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Nematode assemblages from Mountain Pine (*Pinus mugo* Turra) communities in Pirin Mountain, Bulgaria

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Summary

The structural and functional diversity of nematode communities from *Pinus mugo* sites in Pirin Mountain was assessed. The sampling plots represent different levels of disturbance - next to and outside ski runs. Nematode assemblages from this habitat can be characterised with high diversity (in total, 104 taxa and richness ranging from 41 to 65 genera per site). In general, the trophic structure was dominated by omnivorous and bacterial feeders coupled with low proportion of plant feeding nematodes. The high values of Maturity indices and the results from faunal analysis indicate relatively stable environment and undisturbed conditions for all sites. No clear correlation between the nematode assemblages' characteristics and the level of disturbance (position of the site in relation to ski runs) was revealed.

Keywords: diversity; ecological indices; life strategies; *Pinus mugo*; nematodes; trophic structure

Introduction

The human pressure on upland ecosystems has been increasing during the last decades (Kuzniar *et al.*, 2004). It has a negative impact on ecosystem functioning and often leads to habitat fragmentation and loss of biodiversity. High mountain regions represent fragile and vulnerable ecosystems with a slow recovery after disturbance caused by both natural and human-driven factors. Mountain Pine (*Pinus mugo* Turra) shrublands are of great conservation value and have been included in the Habitat Directive (Directive 92/43/EEC). They protect soils against erosion and retard avalanching. However, outside the native ranges of distribution, *P. mugo* is regarded as an invasive species (Jørgensen, 2006).

Nematodes (free living and plant parasites) are suitable for environmental change assessment. The indicator potential of nematodes has been used previously to estimate soil

characteristics and soil health (de Goede & Bongers, 1994; Neher, 2001; Yeates, 2003), climate change (Ruess *et al.*, 1999a, b; Sohlenius & Boström, 1999a, b), heavy metal pollution (Korthals *et al.*, 1996a, b), and habitat disturbance (Noblack, 1989). In alpine areas, nematode assemblages have been studied with regard to spatial variation between sites and influence of microclimate (Hoschitz, 2003; Hoschitz & Kaufmann, 2004a, b).

Data on composition and structure of nematode communities from *P. mugo* habitats are insufficient and fragmentary (Tsaryk & Kozlowsky, 1999; Lazarova, 2000; Ilieva, 2007,).

In the present study, we compared taxonomic composition and assemblage parameters (diversity and functional group distribution) of nematodes from seven *P. mugo* sites.

Materials and methods

Site description

The study area is situated in northern Pirin Mountains within the Pirin National Park, above the mountain resort of Bansko. Seven plots of mature, over hundred years old Mountain Pine shrub lands were sampled (Table 1). Yulen, Dolno Vassilashko Lake and Academica sites were not or slightly disturbed by anthropogenic influence, though Yulen's site was naturally fragmented. The rest of the sites - Plato, Todorka 1, Todorka 2 and Todorka 3 - were situated next to the ski runs in the sub-alpine belt of Todorka peak. The soil type is Humic Cambisols on granite substratum. The average annual temperature is 3.3 – 3.7 °C, the precipitation rate - 1200 – 1270 mm per year (Raev, 2005).

Sampling, nematode extraction and identification

A total of 70 samples were collected in July 2005 from the *P. mugo* sites with 10 replicates per site. The samples were taken from 0 – 15 – 20 cm depth after removing the litter. Nematodes were recovered from 100 cm³ soil by sieving

Table 1. Description of the studied *Pinus mugo* sites

Locality	Abbreviations	Coordinates		Elevation meters (a.s.l.)	Exposition	Vegetation cover
		N	E			
Yulen	uM	41°41'33.7"	023°28'39.3"	2160	W	<i>P. mugo</i> , <i>Festuca valida</i> (Uechtr. Penzes), <i>Luzulla</i> sp., <i>Juniperus sibirica</i> (Burgsd.), <i>Vaccinium myrtillus</i> (L.)
Dolno Vassilashko lake	dvM	41°44'32"	023°27'09"	2135	SE	<i>P. mugo</i> , <i>Thymus</i> sp., <i>F. valida</i>
Plato	pM	41°45'27.6"	023°26'29.6"	2375	NE	<i>P. mugo</i> , <i>V. myrtillus</i> , <i>Luzulla</i> sp.
Todorka	t1M	41°45'45"	023°26'20"	2400	NE	<i>P. mugo</i>
Todorka	t2M	41°45'47.3"	023°26'16.7"	2400	NE	<i>P. mugo</i>
Todorka	t3M	41°45'53.6"	023°26'26.1"	2200	NE	<i>P. mugo</i> , <i>V. myrtillus</i>
Academica	aM	41°47'16.4"	023°25'21.1"	2140	NE	<i>P. mugo</i> , <i>Luzula albida</i> (Hoffm.), <i>Poa</i> sp.

and decanting technique, using two sieves with apertures of 1 mm and 64 µm, respectively. The final extraction was on small-sized sieves (aperture ca. 500 µm) in water filled Baerman funnels for 48 h. The remnants of roots were placed on the small sieves in order to extract higher percentage of the nematode populations. Extracted nematodes were heat killed at 60 °C, fixed in 4 % formaldehyde and counted. At least 200 specimens per sample were processed in anhydrous glycerine and mounted on permanent slides (Seinhorst, 1959) for identification.

