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三峡库区 2 种马尾松混交林土壤团聚体酶活性分布特征

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摘要:选取三峡库区典型马尾松杉木混交林和马尾松杉木栎类混交林为研究对象,对其表层土壤(0—10 cm) 3 种团聚体等级(大团聚体(>2 mm),中团聚体(0.25—2 mm),微团聚体(<0.25 mm))分布特征,团聚体 5 种水解酶活性(β -葡糖苷酶,酸性磷酸酶,N-乙酰-葡糖苷酶,纤维二糖水解酶,亮氨酸氨基肽酶)和 2 种氧化还原酶活性(多酚氧化酶和过氧化物酶),以及团聚体酶活性与团聚体有机碳、全氮、全磷、碳氮比的关系进行了分析,旨在理解不同马尾松混交林类型下土壤团聚体及其酶活性的分布特征,为科学制定营林措施提供基础数据。结果表明:(1)各等级土壤团聚体分布随着粒径的增加而呈现显著增加的趋势,其中大团聚体所占比例最高,为 60%左右;马尾松杉木混交林的中团聚体分布比例(39.53%±1.65%)显著高于马尾松杉木栎类混交林(32.24%±2.51%);(2)微团聚体 5 种水解酶活性、有机碳含量以及全氮含量最高,而大团聚体中 2 种氧化还原酶活性最高;(3)马尾松杉木栎类混交林大团聚体和微团聚体纤维二糖水解酶、亮氨酸氨基肽酶、土壤酶活性几何平均数、土壤碳氮比均显著高于马尾松杉木混交林;团聚体全氮含量的差异是造成上述酶活性差异的主要原因。马尾松杉木栎类混交林中栎类阔叶树种的增加显著提高了土壤团聚体酶活性,有利于土壤养分质量的提高。

关键词:土壤酶活性;马尾松混交林;团聚体;土壤酶活性几何平均数

Distribution of enzymatic activities within soil aggregates in two types of *Pinus massoniana* mixed plantations in the Three Gorges Reservoir area

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Abstract: Soil enzymes, which were secreted by soil microorganisms, play important role in soil nutrients cycles through mediating the degradation, transformation and mineralization of soil organic matter. And soil aggregate structure can affect the soil enzyme activities by influencing microbial activities and accessibility of soil organic matter. Thus, study of soil enzyme activities on an aggregate level could provide insight into nutrient cycling and could also be used as sensitive indicators for soil fertility. *Pinus massoniana* Lamb., as the top 5 plantation species in China, is also the main vegetation type with key ecological and economic importance in the Three Gorges Reservoir Area, China, but the productivity of

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P. massoniana forests is low due to extensive management. Quantifying the enzymatic activities within soil aggregates in *P. massoniana* forests could provide basic data for forest managements in this area. Hence, in this study, we chose two typical mixed *P. massoniana* plantations in the Three Gorges Reservoir area, *P. massoniana* and *Cunninghamia lanceolata* mixed plantations (MS) and *P. massoniana*, *C. lanceolata* and *Quercus* mixed plantations (MH), as the objects. The soil samples in top 10 cm were collected from six 20 m × 20 m plots (three plots in each mixed plantation) to test distribution of soil aggregate (i.e. large macroaggregates (>2 mm), small macroaggregates (0.25—2 mm), and microaggregates (<0.25 mm)) through modified dry-sieving method, and to analyze the activities of 5 hydrolases (i.e. soil β -glucosidase, cellobiohydrolase, N-acetyl-glucosaminidase, acid phosphatase and leucine aminopeptidase) and 2 oxidase (phenoloxidase and peroxidase) within soil aggregates. The relationships between soil enzymes activities, soil nitrogen, soil organic carbon, soil total phosphorus and soil carbon to nitrogen ratio within aggregate were also observed. The results showed that: 1) the distribution of soil aggregates significantly increased as the aggregate size increased in both two mixed plantations, and the proportion of large macroaggregates was the highest, which accounting for 60% in the soil. The distribution of small macroaggregates was significantly higher in MS (39.53%±1.65%) than that in MH (32.24%±2.51%) but no significant differences were found in other two aggregate sizes. 2) The activities of 5 hydrolases, soil organic carbon and soil total nitrogen were higher in microaggregates than those in other two aggregates, while the activities of 2 oxidase were highest in large macroaggregates in both two mixed plantations. 3) The activities of cellobiohydrolase and leucine aminopeptidase, geometric mean of soil enzymes activities and soil carbon to nitrogen ratio in large macroaggregates and microaggregates were significantly higher in MH than those in MS, and variation of soil nitrogen within soil aggregates attributed to the significant differences of soil enzymes discussed above. Our results indicated that *Quercus* in MH improved the enzymatic activities within soil aggregates and was beneficial to improvement of soil fertilities in the study area.

