. The layer of leaf litter was not included because it was not part of the soil itself. The plot means of each site represented a site level measurement. We followed standardized techniques to quantify faunal diversity in terms of number, size, weight and biomass. Most visible macro-organisms, such as earthworms, were hand-sorted in the top 15 cm soil

layer, but the other taxa such as microarthropods were extracted from the collected soil using modified Berlese–Tullgren dry funnels. Nematodes and enchytraeids were extracted from the soil samples using Baermann wet funnels. All identifications were carried out at taxonomic levels of class, sub-class, order, sub-order or family.

Corresponding sites with greater gradients e.g. conversions of plantations into secondary forests or grassland through fallow, human disturbance regimes differ in both intensity and frequency. For example, site A (site code: HTFFZ18) was established with Chinese fir (*Cunninghamia Lanceolata*) plantations in 1990, where

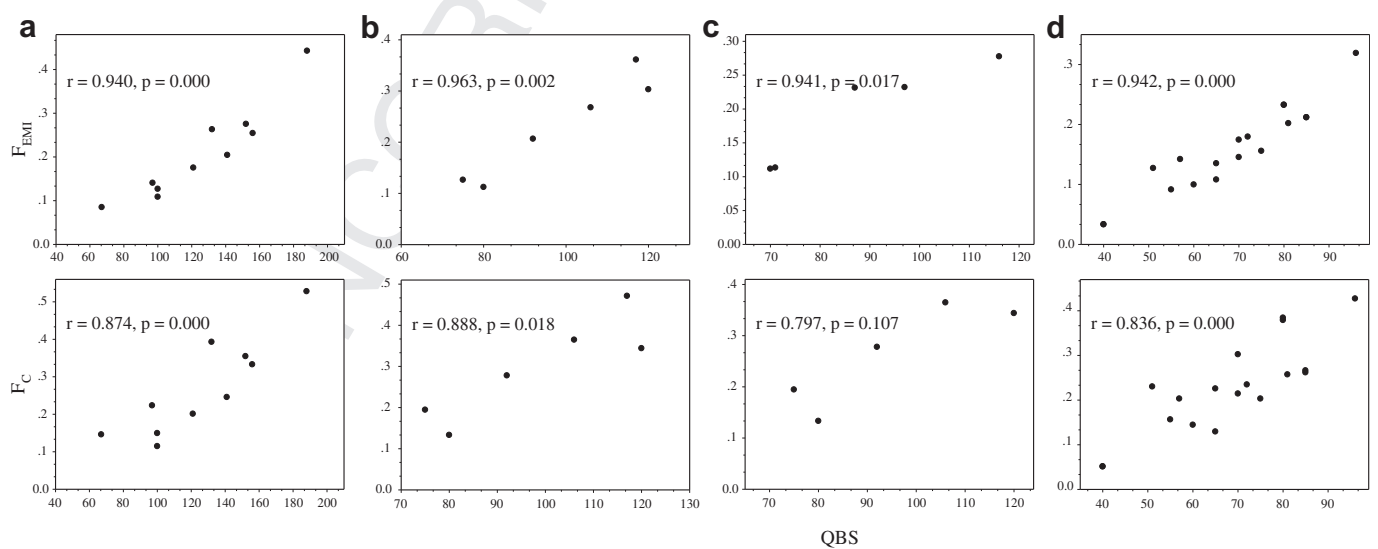


Fig. 3. Association between FAI and QBS using the presence/absence data. a: land use case in Rubbiano sites (source: Parisi et al., 2005), b: sewage sludge case in Cremona sites (source: Parisi et al., 2005), c: agricultural land uses case for the microarthropods (source: Gardi et al., 2002), d: ARS case in corn cultivation (source: Paolo et al., 2010). Because soil faunal quality index is a relative measure and can show soil quality class for evaluated sites, it allows that the reference site is alterable considering the integrated information of all sample sites, in Fig. 3a, 10 Rubbiano sites have combined to form a study region for calculating the F_{EMI} and F_C for each of sites, in the same way, 6 Cremona sites combined in Fig. 3b, 5 sites in Fig. 3c and 18 sample sites in Fig. 3d.