Community parameters and analyses

Based on their relative abundance, the nematode genera were divided into eudominants (40 – 100 %), dominants (12.5 – 39.9 %), subdominants (4 – 12.4 %), recedents (1.3 – 3.9 %) subrecedents (0.1 – 1.2 %) according to Engelmann (1978). The nematode taxa were assigned to five feeding groups following the classification of Yeates *et al.* (1993). Plant feeding nematodes belonging to the sub-group "f" were regarded separately from the groups "a-e" and denoted below as algal feeders (AF). The Maturity indices, MI and PPI (Bongers, 1990), MI 2 – 5 (based on the cp groups 2 – 5, e.g. Korthals *et al.*, 1996) and ΣMI (Yeates, 1994) were calculated. The following diversity measures: generic richness (S), Shannon's diversity index (H') and Simpson's concentration of dominance index (C)(Krebs, 1989) were calculated for each sample. Additionally, Enrichment index (EI), Channel index (CI) and Structure index (SI), (Ferris *et al.*, 2001) were used to characterise the soil food webs.

The diversity parameters, similarity measures and cluster analysis were performed using the program BIODIV 5.2 (Baev & Penev, 1995).

The linear-response model of Principal Components Analysis (PCA) based on generic abundance data, log-transformed prior to analyses was most appropriate for analysing the nematode communities of studied sites (gradient length in CA/DCA did not exceed 3.0 (4.0) SD, a general limits for the acceptance of linear models (ter Braak, 1996). Further, an indirect gradient analysis was applied in order to visualize the relation of generic composition and community measures. All gradient analyses and ordination graphs were performed using CANOCO version 4.5 (ter Braak & Smilauer, 2002). Multiple comparisons of samples datasets were made with non-parametric Kruskal-Wallis *H* test; significant differences were tested using the Mann-Whitney *U* test (Statistica 8.0).

Results and discussion

Diversity, abundance, occurrence and dominance

A total of 104 taxa (a hundred determined to generic, three to subfamily and one to family level) were recorded from all studied sites, with the greatest number identified at Academica (aM, 65) and the least at Todorka (t3M, 41)(Table 2). Thus, the nematode assemblages from the northern Pirin were characterised by high generic richness compared to the data from other Mountain Pine sites: 34 genera reported from Rila Mt. (Ilieva, 2007) and 46 - from Vitosha Mt. (Lazarova, 2000).

The total number of nematodes varied significantly among sites (Table 3) with average values ranging from 177 (at uM) to 2257 (at t1M). With regard to their frequency of occurrence, the nematode taxa could be divided into the following groups: common - found at all seven sites (17); less common - found in four to six sites (34) or three sites (16); and rare - found in one or two sites (35) (Table 2). In general, *Tylencholaimus* (11.4 %), *Aporcelaimellus* (10.3 %), *Plectus* (10.2 %), *Metaporcelaimus* (6.5 %), *Eudorylaimus* (6.4 %), *Acrobeloides* (5.7 %) were the most abundant in all sites. The taxonomic composition appeared rather uniform among sites, because half of the genera were common for the majority of sites (4 – 7). Among them, only six genera were dominant for at least one plot (*Acrobeloides*, pM; *Plectus*, uM & t2M; *Tylencholaimus*, t1M; *Aporcelaimellus*, dvM, pM & t2M; *Metaporcelaimus*, t3M; *Coomansus*, t3M). Dominant structure of the Mountain Pine sites was composed by 1 – 3 dominant and 4 – 8 subdominant genera, with no eudominant genera present (see Table 2 for details).With few exceptions (*Tylocephalus*, *Labronemella*, *Longidorella*, *Malenchus* and *Clarkus*), all rare taxa which occurred in one to three sites, were present in very low numbers (subrecedents).

A similar pattern in dominance structure was observed for the nematode assemblages from Vitosha and Rila Mts (3 – 2 dominant and 4 – 3 subdominant genera, respectively (Lazarova, 2000; Ilieva, 2007). Only three dominant genera (*Plectus*, *Aporcelaimellus* and *Helicotylenchus*) were common for the *P. mugo* sites in all three mountains. Characteristic features of the nematode assemblages from the other two studied regions were the high proportions of *Alaimus* and *Tripyla* in Vitosha and *Malenchus* in Rila Mts. The variation among the nematode communities in all studied plots was calculated with Principal Components

Table 2. Mean relative abundance (A% per 100 cm³ fresh substrate) and frequency (F% occurrence in the replicates) of nematode taxa from *P. mugo* sites