Key Words: soil enzyme activities; *Pinus massoniana* mixed plantations; soil aggregates; geometric mean of soil enzymes activities

土壤酶作为有机质分解、周转和矿化的主要生物催化剂^[1],是土壤中碳、氮、磷等养分循环的重要参与者^[2]。不同的土壤酶参与不同的生态化学过程,如广泛研究的 β -葡糖苷酶(β -glucosidase, BG)主要参与碳循环,水解纤维素,释放葡萄糖^[3],N-乙酰-葡糖苷酶(N-acetyl-glucosaminidase, NAG)主要参与氮循环,分解几丁质^[4],酸性磷酸酶(Acid phosphatase, AP)则主要影响无机磷的产生,催化水解有机磷转化为无机磷^[5]。土壤酶受多种因素的影响^[1,6-7],且对生态环境系统的变化非常敏感,其活性的改变可直接引起土壤群落代谢过程和可利用养分的变化^[8-9],进而影响养分循环和植物生长,是评价土壤地力变化的重要指标^[4,10]。而土壤团聚体是土壤结构的基本单元,通过控制不同粒径团聚体有机质的可接触性、微生物群落组成、水分等因素直接影响着土壤酶的活性^[11-12]。团聚体分布及其土壤酶活性的高低能够较未进行土壤团聚体分级的混合土壤更为有效、快速的反映土壤养分循环的变化^[12-14]。因此,了解团聚体酶活性变化特征,对掌握土壤养分变化和地力维持能力具有重要的指示作用。

马尾松(*Pinus massoniana*)是我国人工林排名第3位的优势树种,主要分布在南方15个省(区),面积达220万 hm^2 ^[15],也是三峡库区分布面积最大的森林类型^[16]。缘于三峡库区复杂的地形及其所导致的自然气候特征的巨大空间分异性,以及强烈人为干扰和长期相对落后的经济社会发展水平,本区域马尾松林经营粗放,林分结构较差,低产林大面积存在,如何有效提高马尾松地力和生产力对于本区域森林经营十分重要。鉴于土壤团聚体酶活性对于环境变化、植被组成的敏感性^[11-12,14],从土壤团聚体微生境分析不同马尾松森林类型酶活性特征,对于深入探索不同马尾松林地力和生产力差异具有重要意义。然而,目前本区域马尾松林的研究多集中于混合土壤养分及其酶活性^[15]、土壤碳排放^[17-18]、凋落物分解^[19]等方面,土壤团聚体分布及其酶活性变化特征仍待解答。本研究以三峡库区分布面积最广的马尾松杉木混交林和马尾松杉木栎类混交林为

研究对象,分析不同马尾松混交林类型表层土壤(0—10 cm)团聚体分布特征及其酶活性的分布特征,以期为深入认识不同马尾松混交林地力差异和制定营林措施提供科学依据和基础数据。

1 研究区概况

研究地点位于湖北省秭归县(30°38′14"—31°11′31" N, 110°00′14"—111°18′41" E),海拔 156—2030.6 m,年均气温 16.9℃,年降水量 1000—1250 mm,多集中于 4—9 月,属于亚热带大陆性季风气候。土壤类型以黄壤、黄棕壤为主^[15]。选取本区域典型马尾松杉木混交林(MS)和马尾松杉木栎类混交林(MH)为研究对象(其中 MH 混交林中栎类树种主要为短柄枹栎(*Quercus serrata* var. *brevipetiolat*)、栓皮栎(*Quercus variabilis*)),分别设置 3 个 20 m×20 m 样地进行调查,共设置样地 6 个,样地基本情况见表 1。调查样地内灌木主要有火棘(*Pyracantha fortuneana*)、胡枝子(*Lepedeza bicolor*)、微毛柃(*Eurya hebeclados* Ling)等,草本主要有狗脊(*Woodwardia japonica*)、鱼腥草(*Houttuynia cordata* Thunb.)、苔草(*Carex tristachya*)等。

表 1 样地概况

Table 1 General situation of sampling sites

林分 Stand	马尾松杉木混交林 (MS) Mixed plantation of <i>P. massoniana</i> and <i>C. lanceolate</i>	马尾松杉木栎类混交林 (MH) Mixed plantation of <i>P. massoniana</i> , <i>C. lanceolate</i> and <i>Quercus</i>
坡度 Grade	6°	28°
坡向 Exposure	北	北
海拔 Altitude/m	921.00	545.00
胸径 Diameter at breast height/cm	10.57(1.12)	8.70(0.38)
林分密度 Stand density/(tree/hm ²)	3458.00(82.52)	3466.00(78.46)
凋落物层厚度 Litter layer depth/cm	3.81(0.18)	3.59(0.20)
凋落物现存量 Litter standing/(t/hm ²)	9.87(0.54)	8.73(0.63)
凋落物碳氮比 Litter C/N ratio	29.42(2.20)	28.33(1.36)
土壤 pH Soil pH	5.65(0.06)	5.62(0.03)
土壤含水量 Soil water content/%	32.00(2.52)	25.67(0.88)

