Influence of cropping system and nitrogen input on soil fauna and microorganisms in a Swedish arable soil*

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Summary. The development of a number of components was analysed in an agro-ecosystem study with four cropping regimens, barley without and with N fertilization, grass ley, and lucerne. A great variation in N inputs ($1-39$ g N m^{-2} year^{-1}) and cropping systems produced a variation in primary production ($260-790$ g C m^{-2} year^{-1}) and input of organic material to the soil ($150-270$ g C m^{-2} year^{-1}). This was reflected in variations of total soil animal biomass ($1.6-5.1$ g C m^{-2}) and in variations in the abundance of various animal groups, nematodes ($5.6-9.8\times10^6$ m^{-2}), micro- ($2.6-4.8\times10^{-4}$ m^{-2}), and macroarthropods ($0.9-4.2\times10^3$ m^{-2}). In contrast, total bacteria, fungi, flagellates, and amoebae varied quite independently of the organic matter input. Mineralization processes covaried more with C and N inputs and total animal biomass than with microbial biomass. It is suggested that the rather constant microbial biomass was a result of an adjustment in the grazing pressure of microbial-feeding animals to the level of microbial production.

Key words: Barley – Nitrogen fertilization – Lucerne – Microorganisms – Soil animals – Causal connections – Primary production – Microbial biomass – *Hordeum distichum*

Traditionally, physical and climatic conditions, organic matter contents and food input have been considered the most important factors structuring the soil faunal community. However, there is an increasing interest in the effects of foodweb interactions, including predation and competition (Elliott et al. 1988; Whitford 1989). In the present work, these aspects are considered in an analysis of the development of various biotic and abiotic soil components in a Swedish agro-ecosystem study. In particular the role of animals is considered.

Kühnelt (1961) pointed out how destructive agricultural practices can be to the soil animal community. Foissner (1987) found a greater number of protozoa and nematoda and a greater CO_2 release and a greater enzymatic activity in ecofarmed cornfields than in those conventionally managed. However, in conventionally managed fields, also, the abundance and biomass of soil animals may increase to the extent that it is reasonable to assume a considerable influence on soil processes (Andrén and Lagerlöf 1983; Ryszkowski 1985; Hendrix et al. 1986).

Syntheses of results from the Swedish project on the ecology of arable land, focusing on other aspects, have been published earlier (Rosswall and Paustian 1984; Andrén et al. 1988; Paustian et al. 1990).

Materials and methods

Site description and experimental layout

The experimental site at Kjettslinge in central Sweden has been described by Steen et al. (1984). The topsoil down to 27 cm (plough layer) is a loam with 19% clay and 5% organic matter, pH 6.0–6.6, and C and N contents of 2.2 and 0.23%, respectively.

The field was fertilized with 500 kg ha^{-1} of granular NPK at 20:6:6 (percentages of elements) and sown with barley (*Hordeum distichum* L. cv. Gunilla) in 1978. In 1979 the field was left in bare fallow and was fertilized with 1290 kg ha^{-1} of PK at 7:13 in the autumn. In 1980 four plots (40×14 m) were cropped with barley without the addition of N fertilizers. Another four plots were cropped with barley and fertilized with 120 kg N ha^{-1} (calcium nitrate) each year. An additional four barley plots were sown with meadow fescue (*Festuca pratensis* Huds. cv. Mimer) and another four plots were sown with lucerne (*Medicago sativa* L. cv. Sverre). From 1980, meadow fescue and lucerne were grown continuously on these plots. Thus, the field was cropped with two annual (barley) and two perennial (grass, lucerne) crops. The grass ley was fertilized with 120+80 kg N ha^{-1} as calcium nitrate each year whereas the lucerne ley took up atmospheric N through symbiotic N_2 fixers (*Rhizobium*). The leys were harvested once in 1981 and twice annually from 1982 to 1984.

