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Single-tree selection system effects on forest soil macrofauna biodiversity in mixed oriental beech stands

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ABSTRACT

Hyrcanian temperate forests are of importance due to their genetic variation, biodiversity, commercial productions and many other ecosystem services. Over the past decades the selection silvicultural system (mostly single-tree selection) has been the dominant method to manage and utilize these forest ecosystems. This study aimed to assess the effect of single-tree selection silvicultural system on mixed beech stands of eastern Hyrcanian temperate forests using soil macrofauna as bioindicator. Therefore 91 forest treefall gaps have been selected of which 36 gaps were natural gaps in managed stands, 41 gaps were human created gaps and 14 gaps were natural gaps in virgin stands. In each gap 3 soil profiles and in each profile 3 soil samples were taken at 3 depths, including litter layer, shallow (0–10 cm) and deep (10–20 cm) soil. Macrofauna of all soil samples were extracted and identified to class level and weighed. Diversity (Shannon and Simpson) and evenness indices were calculated for all soil samples. Results showed that most important macrofauna based on biomass were Clitellata, Gastropoda, Chilopoda and Diplopoda in the study area. In the litter layer of all gaps Gastropoda (snails) have the most amount of biomass followed by Chilopoda (millipedes), while in shallow and deep soil Clitellata (earthworms) and Chilopoda were the main classes based on biomass. There was no significant difference in diversity and evenness indices among the three gap groups (virgin, natural and artificial) which indicates that the single-tree selection system has not intensive and irrecoverable effects on the soil macrofauna of the studied forest stands after about 10 years.

1. Introduction

Hyrcanian temperate forests are broad-leaved deciduous forests covering southern and south-western coasts of Caspian Sea. They are unique in biodiversity, commercial productions and many other ecosystem services (Behjou et al., 2009; Poorzady and Bakhtiari, 2009; Pourmajidian and Rahmani, 2009; Sagheb-Talebi et al., 2004, 2014). Oriental beech (*Fagus orientalis* Lipsky) and common hornbeam (*Carpinus betulus* L.) trees compose 54% of stem number and 60% of standing volume of these forests. Due to the importance of beech forests among Hyrcanian forests, most of the studies on these ecosystems were done in beech stands (Sagheb-Talebi et al., 2014).

Over the past decades the selection silvicultural system (mostly tree-selection) has been the dominant method to manage and utilize these forest ecosystems and replaced the classic methods such as the shelterwood system (Pourmajidian and Rahmani, 2009; Sagheb-Talebi et al., 2014). The selection silvicultural system is a method of tree harvesting in which one (tree-selection) or a few (group-selection) numbers of trees are being cut at each intervention. Regarding the uniqueness of Hyrcanian temperate forests (Akhani et al., 2010; Browicz, 1989; Karami et al., 2012; Sagheb-Talebi et al., 2014), assessing the impacts of this recent silvicultural system on these forest ecosystems is of importance.

The soil macrofauna community has been used as a bioindicator of temperate forest ecosystem condition and change and for monitoring the responses of ecosystems to forest management practices (Antunes et al., 2008; Bird et al., 2004, 2000; Curry and Good, 1992; Donegan et al., 2001; Gerlach et al., 2013; Hoekstra et al., 1995; Moffat, 2003).

This study aimed to assess the effect of the tree-selection silvicultural system on mixed beech stands of Hyrcanian temperate forests using soil macrofauna as bioindicator.

2. Materials and methods

2.1. Study site

This investigation was done in Dr. Bahramnia (Shast Kalate) Forest, the experimental forest of the Gorgan University of Agricultural

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Table 1
The gap size status in the study area.

	Minimum	Maximum	Mean	Std. Deviation
Virgin gaps	10	329	87	92.3
Natural gaps	12.1	422	116.2	89.6
Artificial gap	8	373.6	120.4	112.1
Total	8	422.3	114.31	98.83

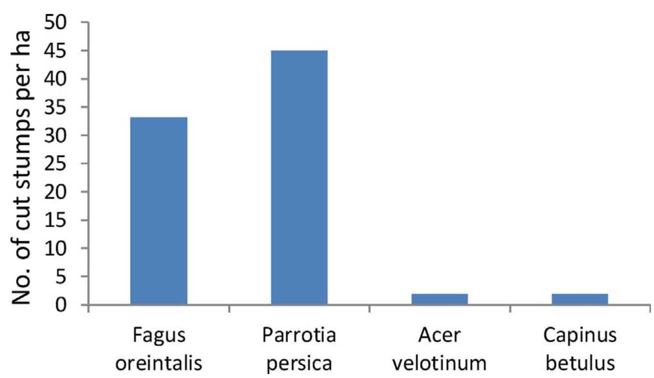

Fig. 1. Species composition of cut trees in artificial gaps.

Table 2
Main soil macrofauna groups found in the study site.