括号内数值为标准误

2 研究方法

2.1 土壤样品采集与土壤团聚体筛分

2017 年 8 月,在 2 种马尾松混交林的每个固定样地内(每种林型 3 个固定样地,共计 6 个固定样地)按照“S”形随机设置 9 个 1 m×1 m 的观测小区使用直径 6 cm 的 PVC 管对观测小区内 0—10 cm 土壤采取 5 个原状土。采样后 12h 内带回实验室,按照土壤纹理轻柔掰开,去除可见的根系和石砾,过 8 mm 筛并将同一样地样品混合。为减少对土壤酶活性的影响,采用 Dornodnikov 等^[20]改良的干筛法进行土壤团聚体的筛分。将过 8 mm 的鲜土,每次称量 500 g,采用 AS200 震筛仪(德国莱达公司)2 mm,0.25 mm 土壤筛以振幅 1.5 mm 震动 3min,根据筛分粒径,将土壤团聚体从大到小分为大团聚体(>2 mm),中团聚体(0.25—2 mm)与微团聚体(<0.25 mm)3 个等级^[20],并对各级团聚体进行称重,用于计算各等级分布。

2.2 土壤有机碳、全氮与酶活性测定

筛分后的各团聚体土壤一部分风干后通过重铬酸钾外加热法测定土壤有机碳(Soil organic carbon, SOC)^[21],凯氏定氮法测定全氮(Total nitrogen, TN)^[22];一部分存于 4℃ 冰箱,于两周内进行土壤酶活性的测定。土壤酶活性测定方法:把相当于 1 g 干土的土壤样品加入至 125 mL 醋酸钠缓冲液(50 mmol/L, pH=5.5)中,在搅拌机中处理 1min 制成均质土壤悬液^[23-25],加入不同酶底物进行培养测定,底物、测定波长等信息详见表 2。本研究共测定了 7 种参与碳氮磷循环的酶活性,5 种水解酶活性采用荧光微孔板方法,25℃ 暗中培

养 3 h 后采用酶标仪(PerkinElmer Enspire, USA)进行测定^[23-24]; 2 种氧化还原酶活性采用比色法, 其中, 过氧化物酶通过添加底物 L-3,4-二羟基苯丙氨酸(L-3,4-dihydroxyphenylalanine, DOPA)和过氧化氢(浓度:3%)测定^[1], 氧化还原酶均室温震荡暗中培养 1h 后, 采用酶标仪进行测定^[24-25]。土壤酶活性的几何平均数^[26-27](Geometric mean, GMea)可用来综合评价土壤酶活性指标, 计算公式为:

$$GMea = \sqrt[7]{E_{BG} \times E_{CB} \times E_{NAG} \times E_{LAP} \times E_{AP} \times E_{POX} \times E_{PER}}$$

式中: E_{BG} 为 β -葡糖苷酶; E_{CB} 为纤维二糖水解酶; E_{NAG} 为 N-乙酰-葡糖苷酶; E_{LAP} 为亮氨酸氨基肽酶; E_{AP} 为酸性磷酸酶; E_{POX} 为酚氧化物酶; E_{PER} 为过氧化物酶。

表 2 测定土壤酶种类、功能以及相应的测定底物

Table 2 Soil enzyme names, function and substrates for assays

土壤酶 Soil enzyme	功能 Function	底物 Substrate	底物浓度 Concentration of substrate/ ($\mu\text{mol/L}$)	测定波长 Measure wavelength/ nm
β -葡糖苷酶 (BG) β -glucosidase	水解纤维素, 释放葡萄糖 ^[3]	4-甲基伞形酮- β -D-葡萄糖苷 4-MUB- β -D-glucoside		
纤维二糖水解酶 (CB) Cellobiohydrolase	水解纤维素, 释放二糖 ^[24]	4-甲基伞形酮- β -D-纤维二糖糖苷 4-MUB- β -D-cellobioside		
N-乙酰-葡糖苷酶 (NAG) N-acetyl-glucosaminidase	分解几丁质 ^[4,28]	4-甲基伞形酮-N-乙酰- β -D-氨基葡萄糖苷 4-MUB-N-acetyl- β -D-glucosaminide	200	365, 450
酸性磷酸酶 (AP) Acid phosphatase	催化水解有机磷转化为无机磷 ^[5]	4-甲基伞形酮-磷酸 4-MUB-phosphate		
亮氨酸氨基肽酶 (LAP) Leucine aminopeptidase	水解亮氨酸以及其他疏水氨基酸 ^[4]	L-亮氨酸-7-氨基-4-甲基香豆素 L-Leucine-7-amido-4-methylcoumarin		
多酚氧化物酶 (POX) Phenoxidase 过氧化物酶 (PER) Peroxidase	分解木质素以及芳香类复合物, 形成腐殖质 ^[1]	L-3,4-二羟基苯丙氨酸 L-3,4-dihydroxyphenylalanine (DOPA)	25000	465

