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封面图说: 站立的仓鼠——仓鼠为小型啮齿类动物,栖息于荒漠、荒漠草原等地带的洞穴之中。白天他们往往会躲在洞穴中睡觉和休息,以避开天敌的攻击,偶尔也会出来走动,站立起来警惕地四处张望。喜欢把食物藏在腮的两边,然后再走到安全的地方吐出来,由此得仓鼠之名。它们的门齿会不停的生长,所以它们的上下门齿必须不断啃食硬东西来磨牙,一方面避免门齿长得太长,妨碍咀嚼,一方面保持门牙的锐利。仓鼠以杂草种子、昆虫等为食。

彩图提供:陈建伟教授 北京林业大学 E-mail: cites.chenjw@163.com

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闫文德, 梁小翠, 郑威, 田大伦, 朱凡, 王光军. 4种绿化树种盆栽土壤微生物对柴油污染响应及对PAHs的修复. 生态学报, 2012, 32(7): 2279-2287.

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4种绿化树种盆栽土壤微生物对柴油污染 响应及对PAHs的修复

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摘要:采用室内盆栽实验,利用柴油按不同比例混合土壤0 g/kg(CK),2 g/kg(L1),10 g/kg(L2)和50 g/kg(L3)制备了含不同浓度PAHs的污染土样,选择1年生樟树(*Cinnamomum camphora*)、广玉兰(*Magnolia grandiflora*)、栾树(*Koelreuteria bipinnata*)、马褂木(*Liriodendron chinense*)幼苗为供试植物,进行了土壤微生物对柴油的响应及对PAHs的修复研究。结果表明:(1)4个树种土壤微生物区系组成以细菌占优势,放线菌次之,真菌最少。(2)在各测定时间树种间土壤微生物总数对污染处理响应差异较大。栾树各污染处理组土壤微生物总数均高于对照组;樟树各污染处理土壤微生物在实验前期低于对照;广玉兰为污染处理组在4月份显著低于对照,而在其他月份多高于对照;马褂木在4月份均低于对照,其他月份为L1处理低于对照,L2、L3处理高于对照(1月L2除外)。(3)4个树种对照土壤中微生物总数随时间的变化都是从10月逐渐增加至翌年4月,然后不断减少至10月;污染处理土壤微生物总数呈现峰值提前或滞后现象,主要出现在1月或7月。真菌是控制PAHs降解的重要因素。(4)经过1a实验,各树种L1、L2处理土壤中的PAHs浓度已与对照土壤相当;L3处理各树种土壤中PAHs含量为马褂木>栾树>广玉兰>樟树。

关键词:多环芳烃; 土壤微生物; 细菌; 真菌; 放线菌; 柴油; 植物修复

Remediation of soils contaminated with polycyclic aromatic hydrocarbons (PAHs) using four greening tree species

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Abstract: Polycyclic aromatic hydrocarbons (PAHs) are an important group of persistent organic pollutants that are widespread in environment. With rapid growth of population, sustained industrial development and urbanization, PAHs have become a growing concern and received much attention. The reason is that PAHs have toxicity to humans and their possible harmful effect on animals, plants and microbes in aquatic and terrestrial ecosystems. In order to reveal the responses of tree species to PAHs and to examine the remediation methods of diesel-oil contaminated soils using higher plants, a pot experiment was conducted to compare degradation of PAH concentrations in diesel-oil contaminated soils under four tree species, and to investigate how soil microbial flora make contributions on such degradation. One-year old seedlings