Table 2
Characteristics of soils in top 15 cm soil layer at each site. Values given in the table as means across replicates of each site and standard errors are in parentheses.

	A	B	C	D	E	F	G
pH	4.36(0.07)	4.24(0.07)	4.37(0.08)	4.21(0.09)	4.05(0.03)	4.13(0.08)	4.11(0.06)
Bulk density (g cm ⁻³)	1.20(0.10)	1.24(0.02)	1.17(0.09)	1.21(0.02)	1.12(0.02)	1.10 (0.12)	1.10(0.10)
Total P (g kg ⁻¹)	0.16(0.02)	0.15(0.01)	0.20(0.03)	0.19(0.01)	0.32(0.01)	0.22 (0.01)	0.20(0.01)
Total organic C (g kg ⁻¹)	12.45(1.35)	12.81(0.96)	22.34(1.54)	19.56(0.87)	18.01(0.75)	24.85(1.43)	26.66(1.50)
Total N (g kg ⁻¹)	1.36(0.07)	1.38(0.05)	1.45(0.03)	1.57(0.10)	1.69(0.01)	1.78(0.10)	2.26(0.06)

the main disturbances were intensive forest practices and frequent grazing. Among them, herbaceous diversity was moderately distributed and dominated by *Maesa japonica*, *Achyranthes bidentata* and *Dryopteris sparsa* belonging to different families. Site B (site code: HTFFZ20) was also established in 1990 as a mixed culture plantations (Chinese fir with *Kalopanax septemlobus* or with *Alnus cremastogyne*). Disturbances were similar to those at site "A", understory vegetational cover was almost similar but distribution of herbaceous species was different with these three dominant species- *Rubus rosaefolius*, *Parathelypteris glanduligera* and *Dryopteris chinensis*. Whereas site C (site code: HTFZH01) was established in 1983 as a Chinese fir plantation, where grazing was forbidden, and disturbances were moderate forest practices. Comparing with site "A" and site "B", its understory vegetation was substantially covered with better species richness with following dominant species *Mussaenda esquirolii* in association with *Actinidia fulvicoma* and *Microlepis marginata*. Site D (site code: HTFFZ02) was established as a secondary broad leaved forest since earlier from Chinese fir monoculture planted in 1996. This site was characterized by young *Lithocarpus glabra* and *Machilus pauhoi*. The canopy was relatively open and produces an understory of dense shrub dominated by *Cyclobalanopsis glauca*, *Camellia oleosa*, *M. japonica* and a few herbs such as *Piper martini* and *Triblemma lancea* in the stand. Site E (site code: HTFFZ03) was established as a grassland in 1960. Previously, it was an agricultural field under rice cultivation, ground vegetation was significantly better than other sites which was covered with diverse species but dominated by *Pueraria lobata* and *Miscanthus sinensis*. Site F (site code: HTFZH02ABC_02) is established as secondary broad leaved forest following since 1960

and following low human activity, where a few indigenous people occasionally gathered medicinal herbs. This site was characterized by large, old growth trees such as *Castanopsis fargesii*, *Machilus pauhoi* and *Cyclobalanopsis glauca*, whereas, understory was dominated by *Indocalamus longiauritus*, *M. japonica* and *Camellia oleifera*. Last, site G (site code: HTFZH02ABC_01) is established with secondary broad leaved forests following since 1960 and almost without human disturbance. The site was also characterized by large, old growth trees such as *Castanopsis fargesii*, *Machilus pauhoi* and *Cyclobalanopsis glauca*. The canopy is relatively closed and produces an understory of sparse shrubs (*Millettia dielsiana* and *Eurya loquaiana*) as well as with a few herbaceous species such as *Woodwardia japonica* and *Carex cruciata*.

These sites are included in a national ecosystem monitoring program for investigating long term changes of biodiversity in ecosystem under CERN's supervision. Soils of these sites are predominantly derived from slate and shale, and classified as Oxisols. The main physic-chemical characteristics of these sites are listed in Table 2. Details about present site parameters are also available online (<http://www.cerndata.ac.cn>).