2.3 数据统计分析

利用单因素方差分析 (one-way ANOVA) 检验不同等级土壤团聚体酶活性、有机碳、全氮的差异 ($P < 0.05$), 利用独立样本 t 检验对比不同马尾松混交林同等级团聚体土壤酶活性以及土壤有机碳、全氮的差异, 利用 Pearson 分析团聚体有机碳、全氮与土壤酶活性的相关性。所有分析处理在 SPSS 19.0 中进行, 用 SigmaPlot 14.0 软件作图。

3 结果与分析

3.1 各等级土壤团聚体分布以及碳氮含量

MS 与 MH 各等级土壤团聚体分布均呈现显著差异 ($P < 0.05$), 不同等级团聚体所占比例均值由大到小为: 大团聚体 ($> 2 \text{ mm}$, $59\% \pm 2.18\%$) $>$ 中团聚体 ($0.25\text{--}2 \text{ mm}$, $35.89\% \pm 1.65\%$) $>$ 微团聚体 ($< 0.25 \text{ mm}$, $2.56\% \pm 0.22\%$)。不同混交林土壤大团聚体与微团聚体分布并无显著差异, 而 MS 的中团聚体分布比例 ($39.53\% \pm 1.65\%$) 显著高于 MH 的中团聚体 ($32.24\% \pm 2.51\%$) (图 1)。

2 种马尾松混交林土壤团聚体有机碳、全氮、全磷均随着团聚体等级的降低而呈现增加的趋势, 且微团聚体的有机碳、全氮含量差异高于大团聚体 ($P < 0.05$)。不同混交林同等级团聚体的有机碳并无显著差异, 而 MH 大团聚体与微团聚体的全氮显著高于 MS, MH 大团聚体全磷也显著高于 MS, MS 各团聚体土壤碳氮比显著高于 MH (图 2)。

3.2 不同马尾松混交林土壤团聚体酶活性

团聚体分级以及马尾松混交林类型对 2 种氧化还原酶活性并无显著影响。MS 不同粒径团聚体的 7 种土壤酶活性均无显著差异。MH 微团聚体 N-乙酰-葡萄糖苷酶(NAG, $(3276.04 \pm 160.63) \text{ nmol g}^{-1} \text{ h}^{-1}$)显著高于中团聚体($(2214.92 \pm 395.56) \text{ nmol g}^{-1} \text{ h}^{-1}$),微团聚体的亮氨酸氨基肽酶(Leucine aminopeptidase, LAP, $(21.76 \pm 0.47) \text{ nmol g}^{-1} \text{ h}^{-1}$)显著高于大团聚体($(4.33 \pm 0.95) \text{ nmol g}^{-1} \text{ h}^{-1}$)和中团聚体($(7.16 \pm 2.45) \text{ nmol g}^{-1} \text{ h}^{-1}$),其余不同等级团聚体的酶活性均无显著差异。2 种马尾松混交林的中团聚体土壤酶活性均无显著差异,MS 的大团聚体和微团聚体纤维二糖水解酶(Cellobiohydrolase, CB)和 LAP 均显著高于 MH,同时,MS 大团聚体的 β -葡萄糖苷酶(BG)和 NAG 也显著高于 MH(图 3)。

由表 3 可知,除酸性磷酸酶(AP)外,MS 各团聚体水解酶均值低于 MH,而其氧化还原酶均值则高于 MH。

MS 的大团聚体、微团聚体的土壤酶活性几何平均数显著高于 MH,分别是 MH 的 1.98 倍和 1.49 倍。MS 各等级团聚体的土壤酶活性几何平均数无显著差异,MH 的微团聚体土壤酶活性几何平均数显著高于大、中团聚体(表 4)。

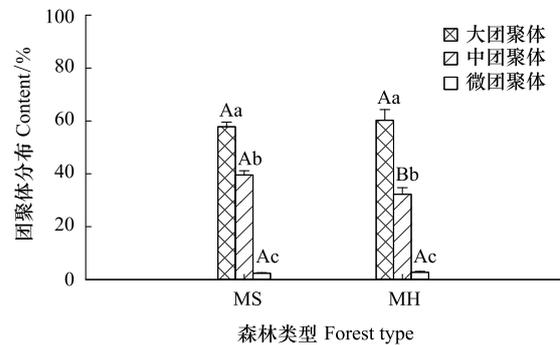


图 1 2 种马尾松混交林各粒径土壤团聚体分布

Fig. 1 The distribution of soil aggregate-size classes in two different *Pinus massoniana* mixed plantations