Genera	Yulen		Dolno Vassilashko lake			Plato		Todorka 1		Todorka 2		Todorka 3		Academica	
	A	F	A	F	A	F	A	F	A	F	A	F	A	F	
Bacterial Feeders															
<i>Acrobeloides</i>	3.0	90	8.3	100	14.4	90	0.5	40	8.2	90	2.0	70	3.4	100	
<i>Alaimus</i>	3.3	60	4.5	100	0.6	60	0.7	60	0.2	40	0.1	10	1.9	70	
<i>Amphidelus</i>	0.2	20	-	-	-	-	-	-	-	-	-	-	-	-	
<i>Anaplectus</i>	2.1	40	0.8	50	0.7	50	0.1	20	-	-	-	-	0.9	60	
<i>Aulolaimus</i>	-	-	-	-	-	-	-	-	-	-	-	-	0.1	30	
<i>Bastiania</i>	0.2	20	0.9	60	0.3	30	0.8	70	+	10	+	10	0.7	50	
<i>Bunonema</i>	-	-	-	-	-	-	-	-	-	0.1	10	-	-		
<i>Cephalobus</i>	-	-	-	-	-	-	+	10	-	-	-	-	1.2	80	
<i>Ceratoplectus</i>	0.2	20	+	10	-	-	-	-	-	-	-	-	-	-	
<i>Cervidellus</i>	0.7	40	2.7	70	0.6	60	+	10	0.1	10	0.1	10	2.1	90	
<i>Chiloplacus</i>	0.1	10	0.5	50	-	-	0.2	30	-	-	-	-	0.8	60	
<i>Chromadorina</i>	-	-	0.1	10	-	-	-	-	-	-	-	-	-	-	
<i>Cylindrolaimus</i>	-	-	0.3	30	-	-	-	-	-	-	-	-	0.2	20	
<i>Eucephalobus</i>	0.4	20	0.5	40	-	-	-	-	-	-	0.1	10	4.2	70	
<i>Eumonhystera</i>	-	-	0.2	50	0.2	40	-	-	-	-	0.1	20	0.4	50	
<i>Euteratocephalus</i>	-	-	-	-	-	+	10	0.2	10	-	-	-	-	-	
<i>Geomonhystera</i>	-	-	0.3	10	0.1	10	-	-	-	-	-	-	0.1	10	
<i>Heterocephalobus</i>	-	-	1	80	1.2	70	0.4	10	-	-	-	-	0.2	40	
<i>Metateratocephalus</i>	0.1	10	0.1	20	0.1	10	-	-	0.2	40	0.1	20	0.3	20	
<i>Monhystrrella</i>	-	-	-	-	-	-	-	-	-	-	0.1	10	-	-	
<i>Odontolaimus</i>	-	-	-	-	-	-	+	10	-	-	-	-	-	-	
<i>Panagrolaimus</i>	-	-	0.1	20	-	-	0.1	10	-	-	0.6	20	+	10	
<i>Paramphidelus</i>	0.1	10	0.1	20	-	-	-	-	-	-	-	-	1.3	50	
<i>Pelodera</i>	0.5	10	-	-	-	-	-	-	-	-	-	-	+	10	
<i>Plectus</i>	15.6	100	8.9	100	7.4	100	4.7	100	15.4	100	13.1	100	6.3	100	
<i>Prismatolaimus</i>	0.1	20	0.9	60	1.1	70	2.2	100	0.7	40	-	-	1.0	70	
<i>Prodesmodora</i>	0.1	10	+	10	0.1	10	0.4	40	+	10	-	-	0.2	30	
<i>Rhabditis</i>	-	-	0.1	10	-	-	-	-	-	-	0.4	20	-	-	
<i>Rhabdolaimus</i>	-	-	0.1	20	1.6	40	9.2	100	0.7	60	-	-	0.6	60	
<i>Seleborca</i>	-	-	+	10	-	-	1.7	70	-	-	-	-	0.1	20	
<i>Stenonchulus</i>	-	-	-	-	-	-	+	10	-	-	-	-	0.1	20	
<i>Teratocephalus</i>	1.0	70	3.4	70	5.6	100	2.4	100	1.6	100	1.7	80	1.6	60	
<i>Theristus</i>	-	-	-	-	-	-	-	-	-	-	-	-	+	10	
<i>Tylocephalus</i>	-	-	-	-	-	-	-	-	0.1	10	-	-	1.3	60	
<i>Wilsonema</i>	0.1	10	0.3	30	0.1	20	-	-	0.1	10	-	-	-	-	
Animal Parasites															
<i>Howardula</i>	-	-	-	-	-	-	-	-	0.3	10	-	-	-	-	
<i>Steinernema</i>	0.2	10	0.4	30	2.7	30	-	-	0.5	60	0.4	40	0.4	30	
<i>Mermithidae</i>	0.1	10	-	-	-	-	-	-	-	-	-	-	+	10	
Fungal Feeders															
<i>Aphelenchoïdes</i>	1.1	50	5.3	100	5.4	100	3.2	100	2.5	90	4.7	100	4.2	100	
<i>Aphelenchus</i>	-	-	-	-	0.4	10	0.05	10	-	-	0.1	10	-	-	
<i>Deladenus</i>	-	-	-	-	-	-	-	-	0.3	20	0.7	40	+	10	
<i>Diphtherophora</i>	0.6	30	0.8	70	0.3	60	0.6	50	1.8	70	0.3	40	0.1	40	
<i>Ditylenchus</i>	0.8	80	0.4	60	1.3	80	0.6	70	0.6	60	1.0	60	0.2	20	
<i>Dorylaimellus</i>	0.7	10	2.5	80	4.7	80	12.3	100	0.5	30	-	-	-	-	
<i>Hexatylus</i>	-	-	0.6	10	-	-	0.1	10	-	-	0.1	10	0.1	20	