Table 1. Mean values, sequence, and range of variation (%) of C and N fluxes and C contents in various components of four cropping systems: Barley without N (B0); barley with $120 \, kg \, N \, ha^{-1} \, year^{-1}$ (B120); grass ley (GL); and lucerne ley (LL)

Component	Mean	Sequence	Range (%)
N input	$18.5 \, g \, N \, m^{-2} \, year^{-1}$	B0 < B120 < GL < LL	205
Net C assimilation	$568 \, g \, C \, m^{-2} \, year^{-1}$	B0 < B120 < GL < LL	93
C input	$215 \, g \, C \, m^{-2} \, year^{-1}$	B0 < B120 < GL < LL	56
N mineralization	$13.3 \, g \, N \, m^{-2} \, year^{-1}$	B0 < B120 < LL < GL	101
Heterotrophic soil respiration	$220 \, g \, C \, m^{-2} \, year^{-1}$	B0 = B120 < GL < LL	55
Ammonium	$3.2 \, \mu g \, N \, g \, (dry \, weight)^{-1}$	B0 < B120 < GL < LL	43
Total C in soil	$8708 \, g \, C \, m^{-2}$	B0 < LL < GL < B120	36
Total C in biomass	$473 \, g \, C \, m^{-2}$	B0 < B120 < GL < LL	83
Root biomass	$198 \, g \, C \, m^{-2}$	B0 < B120 < GL < LL	177
Fungal hyphae	$180 \, g \, C \, m^{-2}$	B0 < GL < LL < B120	44
Bacteria	$85 \, g \, C \, m^{-2}$	B0 < B120 = GL = LL	24
Total metazoan soil fauna	$2.8 \, g \, C \, m^{-2}$	B0 < B120 < GL < LL	127

Data used in the investigation

Data for soil organism are taken from various publications of follows: Bacteria, fungi, and protozoa (Schnürer et al. 1986); ammonium and nitrite oxidizers (Berg and Rosswall 1987); nematodes (Sohlenius et al. 1987, 1988); enchytraeids (Lagerlöf et al. 1989); earthworms (Boström 1988); Pauropoda and Symphyla (Lagerlöf 1987); Acari (Lagerlöf and Andrén 1988); Collembola, Protura, and Diplura (Lagerlöf and Andrén 1990); macroarthropods (Carter et al. 1985); above-ground fauna (Curry 1986); N and C and other nutrient inputs (Paustian et al. 1990). Details on taxonomic composition of the fauna have been provided by Andrén et al. (1989).

The values given in the present paper may differ slightly from those in the other papers, depending on sampling period and depth. Since the pattern of variation of the components in the four treatments is the chief concern of the present paper unmodified data were used, in order to avoid various errors in calculation and extrapolation. The analysis was undertaken by comparisons of the variation of various soil components. The range of variation was estimated as the difference between the highest and lowest values as a percentage of the mean value for all four treatments (Tables 1 and 2). The mean time from the start of the experiment to the sampling period was 2–3 years.

Results

Variation in components

The total N input by atmospheric deposition (1 g N m^{-2} over all treatments), fertilization, and N$_2$ fixation increased from the unfertilized barley to the lucerne (Fig. 1 A). This was also the case with net C assimilation

Table 2. Mean values, sequence, and range of variation (%) of hyphal length and abundance of various groups of soil organisms (number per m^2 except as indicated) in four cropping systems (crops abbreviated as in Table 1)

Component	Mean	Sequence	Range (%)
Total hyphae[a]	1.1×10^3	B120 = LL < GL < B0	12
FDA-hyphae[a,b]	79.5	B120 < B0 < GL < LL	48
Bacteria[c]	5.5×10^9	B0 < B120 = LL < GL	25
Ammonium oxidizers[c]	3.3×10^4	B0 < B120 < GL < LL	65
Nitrite oxidizers[c]	59×10^4	B0 < B120 < GL < LL	118
Flagellates[c]	8×10^4	B120 < LL < B0 < GL	55
Amoeba[c]	3.8×10^4	B120 < LL < GL < B0	145
Nematoda total	7.7×10^6	B0 < B120 < GL < LL	54
Nematoda			
Plant feeders	2.4×10^6	B0 < B120 < GL < LL	130
Fungal feeders	1.9×10^6	B120 < LL < B0 < GL	86
Bacterial feeders	2.9×10^6	B0 < GL < B120 < LL	42
Rhabditis + Panagrolaimus	7.2×10^5	B120 < B0 < GL < LL	174
Enchytraeidae	8.4×10^3	GL < B120 < LL < B0	54
Lumbricidae	48	B0 < B120 < GL < LL	127
Microarthropods	3.2×10^4	B120 < B0 < GL < LL	76
Acari	1.3×10^4	B0 < B120 < Gl < LL	44
Pauropoda	1.4×10^3	GL < B120 = LL < B0	59
Symphyla	213	LL < B120 < GL < B0	104
Collembola	1.8×10^4	B120 < B0 < GL < LL	108
Protura + Diplura	505	B120 < GL < LL < B0	133
Macroarthropods	1.9×10^3	B0 < B120 < GL < LL	176