MS: 马尾松杉木混交林 Mixed plantation of *P. massoniana* and *C. lanceolata*; MH: 马尾松杉木栎类混交林 Mixed plantation of *P. massoniana*, *C. lanceolata* and *Quercus*; 大写字母表示同等级团聚体不同混交林之间的显著差异;小写字母表示同种混交林类型不同等级团聚体之间的显著差异

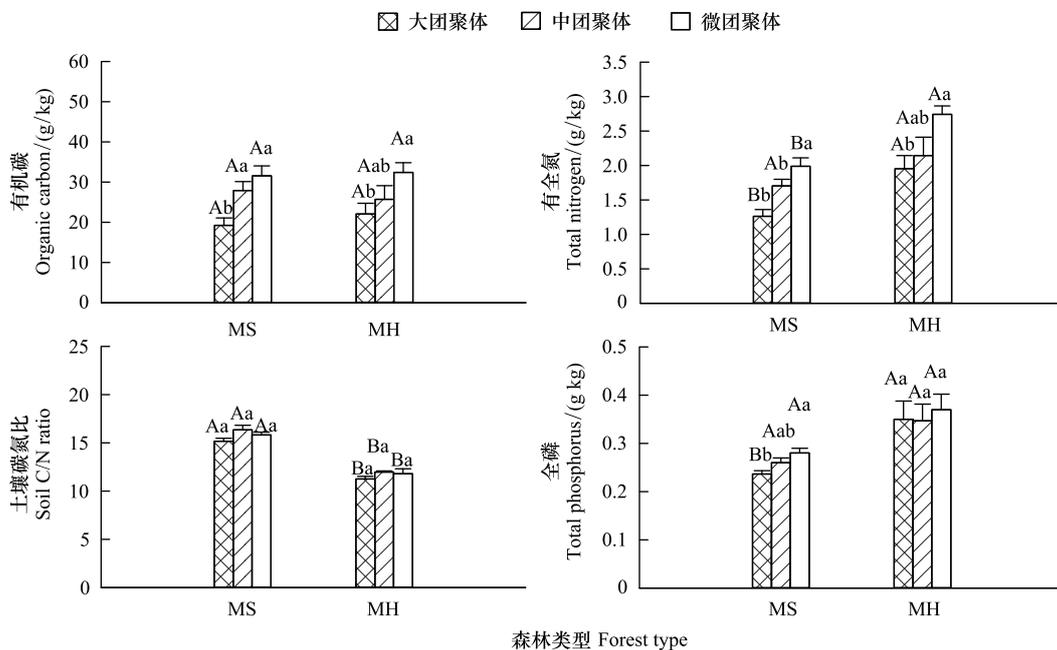


图 2 马尾松混交林土壤团聚体养分含量

Fig. 2 Nutrient content of soil aggregates in two different *Pinus massoniana* mixed plantations