<i>Nothotylenchus</i>	-	-	0.8	50	+	10	-	-	-	-	0.1	10	-	-
<i>Paraphelenchus</i>	-	-	-	-	+	10	0.1	10	+	10	0.0	0	-	-
<i>Pseudhalenchus</i>	0.1	10	0.4	40	0.6	20	0.6	50	0.3	40	0.1	10	-	-
<i>Safianema</i>	-	-	+	10	1.4	100	0.3	50	1.3	70	-	-	-	-
<i>Tylencholaimellus</i>	-	-	-	-	-	-	0.05	10	-	-	-	-	-	-
<i>Tylencholaimus</i>	2.3	50	7.1	100	5.7	80	18.9	100	10	100	2.8	60	33.3	100
<i>Tyloclaimophorus</i>	0.1	10	0.8	40	-	-	0.2	20	-	-	-	-	-	-
Omnivorous														
<i>Allodorylaimus</i>	0.2	30	0.3	10	0.7	60	0.5	40	0.8	30	0.5	40	+	10
<i>Aporcelaimellus</i>	5.8	90	12.5	100	16.7	100	11.8	100	15.3	100	1.7	80	8.1	100
<i>Aporcelaimus</i>	0.7	30	1.3	100	0.4	70	0.3	50	2.7	80	2.8	90	0.5	50
<i>Dorylaimoides</i>	0.2	20	1.4	70	1.5	90	2.9	90	0.4	60	0.2	10	1.0	50
<i>Enchodelus</i>	0.9	40	0.1	20	0.1	10	-	-	0.1	20	0.2	30	0.2	40
<i>Epacrolaimus</i>	0.2	10	-	-	-	-	-	-	-	-	-	-	-	-
<i>Epidorylaimus</i>	-	-	-	-	+	10	1.1	30	0.4	40	-	-	0.4	40
<i>Eudorylaimus</i>	12.2	100	4.6	90	2.1	90	3.2	90	9.4	100	5.6	100	7.8	80
<i>Labronemella</i>	-	-	-	-	1.4	60	0.6	70	0.5	20	-	-	-	-
<i>Metaporcelaimus</i>	7.3	100	7.6	100	6.2	100	+	10	8.9	90	15.6	100	+	10
<i>Microdorylaimus</i>	-	-	-	-	-	-	-	-	-	-	-	-	0.7	60
<i>Morasia</i>	-	-	-	-	-	-	+	10	-	-	-	-	-	-
<i>Oonaguntus</i>	-	-	0.9	60	0.3	50	-	-	-	-	-	-	+	10
<i>Thonus</i>	5.9	80	7.5	80	1.1	50	-	-	5.1	50	11.5	100	2.3	80
Plant Feeders														
<i>Rotylenchus</i>	0.1	10	0.6	20	0.4	30	-	-	-	-	-	-	-	-
<i>Pratylenchoides</i>	-	-	-	-	0.1	10	-	-	+	10	-	-	-	-
<i>Pratylenchus</i>	-	-	-	-	0.1	10	0.8	70	0.5	40	-	-	0.2	10
<i>Helicotylenchus</i>	4.3	40	0.5	50	2.2	60	1.7	40	0.1	10	1.0	50	+	10
<i>Amplimerlinius</i>	-	-	-	-	-	-	-	-	-	-	-	-	0.1	10
<i>Bitylenchus</i>	-	-	-	-	0.1	10	0.1	10	-	-	-	-	-	-
<i>Cephalenchus</i>	-	-	0.2	30	0.1	20	0.1	10	0.4	30	-	-	-	-
<i>Criconemooides</i>	-	-	-	-	-	-	-	-	-	-	0.1	10	+	10
<i>Longidorella</i>	2.4	30	0.2	10	-	-	-	-	-	-	-	-	1.8	70
<i>Longidorus</i>	-	-	-	-	+	10	-	-	-	-	-	-	-	-
<i>Merlinius</i>	0.8	30	0.1	20	1.3	30	+	10	0.1	20	-	-	-	-
<i>Mesocriconema</i>	0.1	10	0.1	30	0.2	30	2.9	80	-	-	-	-	-	-
<i>Nagelus</i>	-	-	0.2	10	-	-	-	-	-	-	-	-	+	10
<i>Paratylenchus</i>	0.8	50	1.6	80	1.5	60	1.3	80	1.2	90	1.7	70	-	-
<i>Pungentus</i>	-	-	0.2	20	-	-	-	-	-	-	-	-	+	10
<i>Trichodorus</i>	-	-	-	-	-	-	-	-	-	-	-	-	0.6	20
<i>Tylenchorhinchus</i>	+	10	+	10	0.3	30	2.5	80	-	-	-	-	0.1	10
<i>Basiria</i>	0.1	10	0.5	70	0.5	40	0.1	10	-	-	-	-	0.2	40
<i>Coslenchus</i>	0.4	40	-	-	1.1	50	-	-	0.4	10	0.1	10	+	10
<i>Filenchus</i>	-	-	1	80	0.2	20	0.5	70	+	10	0.3	40	0.3	30
<i>Malenchus</i>	-	-	+	10	-	-	-	-	-	-	1.7	50	3.6	60
<i>Miculenchus</i>	-	-	-	-	0.7	10	0.3	30	0.1	20	-	-	0.1	20
<i>Ottolenchus</i>	-	-	0.5	30	0.6	40	0.1	20	0.2	40	-	-	-	-
<i>Tylenchus</i>	4.4	80	1.3	70	3.1	100	2.4	90	3.7	100	4.5	100	1.4	90
Predators														
<i>Nygolaimus</i>	0.1	10	-	-	-	-	+	10	-	-	-	-	-	-
<i>Paravulvus</i>	0.4	20	-	-	0.2	20	5.9	90	-	-	-	-	0.7	40
<i>Clarkus</i>	3.7	70	2	50	-	-	-	-	-	-	-	-	0.1	20

<i>Coomansus</i>	9.9	80	-	-	-	-	+	10	3.4	90	18.7	100	0.4	10
<i>Mylonchulus</i>	-	-	-	-	+	10	-	-	-	-	-	-	0.8	70
<i>Prionchulus</i>	-	-	-	-	-	-	-	-	-	-	-	-	0.2	30
<i>Solididens</i>	0.1	10	+	10	-	-	0.2	30	-	-	-	-	-	-
<i>Tripyla</i>	5	60	-	-	0.3	20	-	-	+	10	3.3	70	-	-
Actinolaimoidinae	0.1	10	-	-	-	-	-	-	-	-	-	-	-	-
Dauer larvae	0.5	50	1.4	70	0.1	10	-	-	0.4	30	1.9	60	0.7	90
unidentified	-	-	+	10	0.1	20	-	-	-	-	+	10	+	10

Note: Values less than 0.05 marked with '+'.