[a] Metres per gram dry weight
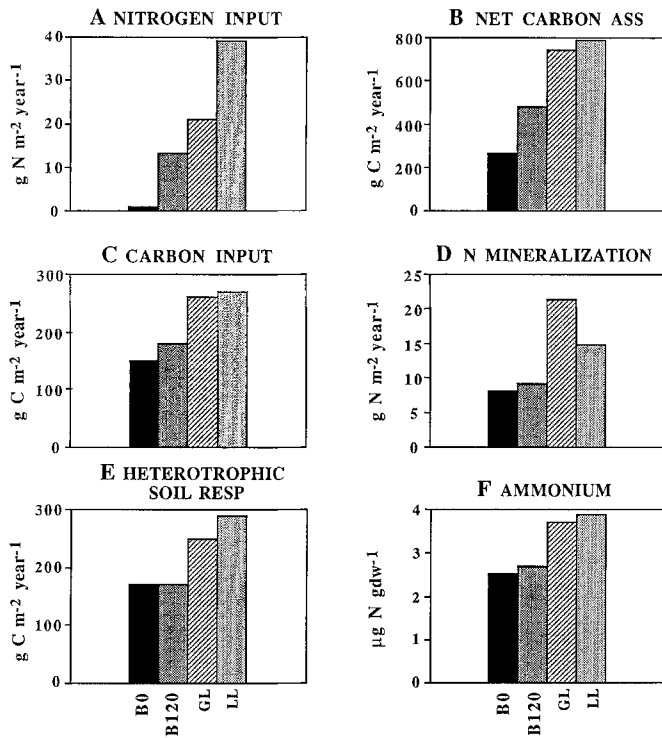[b] FDA, fluorescein diacetate stain
[c] Number per gram dry weight

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Fig. 1 A–F. C and N dynamics in four cropping systems: Barley without N (*B0*), barley with 120 kg N ha^{-1} year^{-1} fertilization (*B120*), grass ley (*GL*), and lucerne ley (*LL*). Bars are mean values of samplings during 1980–1984. *ASS*, assimilation; *RESP*, respiration

(= primary production) (Fig. 1B), root biomass (Fig. 2A), and organic matter input to the soil (Fig. 1C).

The rate of N and C mineralization was higher in the perennial than in the annual systems (Fig. 1D and E) and the amount of ammonium increased from the unfertilized barley to the lucerne (Fig. 1F).

Root biomass varied considerably (Table 1), with higher values in the perennial than in the annual systems (Fig. 2A). The total hyphal length per g soil (Fig. 2B) was uniform under the various treatments (Table 2). Viable, fluorescein-diacetate stained hyphal lengths (Fig. 2C) varied more, and were significantly lower in the unfertilized barley for some samplings. The total fungal biomass (from Paustian et al. 1990) was highest in the fertilized barley (Table 2). The number and biomass of total bacteria (Fig. 2D and Table 1) did not vary much between the treatments. However, ammonium and nitrite oxidizers clearly increased from the unfertilized barley to the lucerne (Figs. 2E and F). The highest abundance of flagellates and amoebas was found in the unfertilized barley and the grass and the lowest in the fertilized barley (Fig. 2G and H).

Total nematodes increased evenly from the unfertilized barley to the lucerne (Fig. 3A). Much of this increase was due to plant feeders (Fig. 3B), which had a wide range of variation. Variation in the number of bacterial feeders was rather low. The number of fungal feeders (Fig. 3D) was lower in the fertilized barley and the lucerne and higher in the unfertilized barley and the grass. *Rhabditis + Panagrolaimus* (Fig. 3E), which are consid-

ered good indicators of rapid microbial processes, were especially abundant in the lucerne.

The greatest abundance of enchytraeids was found in the unfertilized barley and the lowest in the grass (Fig. 4A). The abundance of earthworms was higher in the lucerne than in the other treatments (Fig. 4B).

The variability in numbers of Acari (Fig. 4C) was lower than that of Collembola (Fig. 4D, Table 2). Pauropoda, Symphyla (Fig. 4E and F), and Protura + Diplura (Table 2) reached their highest abundance in the unfertilized barley (Table 2). The macroarthropods (Fig. 4G) increased considerably from the unfertilized barley to the lucerne.

The influence of N fertilization on the above-ground animal biomass in barley was considerable (Fig. 4H).

Some general patterns of variation

Some particular pattern of variation were evident.