大写字母表示同等级团聚体不同混交林之间的显著差异;小写字母表示同种混交林类型不同等级团聚体之间的显著差异

3.3 土壤团聚体土壤养分与酶活性相关性

测定的 2 种土壤氧化还原酶活性、以及水解酶 AP 与土壤团聚体的有机碳、全氮、全磷含量均无显著相关

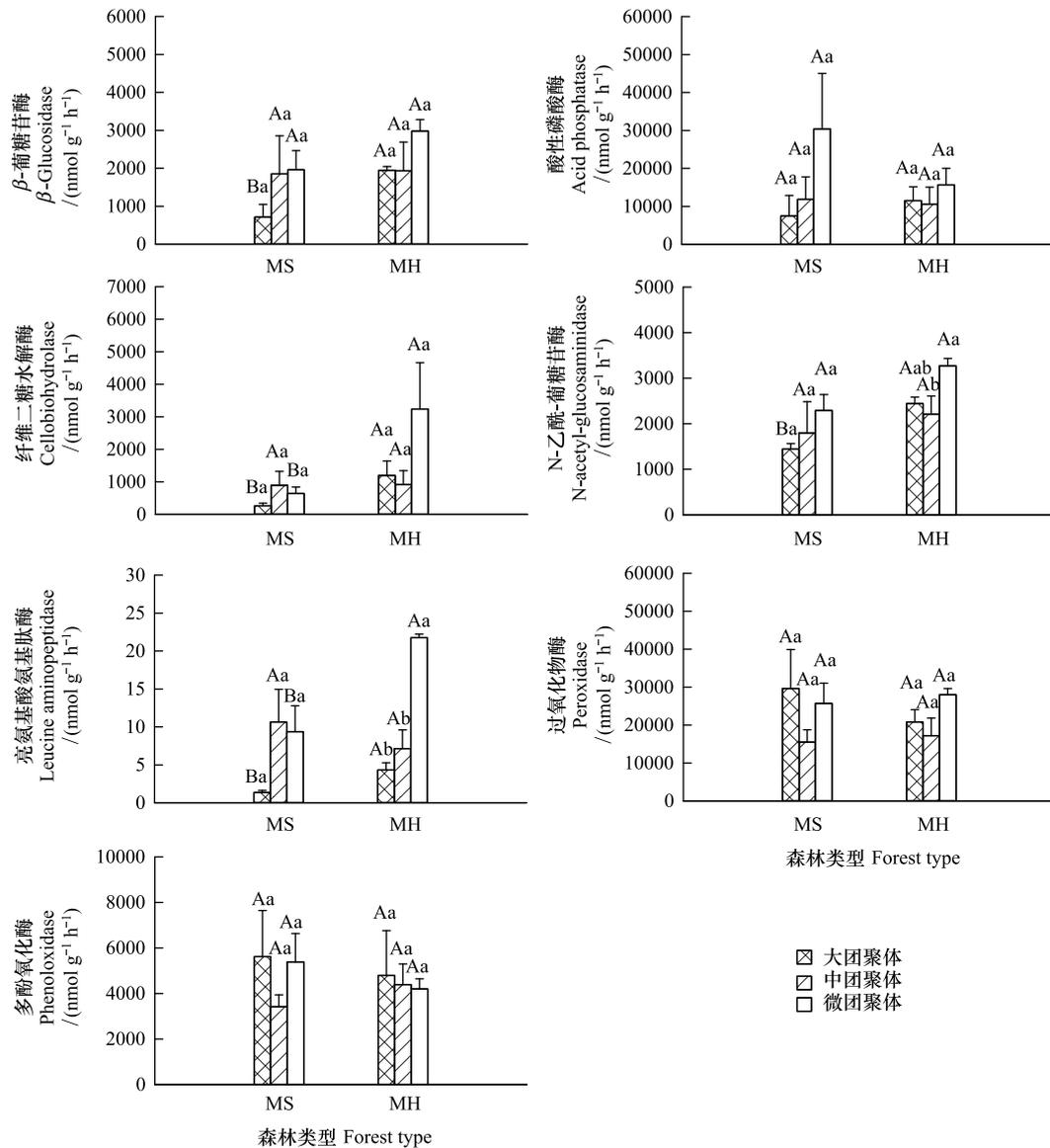


图3 马尾松混交林土壤团聚体土壤酶活性

Fig.3 Enzyme activities of soil aggregates in two different *Pinus massoniana* mixed plantations

大写字母表示同等级团聚体不同混交林之间的显著差异;小写字母表示同种混交林类型不同等级团聚体之间的显著差异

性。土壤全氮含量与其余4种水解酶呈现显著的正相关关系。土壤有机碳含量仅与NAG、LAP呈现显著的正相关关系。土壤全磷与CB和NAG呈现显著的正相关关系。土壤酶活性几何平均数随着有机碳、全氮、全磷的增加而呈现显著的增加。土壤碳氮比与测定的酶活性以及土壤酶活性几何平均数均无显著相关性(表5)。

4 讨论

不同等级团聚体通过控制水分、温度、空气以及有机质的可接触性影响土壤酶活性^[11,29],各粒径团聚体的分布对于酶活性影响显著。本研究中,森林植被类型的不同并未造成各等级团聚体分布的显著差异,2种马尾松混交林团聚体分布比例均随着团聚体等级的增加而显著增加,大团聚体最高,占据土壤60%左右,这与相关研究结果一致^[12,30],如Fang等对3种亚热带森林类型的土壤团聚体等级分布研究结果表明各等级团

聚体分布差异显著,大团聚体 ($58.5\% \pm 2.6\%$) > 中团聚体 ($35.6\% \pm 3.0\%$) > 微团聚体 ($6.0\% \pm 0.7\%$)^[12]。而马尾松杉木混交林的中团聚体分布显著高于马尾松杉木栎类混交林,可能是由于地上植被组成的影响,阔叶林真菌生物量高于针叶林^[31],且其根系的高分子黏质高,根系分布广,能够促进较小等级团聚体胶结成团聚体^[32],因此,马尾松杉木栎类混交林的大团聚体分布比例高于马尾松杉木混交林,而中团聚体则低于马尾松杉木混交林。