Phylum	Subphylum	Class
Arthropoda	–	Insecta
	Myriapoda	Chilopoda
		Diplopoda
	Crustacea	Malacostraca
	–	Arachnida
Annelida	–	Clitellata
Mollusca	–	Gastropoda

Sciences and Natural Resources (GUASNR). A natural mixed deciduous semi-mountain forest is located on northern slopes of the Alborz mountain in the north of Iran (36°41′–36°45′N and 54°20′–54°24′E), covering an area of about 3716 ha and the altitude ranging from 100 to 1000 m above sea level. This forest is a part of the Hyrcanian forests and receives about 650 mm precipitation annually. Also according to Izadi et al. (2017) Soil types of the study area based on WRB classification are “Chromic Cambisols including Cambisols with having base saturation more than 50% at depth of 20–50 cm, with a Cambic B horizon”, with a mostly sandstone bedrock.

2.2. Sample collection

In order to assess the effects of tree-selection system on soil macrofauna biodiversity in the mentioned forest compartments 27 and 28 were selected with an area of 68 and 51 ha, respectively, in which tree-selection cutting was executed from 1997 to 2006. Also 16 ha of unmanaged virgin stands in the adjacent compartment 32 were selected as control. The mentioned compartments are mostly covered with *Fagus orientalis* Lipsky (Oriental Beech), mixed with *Parrotia persica* (DC.) C.A. Mey (Persian iron wood tree) and *Carpinus betulus* L. (common hornbeam). Then in compartments 27 and 28, the managed compartments, 36 natural and 41 human created (cut) treefall gaps were randomly selected. Also 14 natural gaps were chosen in the unmanaged virgin stands of compartment 32. We briefly name the first 36 natural gaps in managed stand as “natural gaps”, the next 41 human-created gaps in managed stands as “artificial gaps” and the last 14 gaps in unmanaged stand as “virgin gaps”. The area of each gap was calculated by measuring the longest and shortest axes of an ellipsoid (Runkle, 1982). All dead trees inside the gaps were recorded. Also tree species cutting of which caused the formation of artificial gaps were (if possible) identified based on remaining stumps. Also in order to assess the effect of gap opening size on macrofauna biodiversity, gap opening sizes have been divided in 5 classes including under canopy cover, smaller than 50, 50–100, 100–200 and 200–400 m^2.

Within each gap 3 soil profiles were sampled in summer using a 10 × 10 cm metal frame, one sample at the gap center and two others at one meter distance from the gap center (on different sides of the center) and all on the longest axis of the gap. In each profile soil samples were taken at 3 depths, including litter layer, shallow (0–10 cm) and deep (10–20 cm) soil. A total of 91 gaps, 91 × 3 soil profiles = 273 profiles and 273 × 3 depth levels = 819 soil samples were studied. Soil samples were packed and transported to the soil lab of GUASNR where macrofauna were extracted by hand sorting (Coleman et al., 2004). The macrofauna extracted from each sample were identified to class level, counted, dried and weighed to milligram for the calculation of biomass.

2.3. Data analysis

Diversity (Shannon and Simpson) and evenness indices were used as indicators of macrofauna biodiversity. The mentioned indices were calculated using PAST 2.06 software. Statistical analyses and comparisons were done using SPSS 16 software. Parametric analyses were done by Analysis of Variances (ANOVA) and non-parametric analyses were done by Kruskal-Wallis test.

3. Results

The gap size status in the study area is shown in Table 1. According to this census the smallest gap studied measures 8 m^2 and the biggest one 402 m^2. The mean gap size is 114.3 m^2.

Results showed that among the total volume of recorded dead trees, 89% were laid down dead trees and 11% standing dead trees. Also among trees cutting of which caused the creation of artificial gaps *Parrotia persica* was the most abundant species (54%) followed by *Fagus orientalis* (42%) (Fig. 1).

Among the extracted soil macrofauna 3 phylums and 7 classes of soil macrofauna were identified (Table 2). The phylum Arthropoda with 5 classes can be considered as the main phylum among soil macrofauna in the study area.

Results also showed Arthropoda, Clitellata, Gastropoda, Chilopoda, Diplopoda and Malacostraca were the main macrofauna classes by abundance and Clitellata, Gastropoda, Chilopoda and Diplopoda were the main macrofauna classes by biomass. The other classes had a very small abundance and biomass per unit area and therefore have been neglected in the following figures. In the litter layer of all gap classes Diplopoda have the highest amount of abundance per unit area while in shallow (0–10 cm) and deep (10–20) soil Clitellata were the most abundant class (Fig. 2). In the litter layer of all gap classes Gastropoda (snails) have the highest amount of biomass per unit area followed by Diplopoda (millipede). In shallow (0–10 cm) and deep (10–20 cm) soil Clitellata (earthworms) have the highest amount of biomass again followed by Diplopoda (Fig. 3a).

Results of ANOVA showed that biodiversity indices were not significantly different among the three gap groups (Table 3) while there