1. A regular increase from the unfertilized barley to lucerne was found in N and C inputs (Fig. 1A and C), root biomass (Fig. 2A), and total nematode numbers (Fig. 3A).

2. A pattern quite similar to pattern 1, with a smooth increase from the unfertilized barley to the grass and then
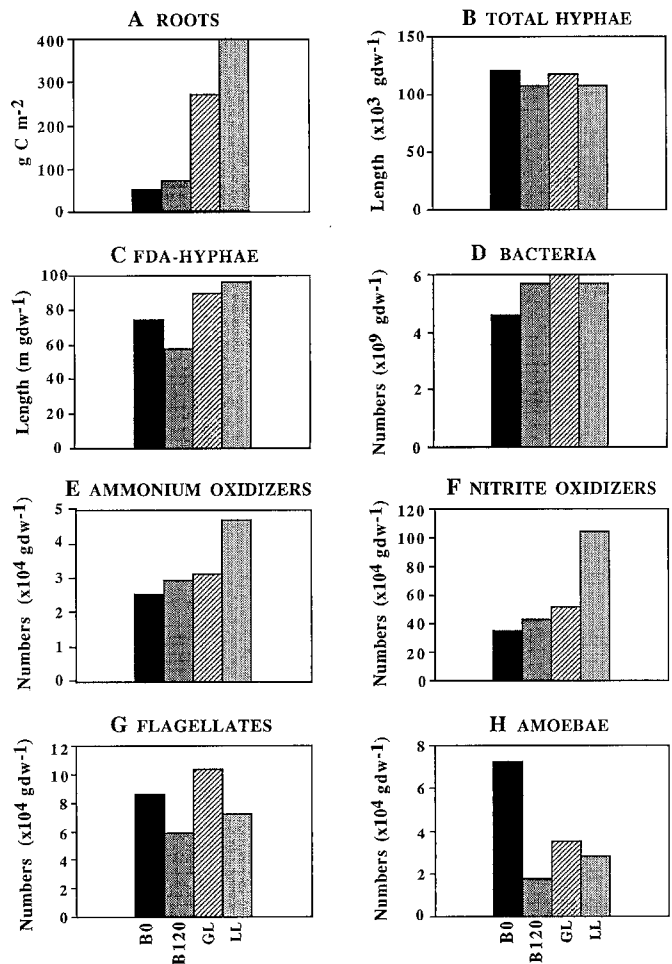

Fig. 2 A–H. Hyphal length and abundances of bacteria and protozoa in four cropping systems (crops abbreviated as in Fig. 1). *FDA*, fluorescein diacetate stain; *gdw*, gram of dry weight
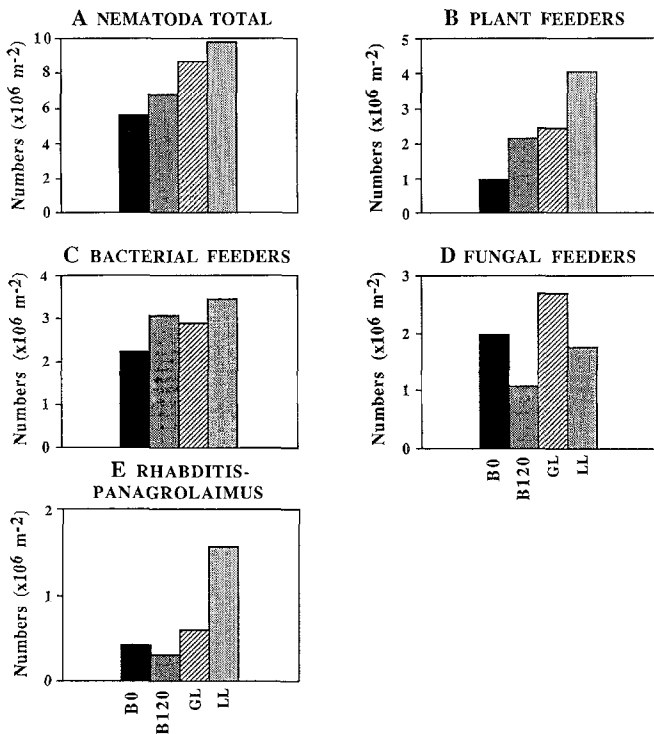
Fig. 3 A—E. Abundance of total nematodes and of various feeding groups in four cropping systems (crops abbreviated as in Fig. 1)

a distinctly higher value in the lucerne, was found for the total soil animal biomass (Table 1), abundance of earthworms (Fig. 4B), macroarthropods (Fig. 4G), and ammonium and nitrite oxidizers (Fig. 2E and F).