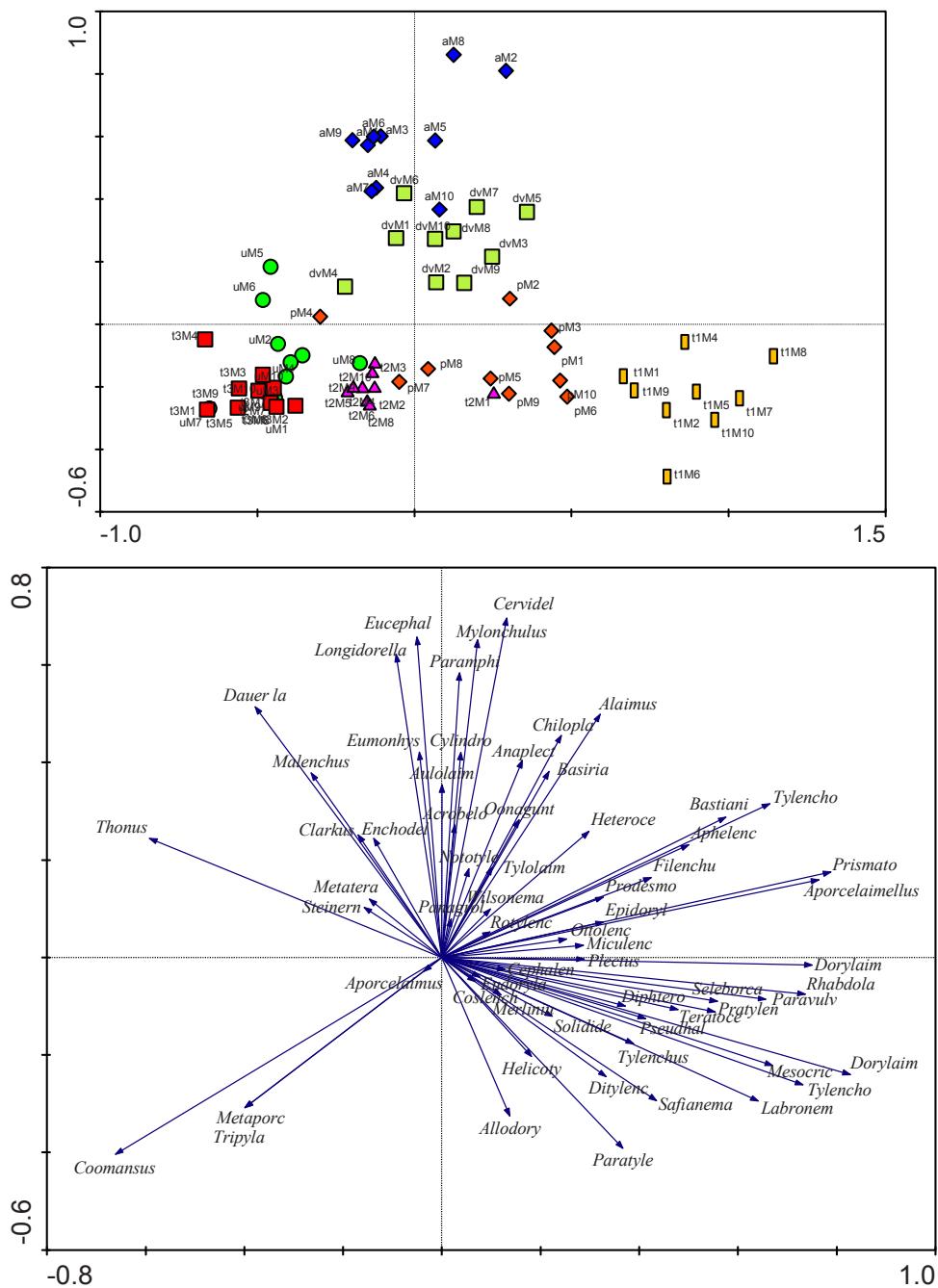


Fig. 1. Principal Component Analysis of the nematode communities based on generic abundance data:
A - sites (abbreviations are the same as in Table 1); B - generic distribution

Analysis, presented separately at Fig. 1a and Fig 1b, for sites and genera, respectively. The three ordination axes explain 39 % of the variance of generic composition data. The first axis of the PCA (eigenvalue 0.210) represents a gradient from sites with the lowest abundance and diversity (uM, t3M, t2M) to sites with more diverse and numerous nematode communities (pM, dvM, aM and t1M) (see also Table 3). Further, the second axis of the PCA (0.091) divided the the sites of higher human impact - in close vicinity to ski runs (t3M, uM, t2M, pM and t1M), from those that were non disturbed (aM and dvM). The nematode communities of the latter two sites also formed well

distinguishable groups at the third ordination axis (0.084, figure not included), which revealed specific genera occurring at one of the two sites (Table 2). Among the common genera, *Alaimus*, *Aporcelaimus*, *Diphtherophora*, *Filenchus*, *Heterocephalobus* and *Metaporcelaimus*, prevailed significantly at dvM site ($p < 0.05$) and *Eucephalobus*, *Malenchus* and *Tylencholaimus* - were significantly more abundant at aM site ($p < 0.05$).