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of four tree species, *Cinnamomum camphora*, *Magnolia grandiflora*, *Koelreuteria bipinnat*, and *Liriodendron chinense* were selected and planted in PAH contaminated soils with different diesel-oil (0g/kg (control), 2g/kg (L1), 10g/kg (L2) and 50g/kg soil (L3)). The composition, abundance and dynamics of soil microbes in the four groups of soils were measured to provide theoretic evidences for assessing and selecting tree species for remediation of PAHs contamination. The results showed that (1) bacteria were the most dominant group in soil microbial flora in the four tree species, and accounted for 69.70%—93.87% of the total microorganism. The percentage of bacteria usually increased with increasing of diesel-oil concentration levels. Compared with in control treatments, the proportion of bacteria in soil microorganisms in PAH treatments were inhibited by diesel-oil concentrations, except in soil of *Koelreuteria bipinnat*. Actinomyces accounted for 2.71%—25.29% of total microbeorganisms, and the percentage decreased with the increases of diesel-oil concentrations in all treatments. For *Koelreuteria bipinnat* species, the percentages of Actinomyces in total soil microbial flora were smaller in contaminated treatments than in control. But the situation was opposite for *Cinnamomum camphora* species. The proportion of fungi in total soil microorganisms was 0.88%—5.83%, and the values were relatively promoted in low and medium diesel-oil concentration treated soils. (2) The microorganisms in the studied tree species soils exhibited different seasonal patterns to response to PAHs treatments. In *Koelreuteria bipinnat* soils, the number of total microbes was higher in contaminated treatments than in control; In *Cinnamomum camphora* soils, only at the early stage were the total microbes high in polluted treatments than in control. For *Magnolia grandiflora* species, the abundance of total microorganisms was higher in all diesel-oil treated soils than in control soils for the studied period, except in the month of April, when the number of microbes was higher in control than in other treatment soils. The total microbes were lower in polluted treatments than in control in *Liriodendron chinense* soils in April. But in other months, all treatment soils had higher microbes than in control except in L1 treatment. (3) In control soils, the quantity of total microbes gradually increased at the early stage of the study (from October, 2009), reaching the peaking value in April, 2010, and then decreased until in October, 2010. PAHs contaminations disturbed such dynamic patterns of microbial abundance. The maximum values of total microorganisms in were appeared in January or July in the treatments. It was found that fungi played an important role in controlling the degradation of PAHs in this study. One year later of the treatment, PAHs contents were similar in L1, L2 treatments' soils and in control soils for all four tree species plots. PAHs contents in L3 treatment's soils of each tree species were in the order of *Liriodendron chinense* > *Koelreuteria bipinnat* > *Magnolia grandiflora* > *Cinnamomum camphora*.

Key Words: PAHs; soil microbes; bacteria; fungi; actinomyces; diesel-oil; remediation

多环芳烃属于持久性有机污染物(POPs),难以降解,能在环境中长期停留,具有潜在环境危害^[1],在世界范围受到普遍关注^[2]。中国PAHs(美国环保局EPA优先控制16种PAHs)的排放量约占全球的22%,居世界第一^[3],而PAHs已成为中国最严重的土壤污染物(达到28 mg/kg干土)^[4]。土壤中PAHs去除最重要的途径是土壤中微生物对PAHs的分解代谢。许多研究证明了PAHs降解微生物与PAHs含量密切关系^[5-7]。然而PAHs重度污染土壤会对土壤中微生物群落造成毒害,降低其修复效率^[8],因此许多研究通过向土壤中接种专性降解细菌或真菌,来提高修复效果^[9-10],但此法更适用于较小面积的点污染源,无法应对受到普遍污染的大尺度地域。

植物可以显著的增强微生物对PAHs的降解能力^[11-16],主要是通过改善微生物生长条件^[17]、提供营养^[18]、共生代谢作用^[19]等途径,植物本身也可以释放大量降解酶^[20]进入土壤。由于根系的促进作用,植物根系周围土壤中PAHs降解菌会出现选择性地增加^[21-24]。植物-微生物的联合降解系统不仅受根际微生物影响,也取决于宿主植物本身特性^[25]。植物物种间根系特征、分泌物组成(如碳源、表面活性剂)的差异会影响微生物的降解、土壤特性和PAHs转移^[26],同时植物本身吸收、同化PAHs的能力也有所不同^[27],因此,植物的选取成为植物修复的重要因素^[15-16]。

由于工业、交通以及集中的燃煤采暖,城市和工业区及其周边区域土壤中的PAHs污染水平高于山区、远郊区^[28],而目前植物-微生物修复PAHs污染的研究多见于草本^[15-16,29-32],对木本植物仅集中于柳树等少数树种^[33],当前研究结论难以适用于南方城市土壤污染修复。同时, Gunther等指出理想的修复植物应具备:根系深,须根系强大;适应性强,生长旺盛,有较大的生物量等特点,所以木本植物拥有成为理想城市污染土壤修复植物的潜力。

本研究选择4种南方绿化植物幼苗为对象,研究其根部土壤中微生物数量特征及季节变化规律,并分析了与土壤中PAHs的降解率的关系。对筛选PAHs污染修复的优良绿化植物具有现实意义,为南方地区城市的绿化和环境保护、城市防污绿化带的营造以及对生态环境中PAHs的生态风险评价提供理论依据。

1 实验地概况与实验材料

1.1 实验地概况

实验地在长沙市中南林业科技大学城市生态站温室内,地处东经112°48',北纬28°03'。当地年平均气温16.8℃,极端最高气温40.6℃,最低气温-12℃。日照时数年均1677.1 h,属典型的亚热带湿润季风气候。