We ranked all these selected sites into five land use intensity classes from low to high based on the tillage operations and disturbance regimes. Class one is having of no tillage and almost without any human intervention (site G), while class two is possessed the same characters except in addition of less human activities by some indigenous people who collects medicinal herbs for their own purpose (site F). Class three is ranked on the characters of no tillage within 10 years (site D and E). Class fourth and fifth is distinguished with opposite characters of the previous class,

Table 3
Abundance (ind. m⁻²) of soil fauna at different sites. Values represented in the table as means across replicates of each site. Standard errors are in parentheses.

Taxa	A	B	C	D	E	F	G
Acari	1203.2 (440.3)	335.3 (335.3)	3018.0 (1040.8)	8595.5 (2469.9)	12701 (2800.6)	8625.3 (2529.9)	36041.8 (8732.8)
Acerentomata				125.8 (125.8)	125.8 (125.8)		251.5 (251.5)
Amphipoda							33.7 (20.6)
Ants	477.5 (318.3)		302.0 (240.9)	2031.0 (1305.7)	84.2 (46.1)	2476.1 (1617.5)	2125.2 (854.2)
Araneae			302.0 (151.9)	125.8 (125.8)	16.8 (16.8)	472.7 (289.5)	159.4 (118.8)
Blattoptera					50.5 (33.7)		
Coleoptera			628.8 (344.4)		352.5 (121.8)	484.0 (296.4)	1236.8 (1086.5)
Collembola	795.8 (616.4)		1559.5 (464.2)	2640.8 (961.8)	4031.9 (1449.4)	7185.3 (1629.8)	4812.3 (1890.2)
Diplopoda	9.9 (9.9)		377.3 (154.0)				125.8 (125.8)
Diplura	9.9 (9.9)	2012.0 (2012.0)	16.8 (16.8)				285.2 (158.8)
Diptera	407.4 (407.4)		471.7 (471.7)	419.7 (249.3)	125.8 (125.8)	2953.8 (2668)	2155 (949.6)
Earthworm	19.9 (12.2)	50.5 (50.5)	16.8 (16.8)	16.8 (16.8)	101.0 (61.9)	16.8 (16.8)	
Enchytraeidae	814.9 (499.0)	6036.1 (2332.4)	7044.0 (3009.1)	12718.6 (4485.9)	6392.7 (1262.1)	10450.4 (1459.6)	1966.4 (1432.9)
Geophilomorpha				16.8 (16.8)		16.8 (16.8)	16.8 (16.8)
Harpacticoida	1629.7 (1187.9)						
Hemiptera	9.9 (9.9)				125.8 (125.8)		
Homoptera				159.4 (118.8)	125.8 (125.8)		
Isopoda			16.8 (16.8)		67.4 (49.1)	16.8 (16.8)	16.8 (16.8)
Isoptera							33.7 (20.6)
Lepidoptera	407.4 (407.4)			125.8 (125.8)		84.2 (37.7)	16.8 (16.8)
Lithobiomorpha			33.7 (20.6)				
Nematoda	19964.4 (8748.0)	80481.3 (40483.6)	237819.8 (234664.3)	135983.8 (18738.8)	213759.1 (38380.6)	76430.0 (69706.6)	367233.0 (59146.6)
Pseudoscorpiones					377.3 (251.5)		
Psocoptera				16.8 (16.8)			16.8 (16.8)
Scolopendromorpha					33.7 (20.6)		
Symphyla							669.9 (505.5)

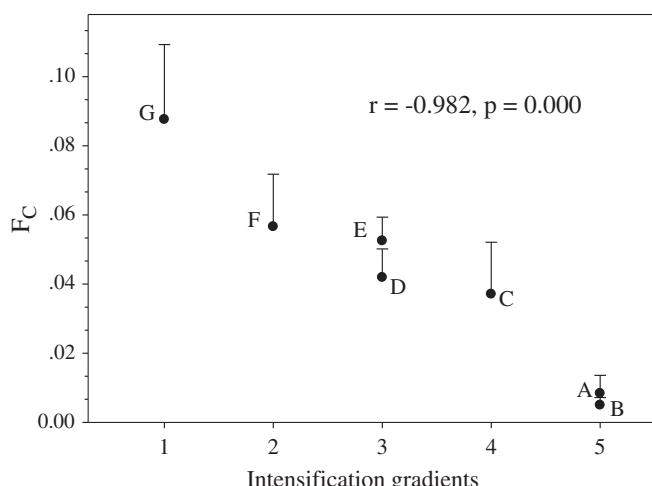


Fig. 4. Plot of the relationship between land use intensity and F_C index. Values represented as one site is means of replicates of each site and standard errors are in tip bars. Spearman rank order correlation and significance is shown.

thus, fourth is contained moderate forest practices with forbidding grazing (site C) while last one is with intensive forest practices with intensive grazing (site A and B).