Classification procedure performed with the Sørensen percentage similarity index (**Ics*b) showed similar patterns (Fig 2). Two main groups of sites (clusters 1 and 2) represented a pattern close to the arrangement of the sites

Table 3. Community parametres of nematode assemblages from seven *P. mugo* sites: mean relative abundance (numbers per 100 cm³ fresh substrate), generic richness, the Shannon-Wiener diversity index (H') and Simpson's dominance index (C), trophic groups, colonizer-persistor (cp and pp) groups, the maturity indices (MI, ΣMI, MI 2-5 and PPI), Channel (CI), Enrichment (EI) and Structure index (SI).

	Yulen		Dolno Vassilashko lake		Plato		Todorka 1		Todorka 2		Todorka 3		Academica		
	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD	
Mean abundance	177	69.6	a	727	244	b	988	828	b	2257	1589	c	357	227	d
Generic richness	20	6.6	a	30	5.38	b	27	5.05	b	26	2.85	b	22	3.8	a
H'	2.30	0.38	ac	2.66	0.32	b	2.50	0.30	abc	2.52	0.16	ab	2.27	0.41	bc
C	0.15	0.05	abc	0.11	0.05	a	0.14	0.06	abc	0.12	0.03	abc	0.17	0.12	abc
Trophic groups															
Sum PF	9.2	11	a	5.7	4.1	a	9.3	7.6	a	10	11	a	3.1	2.2	b
PFb	0	0	a	0	0	a	0.2	0.5	ab	0.8	1	b	0.5	0.9	bc
PFc	4.5	9.2	a	1.1	2.1	a	2.5	4.5	a	1.7	4.2	ab	0.1	0.2	b
PFd	4.3	4.6	a	3.1	3.5	a	4	3.6	ab	7	7.4	b	1.7	1	a
Pfe	0.5	0.7	a	1.6	1.1	b	2.5	3.3	ab	0.9	1	ab	0.7	1.4	a
PFf (= AF)	4.4	9.4	a	1.3	1	a	3.1	2.7	ab	2.4	2	ab	3.7	3.7	ab
BF	28	11	ab	34	12	a	34	16	a	24	10	ab	28	16	ab
FF	5.7	6.3	a	19	8	b	20	12	b	37	8.3	c	17	11	bd
O	33	14	ac	36	16	a	31	16	abc	20	7.2	bc	44	18	a
PR	19	12	a	2.1	2.9	bc	0.4	0.8	b	6.2	6.4	c	3.4	3.9	c
AP	0.3	0.8	ab	0.4	0.8	ab	2.7	8	ab	0	0	a	0.8	0.2	b
DL+U	0.5	0.7	a	1.5	1.9	a	0.2	0.4	b	0	0	b	0.4	0.7	bc
Colonizer -Persistor groups															
cp 1	0.6	1.7	ab	0.7	1	a	0	0	bc	0.3	0.5	ac	0	0	bc
cp 2	23	13	ad	30	16	a	34	23	ad	12	5.7	bc	29	18	ad
cp 3	7.1	9.1	ac	6.3	5.1	ac	9.3	5.9	ab	16	11	b	5.4	3.6	ac
cp 4	39	15	ac	30	14	ac	14	7	b	28	7	a	30	15	ae
cp 5	15	14	ac	24	15	ab	28	15	ab	31	7.8	b	27	21	ab
pp 2	5.7	9	a	5.1	3.4	ab	7.8	6.3	ab	4.9	2	a	6.1	4	ab
pp 3	5.4	9.2	ab	1.5	2.1	a	4.6	7.6	abc	8.1	11	b	0.7	1	cd
pp 4	2.4	4.4	ab	0.4	0.7	a	0	0	a	0	0	a	0	0	a
pp 5	0	0	a	0	0	a	0	0.1	a	0	0	a	0	0	a
MI	3.51	0.35	a	3.47	0.45	a	3.43	0.6	a	3.89	0.18	b	3.60	0.52	ab
ΣMI	3.38	0.37	a	3.39	0.44	a	3.30	0.56	a	3.72	0.15	b	3.50	0.51	ab
MI 2-5	3.55	0.35	a	3.53	0.46	a	3.44	0.6	a	3.9	0.18	b	3.61	0.52	ab
PPI	2.51	0.38	abc	2.30	0.25	b	2.33	0.34	cbd	2.56	0.21	cb	2.09	0.11	d
CI	79.8	38.1	abc	54.3	33.2	ac	94.3	18.1	b	85.8	25.6	bd	88.3	20.1	bd
EI	12.9	18.4	a	33.6	13.8	b	22.6	7.65	cd	31.8	11	b	19.3	14.1	ac
SI	91.3	5.84	a	87.6	12.1	a	82.3	20.5	a	95.7	1.63	b	89.8	8.07	ab

Feeding types: Plant-feeding (PF, a-f subgroups according to Yeates *et al.*, 1993), algal-feeding (AF), bacterial-feeding (BF), fungal-feeding (FF), omnivores (O), predators (PR), animal parasites (AP), Dauer larvae and unidentified (DL+U); in a given line numbers followed by different letters differ significantly ($p < 0.05$, M-W test). The mean relative abundance for the trophic and c-p groups was expressed as % from 100 cm³ soil.

along the first ordination axes by the PCA method. Nematode assemblages from the dvM site were most similar with those from pM and t2M sites (65 and 63 %, respectively). On the contrary, the greatest dissimilarity was exhibited between the nematode communities of t1M plot compared with t3M (23 %) and uM (27 %) sites.