1.2 实验材料

实验土壤分别采自湖南省株洲市夕阳红苗圃园和中南林业科技大学长沙校区,土壤为0—20 cm红壤表土(以1:1比例将两处土壤均匀混合,自然风干,过1 mm筛,待用)。实验采用4种南方城市常见的绿化树种,樟树(*Cinnamomum camphora*)、广玉兰(*Magnolia grandiflora*)、栾树(*Koelreuteria bipinnata*)、马褂木(*Liriodendron chinense*),均为1年生实生苗。

供试污染物:市售0号柴油。将风干过筛后的实验土壤和柴油以3个浓度混合:2、10、50 g/kg土,充分拌匀,放置48 h以充分平衡,可得到含不同浓度PAHs的土壤:低水平(L1)9.85 mg/kg、中水平(L2)23.59 mg/kg、高水平(L3)47.06 mg/kg,此处PAHs指美国环保局(EPA)优先控制的16种PAHs:萘、苊烯、苊、芴、菲、蒽、荧蒽、芘、苯并(a)蒽、屈、苯并(b)荧蒽、苯并(k)荧蒽、苯并芘、茚并(1,2,3-cd)芘、二苯并(a,h)蒽、苯并(ghi)芘。

2 研究方法

将所制备的污染土壤分装到圆形塑料盆($\Phi 35\text{ cm} \times H30\text{ cm}$)中,移栽生长发育良好且大小均一的1年生实生苗木。每个树种每个污染水平下重复3株,以原状实验土作为对照(CK)。实验期为2009年10月至2010年10月,分别于2010年1月、4月、7月、10月取样测定土壤PAHs含量和微生物数量,取土时分上、中、下3层,然后将其混合均匀。实验期间苗木置于温室内培育,开窗对流使温室外温度基本保持一致,采用自来水供给苗木生长水分需求。各处理土壤的基本理化性质见表1。

土壤中PAHs(EPA标准16种PAHs)的含量测定:样品前处理(超声提取、旋转蒸发、柱层析、氮吹),浓缩至1 mL,用Agilent 6890GC/5973MS气质联用仪测定PAHs含量。仪器分析PAHs的基本参数为: $60^{\circ}\text{C} \rightarrow 15^{\circ}\text{C}/\text{min} \rightarrow 100^{\circ}\text{C} (5\text{ min}) \rightarrow 8^{\circ}\text{C}/\text{min} \rightarrow 210^{\circ}\text{C} (3\text{ min}) \rightarrow 2^{\circ}\text{C}/\text{min} \rightarrow 290^{\circ}\text{C} (5\text{ min})$

色谱柱为HP-5毛细管色谱柱30 m \times 0.25 mm。不分流进样,气化温度280℃,载气为高纯He。

土壤pH值用PXS-270型离子计测定,有机碳采用重铬酸钾氧化法,全氮采用凯氏定氮法,含水量采用烘干法。

土壤微生物数量的测定用稀释平板菌落计数法。细菌采用牛肉膏蛋白胨培养基,真菌采用孟加拉红-马丁氏琼脂培养基,放线菌采用改良高氏一号培养基。细菌、真菌、放线菌均采用混菌法接种,接种后置28—30℃生化培养箱内培养,分别在24 h、48 h及4—5 d内检查并进行CFU(Colony Forming Unit)计数^[34]。菌落

表1 供试土壤的pH、碳、氮含量

Table 1 Content of total organic carbon, total nitrogen and pH in studied soils

处理 Treatment	pH	总有机碳 /(g/kg)	全氮 /(g/kg)
CK	4.84	17.21	1.33
L1	5.01	19.06	1.35
L2	4.98	23.36	1.29
L3	4.86	46.26	1.16

计数方法见《环境工程微生物检验手册》^[35]。微生物总数为细菌、真菌、放线菌三者数量之和。

实验数据采用 Excel、Origin7.5、SPSS13.0 软件进行作图和分析。不同浓度 PAHs 污染对不同树种各个时期的指标的差异采用 One-way ANOVA 方法检验,相关性分析采用 Pearson correlation sig. (2-tail) 方法分析, $P<0.05$ 为显著相关, $P<0.01$ 极显著相关。