We used Liao's occurrence ratio (niche breadth trait) as a functional trait option (Liao et al., 1997) because the EMI is limited to soil arthropods, in some plots no soil arthropods were found during sampling. We identified 26 taxa in the study region (Table 3), the number of taxa ranged from 1 to 12, the abundance of soil fauna in these sites ranged from 25,749 to 417,196 individuals m^{-2} , and the estimated FAI ranged from close to zero to 0.16 in each plot. The estimated populations of some groups given in Table 3 seemed very low, however the results were typical, and the other surveys were done with the similar results in the region (Yan et al., 2004, 2009a,b), in practice, the 'absolute efficiency' of extraction for each taxa was not really relevant to this type of 'comparative study'. Among sites, site A and B have low FAI values with forest operation disturbances such as logging and grazing while the high FAI at site number G might be due to little soil disturbance in 46 years since establishment. Thus, land use intensification was strongly associated with FAI where the intensification gradients were closely separated by FAI values (Fig. 4). This indicates that within the study region, soil quality was reduced as land-use intensified. Our study also showed there is a high efficiency incorporating all specimens from dry/wet funnel extraction into a relative integrated community in distinguishing between FAI values when specimen was identified to order or class. If, in a given plot, only non-arthropods were found (such as only one taxa of nematodes in the 4th plot at site A), the F_C was selected as a more feasible method than F_{EMI} and QBS. We provide Excel VBA Macro Code to implement our approach for computing F_C values as given in Appendix S1.

4. Conclusions

Parisi et al. (2005) developed an integrated approach through summing up a simplified functional trait score, namely, the eco-morphological index (EMI) of soil arthropods, for assessment of soil quality. Their approach does not support abundance data and is limited to soil arthropods. We have developed a new approach to extend the application of the functional method. The approach is used to describe how the functional trait method could be generalized into a flexible abundance-based measurement. The index we developed is useful to measure the ability of soils to keep the

biodiversity and soil functioning through selecting appropriate function traits and soil faunal community.

Theoretically, the performance of a trait is an expression of its fitness in a given environment (Webb et al., 2010). We hypothesized that a functional trait with strong effects on an organism's performance can be used as indicator on a scale in which the high values mean "more function". In our study, through analyzing the intrinsic association of new index with existing soil quality index (QBS) using model data and some cases reported, we found two functional traits of morphological adaptive differentiation and niche breadth can be applied in our index for the assessment of soil quality. However we did not test other function traits, especially when using a single taxa as indicator, i.e. c–p scale for nematodes. When function traits were selected to classify the organism, the extent to which the index will assess soil functioning will depend on the accuracy of such classification measuring the capacity of those organisms of performing a certain soil function. In addition, we investigated and developed relationships between FAI and QBS index. Results showed that FAI could assess the soil quality more realistically than QBS. Case analysis further showed that FAI method can extend to soil invertebrate community with more flexible choices in community and functional traits.

One of the challenges in evaluating soil quality lies in selecting a feasible soil faunal community as an indicator. In our approach when using single taxa method, FAI measures biological quality of selected taxa in a specific function, for example, FAI value is soil nematode faunal quality value when using soil nematodes as an indicator. The accuracy of assessment will depend on the capability of the taxa as an indicator. When using the multiple taxa method, FAI measures biological quality of soil faunal community in anticipant function. What taxa should be included, i.e. soil invertebrates, soil arthropods or the other assemblage, determines which classification level should be adopted, i.e. class, order, family, depending on demand of soil quality assessment. In conclusion, our FAI approach provides a new tool for exploring the relationships between soil fauna and soil environment, and useful for soil management.

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Appendix. Supplementary data

Supplementary data associated with this article can be found in the online version, at doi:10.1016/j.soilbio.2011.11.014.

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