表 3 马尾松混交林土壤团聚体酶活性均值

Table 3 The mean of the assayed enzyme activities in all soil aggregates of two different *Pinus massoniana* mixed plantations

森林类型 Forest type	水解酶 Hydrolases/ (nmol g ⁻¹ h ⁻¹)					氧化还原酶 Oxidase/ (nmol g ⁻¹ h ⁻¹)	
	β-葡糖 苷酶	酸性磷 酸酶	纤维二糖 水解酶	N-乙酰-葡 糖苷酶	亮氨酸 氨基肽酶	过氧化物酶	多酚氧化酶
马尾松杉木混交林 Mixed plantation of <i>P. massoniana</i> and <i>C. lanceolate</i>	1509.62± 392.33A	16577.91± 5964.80A	603.72± 165.79A	1845.46± 257.00B	7.13± 2.15A	23641.88± 4054.03A	4803.86± 785.14A
马尾松杉木栎类混交林 Mixed plantation of <i>P. massoniana</i> , <i>C. lanceolate</i> and <i>Quercus</i>	2288.06± 293.78A	12580.47± 2239.36A	1786.74± 577.91A	2644.68± 207.08A	11.08± 2.81A	22015.87± 2329.73A	4461.04± 643.50A

大写字母表示不同混交林之间的显著差异

表 4 马尾松混交林土壤团聚体土壤酶几何平均数

Table 4 The geometric mean of the assayed enzyme activities in soil aggregates of two different *Pinus massoniana* mixed plantations

森林类型 Forest type	团聚体分级 Aggregate size		
	> 2 mm	0.25—2 mm	< 0.25 mm
马尾松杉木混交林 Mixed plantation of <i>P. massoniana</i> and <i>C. lanceolate</i>	764.34±125.58Ba	1356.25±530.75Aa	1784.72±184.06Ba
马尾松杉木栎类混交林 Mixed plantation of <i>P. massoniana</i> , <i>C. lanceolate</i> and <i>Quercus</i>	1507.81±79.94Ab	1400.63±378.40Ab	2653.46±55.67 Aa

大写字母表示同等级团聚体不同混交林之间的显著差异;小写字母表示同种混交林类型不同等级团聚体之间的显著差异

表 5 团聚体酶活性与养分含量相关性

Table 5 Correlations between enzyme activities and nutrient content of soil aggregates ($n = 18$)

	全氮 Total nitrogen	有机碳 Soil organic carbon	全磷 Total phosphorus	土壤碳氮比 Soil C/N ratio
β-葡糖苷酶 β-glucosidase	0.540 *	0.462	0.348	-0.229
纤维二糖水解酶 Cellobiohydrolase	0.587 *	0.367	0.502 *	-0.374
酸性磷酸酶 Acid phosphatases	0.145	0.316	0.092	0.192
N-乙酰-葡糖苷酶 N-acetyl-glucosaminidase	0.672 **	0.480 *	0.513 *	-0.400
亮氨酸氨基肽酶 Leucine aminopeptidase	0.704 **	0.664 **	0.395	-0.141
多酚氧化酶 Phenoloxidase	-0.189	-0.128	-0.277	0.074
过氧化物酶 Peroxidase	0.098	0.122	-0.068	0.047
土壤酶几何平均数 Geometric mean	0.695 **	0.590 **	0.478 *	-0.270

* $P < 0.05$; ** $P < 0.01$

本研究发现,2 种马尾松混交林土壤微团聚体的 5 种水解酶活性均高于大团聚体,其中,马尾松杉木栎类混交林的微团聚体亮氨酸氨基肽酶活性显著高于大团聚体 ($P < 0.05$, 图 3)。由于研究区域、土壤类型、植被类型以及土壤团聚体筛分方法的差异,土壤酶活性在团聚体中的分布特征并无定论^[10,12,33]。本研究微团聚体酶活性高于大团聚体可能主要源于团聚体物理结构越差异的影响,因为团聚体粒径小,水分和养分通过扩散作用进入的速度越快^[34],能够为酶促反应提供更多利用的物质^[35],酶活性越高;而大团聚体孔径大,稳定性低,土壤酶活性易受环境影响^[36]。此外,本区域 2 种马尾松混交林的土壤质地是黏壤土,该土壤质地吸附

力大,较小粒径的团聚体具有较高的比表面积,会吸附更多的土壤有机质^[37-38],能够为酶活性提供充足的养分。与水解酶不同的是,氧化还原酶主要是由真菌产生^[39],而真菌因其菌丝无法穿透土壤微团聚体的气孔,主要存在于大团聚体中^[40],因此本研究中大团聚体的2种氧化还原酶活性最高(图3)。