3. A skewed u-shaped configuration, with the lowest value in the fertilized barley and increasing values from the grass to the lucerne was found to some extent in fluorescein-diacetate stained fungi (Fig. 2C), in Collembola (Fig. 4D), and in Rhabditis + Panagrolaimus (Fig. 3E).

4. Low values in the fertilized barley and lucerne and high values in the unfertilized barley and grass were found for the abundance of fungal-feeding nematodes (Fig. 3D), for both groups of protozoa (Fig. 2G and H), and for Symphyla (Fig. 4F). Although weak, the pattern was also found for total fungal length (Fig. 2B).

5. An increase in the sequence unfertilized barley to lucerne with a distinct jump upwards in the fertilized barley was found for plant-feeding nematodes (Fig. 3B) and above-ground faunal biomass (Fig. 4H).

6. Enchytraeids (Fig. 4A) and Pauropoda (Fig. 4E) did not follow any of these patterns except for having the highest value in the unfertilized barley; this was also the case with amoebae (Fig. 2H) and Symphyla (Fig. 4F).

Discussion

The variation in N input apparently had a great effect on several components in the system. That it directly influenced primary production was demonstrated by the pronounced increase in plant production in the fertilized barley. The increased primary production in the perennial

systems was certainly a combined effect of the N input, a longer growth period, and a more extensive root system.

That the variation in C input to the soil system (56%) was smaller than the variation in C assimilation (93%) is an effect of the removal of a large quantity of plant biomass during the harvest. The amount of material removed in this way largely mirrored primary production (Paustian et al. 1990). Schnürer et al. (1985) found a good correlation between soil C contents and microbial biomass, so it was surprising that the microbial biomass did not follow the increase in input of organic material.

Berg and Rosswall (1987) explained the increase in ammonium and nitrite oxidizers from the unfertilized barley to the lucerne by increases in root exudation and in the organic matter input to the system. The pattern of variation of ammonium and nitrite oxidizers, with an extra large increase in the lucerne, had very close similarities with the variation of total faunal biomass and specifically with lumbricids and macroarthropods. This may indicate a connection between soil animals and ammonium production and nitrification processes.

One hypothesis that explains the lack of correlation between organic matter input and microbial biomass is that the grazing pressure, exerted by the microbial-feeding
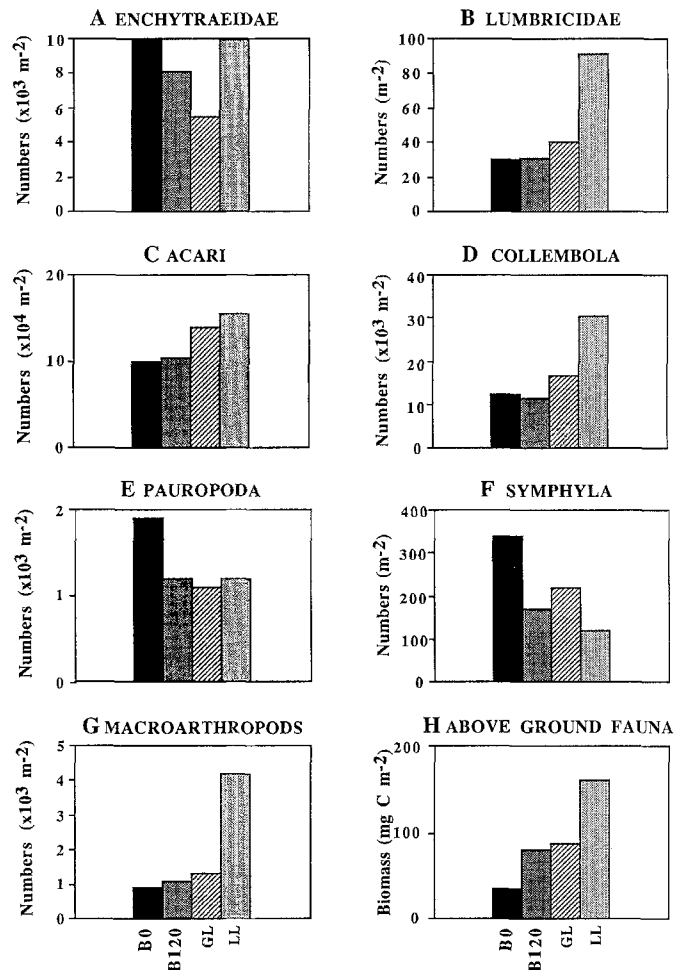