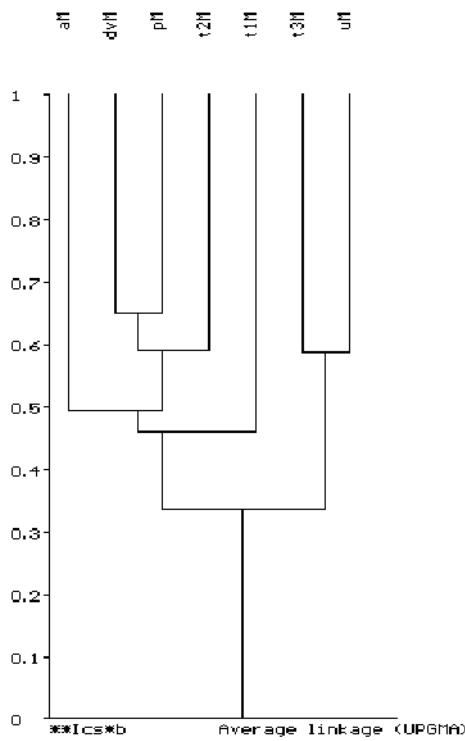


Fig. 2. Dendrogram (UPGMA) representing the classification of the studied *P. mugo* sites.

Functional groups and community indices

The relationships among the different ecological parameters (functional groups, indices, etc.) and the nematode assemblages' distribution along the first and second axes of the ordination biplot are presented on the Fig. 3. The communities of uM, t2M, t3M sites can be characterised with lowest nematode abundance, generic richness and Shannon diversity index (see Table 3 for details). Two of them (t2M and t3M) were situated next to the ski runs, while uM was close to a touristic tour pathways located in a stony area on a steep slope. Among the communities having significantly higher abundance, richness and diversity, two were next to the ski runs (pM, t1M), while the other two were situated in areas being under low anthropogenic pressure (dvM and aM). In comparison, the nematode communities from Vitosha, also located in vicinity of ski runs, exhibited the lowest values for the relative abundance and diversity - av. 327 specimens/200 cm³ soil, av. 1.91 for H' and av. 15 genera per sample (Lazarova, 2000).

Trophic group distribution varied significantly among the studied sites. In general, the communities of all plots had a high proportion of omnivorous (aver. values 20 – 44 %) and bacterial feeding (18 – 34 %) nematodes. Furthermore,

plant feeders (groups belonging to 1b-e) were with relatively low abundance in all sites (aver. values 3.1 – 10 %, lower values assigned to t2M and t3M sites). Some assemblages were dominated by fungal feeders (37 and 38 % for t1M and aM, respectively) but in others the proportion of predators was significantly higher (19 and 22 % for uM and t3M). These sites represented communities with the lowest relative abundance and generic richness, coupled with the highest proportion of omnivorous nematodes (33, 38 and 44 % for uM, t2M and t3M).

Similarly, omnivorous and bacterial feeding nematodes dominated the nematode communities from Vitosha Mt., although their trophic structure showed a characteristic feature - predators and plant feeders were present in similar proportions (ca. 20 %), while fungal feeders had very low number (Lazarova, 2000). In contrast to these observations, in the *P. mugo* site from Rila Mt. the plant and bacterial feeding nematodes prevailed (30 and 27 %), and the other trophic groups were presented in comparable shares (16, 14 and 12 % for predatory, fungal feeders and omnivorous nematodes) (Ilieva, 2007). These differences could be addressed to the seasonal variations – the samples from Rila site have been collected in autumn.

The bacterial feeders and omnivorous nematodes were represented by the highest number of genera, the generic richness of the first group varying in wide ranges (Fig. 4). The distribution of colonizer-persistor groups exhibited higher resemblance among sites for both free-living and plant-feeding nematode taxa (Table 3). The proportion of enrichment opportunists (cp1) was very low for all sites, while the general opportunists (cp2) were well presented

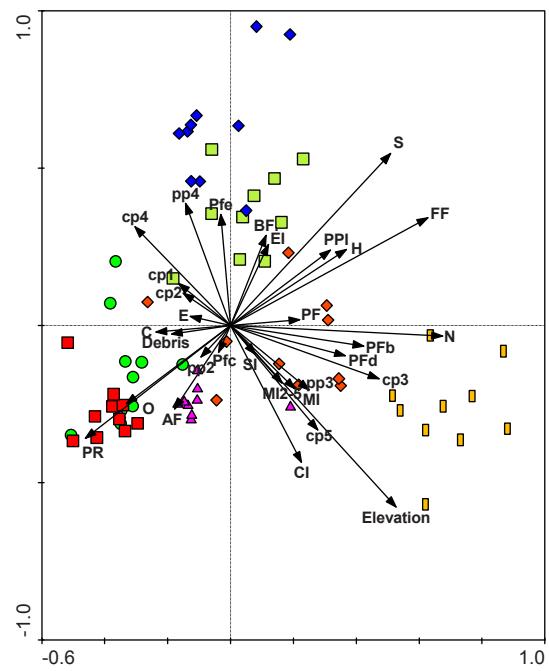


Fig. 3. Principal Component Analysis of the relationship between the ecological parameters (functional groups and indices) and the nematode assemblages' distribution (abbreviations are the same as in Table 3.).

(12 – 34 %) and even dominated in some sites (dvM and pM). The overall abundance of persistors (cp4 and cp5) was generally high (42 – 64 %). The cp4 group of nematodes dominated at several sites (uM, t2M, t3M) and prevailed significantly at aM (55 %), while nematodes of cp5 reached the highest relative abundance (31 %) at t1M. The generic richness of two life strategy groups (cp4 and pp2) had higher average values for all plots (Fig. 5).

blages from Rila, which had the highest reported value (2.71).