对比2种混交林团聚体土壤酶活性发现,马尾松杉木栎类混交林的大团聚体 β -葡糖苷酶、纤维二糖水解酶、N-乙酰-葡糖苷酶、亮氨酸氨基肽酶活性显著高于马尾松杉木混交林,同时其微团聚体纤维二糖水解酶、亮氨酸氨基肽酶活性也显著高于马尾松杉木混交林(图3)。这4种酶活性主要参与土壤碳氮循环^[3,4,24]。然而,究竟是较高的碳循环酶活性(氮循环酶活性)造成了土壤有机碳(或氮)含量的增加,还是较大的土壤有机质库为土壤酶活性提供了充足的底物从而促进了酶活性的提高并无定论^[6]。目前多数学者认为,土壤酶活性同时受到土壤关键理化性质、土壤微生物量、土壤有机质含量的共同影响^[4,41]。本研究中,所测得的 β -葡糖苷酶、纤维二糖水解酶、N-乙酰-葡糖苷酶、亮氨酸氨基肽酶活性均与土壤全氮呈极显著的相关性(表5),马尾松杉木混交林与马尾松杉木栎类混交林的大团聚体与微团聚体全氮的显著差异可能是造成上述土壤酶活性差异的主要原因(图2)。而与上述4种水解酶不同的是,团聚体水解酶酸性磷酸酶与土壤碳氮磷关系并不显著,这主要是因为相较于养分的影响,团聚体酸性磷酸酶更易受到土壤水分的影响^[42]。2种马尾松混交林土壤水分相近(表1),所以其酸性磷酸酶活性并无显著差异。同时,本研究也发现马尾松杉木栎类混交林各团聚体土壤C/N比显著低于马尾松杉木混交林(图2),而低C/N比更适宜主要产生水解酶的细菌生存^[39,43-44],高C/N比则利于主要产生氧化还原酶的真菌生存^[39,43-44],虽然土壤C/N比与各土壤酶活性并无显著相关关系(表5),但其通过影响微生物进而调节土壤酶活性的变化^[44],所以马尾松杉木混交林各团聚体氧化还原酶均值略高于马尾松杉木栎类混交林,而其水解酶活性(除酸性磷酸酶外)则低于马尾松杉木栎类混交林。

多酚氧化酶与过氧化物酶这两种氧化酶活性比水解酶变异性更强^[4],主要影响土壤惰性碳的形成,分解木质素以及芳香类复合物,形成腐殖质^[1]。多酚氧化酶与过氧化物酶活性与土壤有机碳、全氮无显著的相关性^[4],而是随着pH的增加而呈现增加的趋势^[4],本研究也发现,团聚体多酚氧化酶与过氧化物酶与有机碳、全氮并无显著的相关性(表4)。由于马尾松杉木混交林与马尾松杉木栎类混交林的土壤pH分别为 5.65 ± 0.06 和 5.62 ± 0.03 (表1),所以各团聚体的2种氧化还原酶活性相近(图3)。

土壤酶活性几何平均数GMea是基于所测的5种水解酶和2种氧化还原酶活性计算得出的,作为反应土壤质量的综合指标^[26-27],GMea能够反应整体酶活性的变化以及微生物活性变化^[45-46]。相较于马尾松杉木针叶混交林,马尾松杉木栎类阔叶混交林的凋落物C/N比低(表1),分解快^[47],能够为土壤微生物提供丰富的营养,同时不同树种的根系相互作用,根系的代谢也能直接影土壤酶活性^[48-49],这可能是造成马尾松杉木栎类混交林土壤大团聚体和微团聚体酶活性综合指数GMea显著高于马尾松杉木混交林的主要原因(表4)。此外,土壤酶活性一般随着温度的增加而增加^[2],相较于马尾松杉木混交林,马尾松杉木栎类混交林海拔低,土壤温度较高(根据2019年8月表层土壤温度连续监测结果),从而增加了土壤酶活性综合指数GMea(表4)。而为何2种混交林土壤中团聚体酶活性无显著差异仍需进一步对其微生物等指标进行分析。

5 结论

林型对土壤团聚体分布、团聚体氧化还原酶、酸性磷酸酶活性并没有显著影响,而马尾松杉木栎类混交林大团聚体的 β -葡糖苷酶、纤维二糖水解酶、N-乙酰-葡糖苷酶、亮氨酸氨基肽酶显著高于马尾松杉木混交林,同时其微团聚体纤维二糖水解酶、亮氨酸氨基肽酶也显著高于马尾松杉木混交林。2种马尾松混交林团聚体全氮是造成上述4种酶活性不同的主要原因。马尾松杉木混交林大团聚体和微团聚体土壤酶活性几何平均数GMea显著低于马尾松杉木栎类混交林,栎类阔叶树种的增加显著增加了土壤团聚体酶活性,有利于土壤养分质量的提高。

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