Fig. 4 A—H. Abundance of various groups of soil animals and biomass of above-ground fauna in four cropping systems (crops abbreviated as in Fig. 1)

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animals, increased in proportion to microbial production. If this is correct then the microbial production probably increased in sequence from the unfertilized barley to the lucerne in spite of similar biomass values. This production is reflected in increasing soil animal biomass. That the microbial activity increased in proportion to C and N input is indicated by soil respiration (Fig. 1 E), to some extent in N mineralization (Fig. 1 D), and in the amount of ammonium in the soil (Fig. 1 F). The fairly constant abundance and biomass of total bacteria and total fungi might also have been an effect of soil structure, where the narrow pore spaces provided a refuge space from which the microbial feeders were excluded (Elliott et al. 1980). According to this hypothesis, the microorganisms dispersing into larger pore spaces were rapidly consumed. The result of this mechanism would be an adjustment in the number and biomass of microbial-feeding animals to match the production rate of microorganisms.

The abundance and biomass of some animal groups varied in agreement with this hypothesis. However, this does not seem to be the case with the abundance of flagellates, amoebae which varied in quite another, way from the N and C input to the soil (cf. Fig. 1 A and C, and Fig. 2 G and H). Protozoa certainly may reduce bacterial biomass and influence the mineralization rate. Animal groups which varied in agreement with organic matter inputs included nematodes (total numbers), earthworms and most arthropods.

The feeding rate of bacterial-feeding nematodes was estimated at 6.8, 8.6, 9.2, and 12.3 g bacterial C m^{-2} year^{-1} from the unfertilized barley to the lucerne, respectively (Sohlenius et al. 1988). Thus they used a relatively small proportion of the bacterial standing crop. However, it is very difficult to estimate the microbial production. Obviously, the mean metabolic activity of the microbial biomass was very small. Schnürer (1985) estimated a turnover time of 1.1 year.

The high turnover rate of nematodes (9–10) estimated by Sohlenius et al. (1988) indicates a pronounced predation pressure on them. Lagerlöf and Andrén (1988) consider that 20–60% of the nematode production could be consumed by gamasid mites. The numbers of mites and nematodes are correlated (Figs. 4 C and 3 A).

Although the variation in abundance of some animal groups indicates increasing microbial production from unfertilized barley to lucerne it is not clearly apparent from the present data that animal consumption kept the microbial biomass so relatively constant and independent of the input of C and N. However, it is probable that the animals contributed substantially to the increased rate of mineralization in the perennial systems, both by direct excretion of N and by stimulation of microbial activity.

Some results from the present study are in line with results obtained previously in microcosm experiments (Bååth et al. 1978, 1981; Clarholm et al. 1981). In those experiments there was a correlation between the rate of soil respiration and the number of nematodes but no correlation between the microbial biomass and the rate of respiration, showing that the nematode number was a better indicator of mineralization processes than the microbial biomass itself. The observation of a positive correlation between number of nematodes and primary production agrees with observations by Yeates (1987).

It appears as if N fertilization in the fertilized barley led to a decreased length of fluorescein-diacetate-active fungal hyphae. This was also indicated by reduced numbers of fungal-feeding nematodes and perhaps also by a tendency for lower numbers of certain groups of microarthropods.

Certainly, there are reasons other than microbial production for the increase in some animal groups from the unfertilized barley to the lucerne, especially since some of them feed on litter. For these animals food quality is important. Both the above- and below-ground litter of lucerne provides a very suitable food source for animals such as lumbricids (Boström and Lofs-Holmin 1986).

The total metazoan biomass increased from the unfertilized barley to the lucerne more rapidly than the C input (127% against 56%). This can partly be explained by the palatability of lucerne. Many larger animals, especially arthropods, were actually harmed by ploughing. Also, the ploughed plots provided less shelter and a harder climate than the perennial plots. These factors may explain the higher populations, especially in lucerne.

To explain cases where the pattern of animal parameters differed from patterns of organic matter input may be difficult. Lagerlöf et al. (1989) tried to explain the variation in enchytraeids in terms of water contents and noxious effects of N fertilizers. However, competition from larger animals such as earthworms cannot be ruled out.

Although the operation of foodweb interactions is certainly of ultimate importance to the structure and dynamics of the soil faunal community, it is very difficult to prove this, even with access to data from a large-scale ecosystem project such as the Swedish Arable Land Project.

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