Further, the variations of the average values for enrichment and structure indices fall in very narrow limits (EI, 12.9 – 36.5 and SI, 82.3 – 95.7). Data from each replicate plotted along the enrichment and structure trajectories related most of *P. mugo* sites to C quadrant (Ferris et al., 2001). Thus, using functional guilds, the soil food webs in the studied

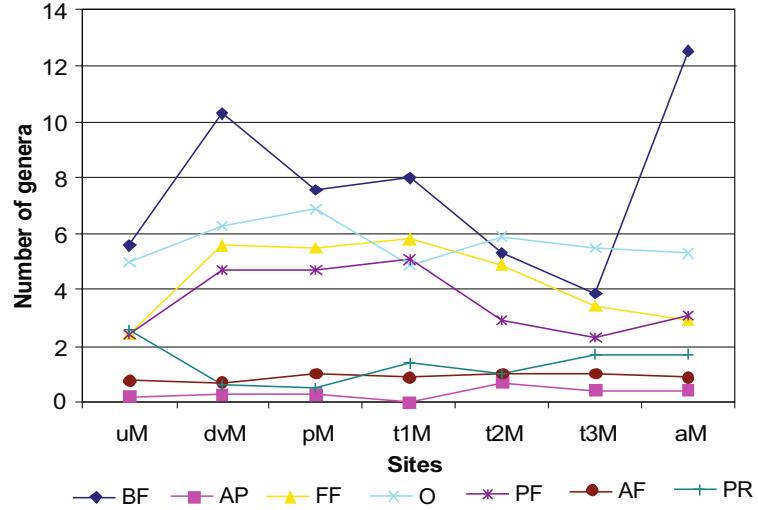


Fig. 4. Generic richness of nematode trophic groups inhabiting Mountain Pine.

The indices characterising the maturity of nematode communities (MI, Σ MI, MI2-5) showed similar trends of variation among sites with significantly higher values detected for t1M site ($p < 0.05$, Table 3). Sites having communities with the lowest nematode abundance and diversity (t2M, t3M) revealed the lowest PPI values compared to the other sites. The values of the maturity indices recorded in previous investigations (Lazarova, 2000; Ilieva, 2007) varied within the ranges revealed for the majority of plots at Pirin Mt, excluding PPI for assem-

plots can be characterised as structured, environment as undisturbed, with low to moderate enrichment (resource-limited) and stable. Similar soil food web conditions were identified in *P. mugo* site at Vitosha Mt (Lazarova, unpublished), while on Rila Mt the food web has been characterised as maturing (Ilieva, 2007). On the opposite to SI and EI, Channel index (CI) varied considerably among the studied sites (Table 3) with lowest and highest values belonging to aM and pM sites, respectively (av. 41.3 vs 94.3). Consequently, the decomposition soil food webs in most of

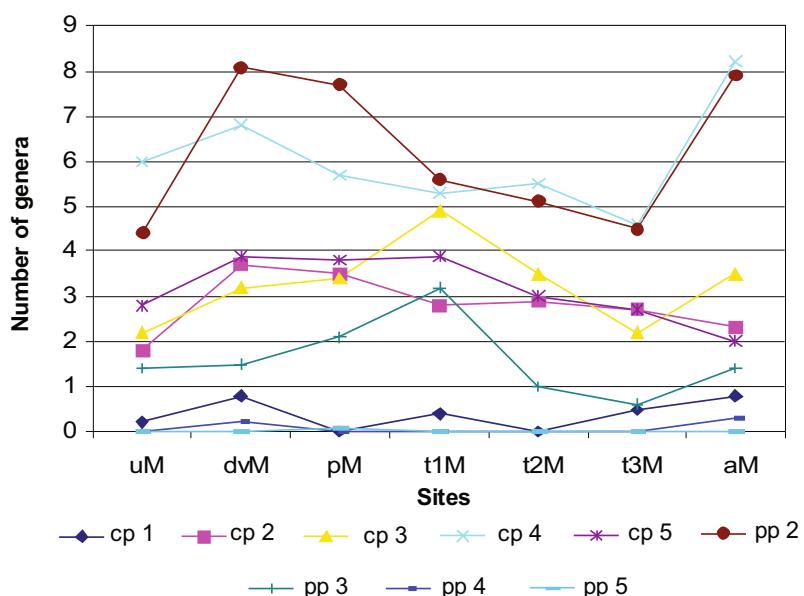


Fig. 5. Generic richness of nematode functional groups inhabiting Mountain Pine.

the sites were dominated by fungal feeders. On the basis of CI, only two plots (dvM and aM) exhibited similarity with *P. mugo* site from Rila Mt (Ilieva, 2007), which reflected the nature of the decomposition pathway dominated by bacterial feeding nematodes.

Concluding remarks

Nematode communities of *P. mugo* habitat from northern Pirin Mountain are very diverse. Although the trophic structure differed among sites, it was dominated by omnivorous and bacterial feeders coupled with a low proportion of plant feeding nematodes. The high values of Maturity indices, and significant participation (key position) of persistors indicated a relative stability of the environment and undisturbed conditions in all sites. This was supported by the nematode faunal analysis characterising the decomposition channels as fungal dominated and food web as structured, the habitat -undisturbed with limited resources. Further, three types of marginal sites can be differentiated: the first represented assemblages with the lowest relative abundance and generic richness, dominated by omnivorous and predatory nematodes; the second one - with the highest abundance, dominated by fungal feeders and the third one with the highest generic richness and strong prevalence of persistors. The rest of the sites occupied an intermediate position regarding community parameters and indices. No clear correlation between the nematode assemblages' characteristics and the proximity of the site to the ski runs was observed.

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