3 结果与分析

3.1 污染处理对土壤微生物数量的影响

由图 1 可知,各处理土壤中微生物类群以细菌占优势,占总数的 69.70%—93.87%,所占比例随污染浓度的升高而变化趋势大体表现为增大;与对照处理相比,污染处理对柰树根际土壤中细菌所占比例起促进作用,但对于其他树种则主要为抑制作用。放线菌占微生物总数比例为 2.71%—25.59%,所占比例随污染浓度的升高的变化趋势与细菌相反,大体表现为减小;柰树污染处理中的放线菌所占比例均低于对照,樟树则相反,其他树种为 L1 处理均高于对照,L2、L3 处理低于对照。真菌在土壤微生物中只占 0.88%—5.83%。各树种低、中污染处理均促进了土壤中真菌所占比例的增大,高浓度处理对各树种影响不一致,真菌在低浓度处理中所占比例最大(马褂木除外)。

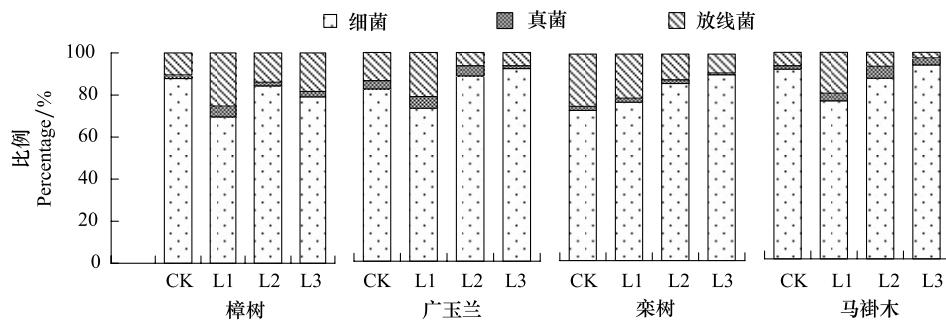


图 1 细菌、真菌和放线菌占土壤微生物总数比例

Fig. 1 Bacteria, fungi and actinomycetes accounted for the proportion of total soil microbial
4 次测定均值

从各季度来看(表 2),不同树种土壤微生物总数对污染处理响应差异较大。樟树各污染处理土壤微生物在 1、4、7 月份均低于对照,而在 10 月份随污染水平的升高而增加。广玉兰污染处理组土壤微生物总数在 4 月份显著低于对照,而在其他月份污染处理多高于对照,但组间无显著差异。柰树各污染处理组土壤微生物总数高于对照组,但组间无显著差异,而在整个研究过程中土壤微生物总数最大值在 L1、L2、L3 组均有出现。马褂木污染处理组土壤微生物总数在 4 月份均低于对照,其他月份为 L1 处理低于对照,L2、L3 组高于对照(1 月 L2 除外)。

如表 2 所示,4 个树种对照组土壤中微生物总数随时间的变化趋势一致,呈单峰型,峰值在 4 月份。但污染处理组土壤微生物总数变化趋势则因树种而不同。樟树、马褂木污染处理组与对照基本一致。广玉兰 L3 处理土壤微生物总数与对照相比峰值提前,出现在 1 月份;L1 处理峰值滞后,出现在 7 月份;L2 处理与对照变化趋势相同。柰树 L1、L3 处理土壤微生物总数变化趋势与对照相同,L2 峰值有滞后现象,出现在 7 月份。

3.2 不同树种土壤中 PAHs 的含量变化

图 2 为 4 种树种土壤中 PAHs 的含量变化情况。可以看出,随着时间的推移,各树种污染处理土壤中 PAHs 浓度均呈现逐渐降低趋势,但各树种情况有所差异。从 2009 年 10 月份实验设置至翌年 1 月份,柰树的 L3 处理 PAHs 浓度已处于较低水平,为 19.28 mg/kg,显著小于其他 3 个树种,马褂木表现较差(41.12 mg/kg);L1 处理各树种土壤中 PAHs 浓度为柰树>樟树>马褂木>广玉兰,L2 处理为樟树>马褂木>广玉兰>柰树;在实验初期阶段,柰树表现出优良的 PAHs 降解能力,对于中、高污染土壤 PAHs 降解尤为明显,但对低浓度污染降解效果不佳;而广玉兰对低、中污染土壤 PAHs 的降解良好,但对高浓度处理 PAHs 降解效果较差。

表2 各时期不同浓度处理土壤微生物总数(10^4 cfu/g)

Table 2 Total microbes in different treated soils at each stage

		CK	L1	L2	L3
樟树	1月	214.00a	36.53b	27.17b	20.87b
	4月	432.18a	126.60b	100.35b	83.60b
	7月	110.25a	49.75a	25.65b	61.72a
	10月	16.55a	22.60a	35.10a	80.51b
广玉兰	1月	30.25a	34.03a	27.85a	85.93a
	4月	245.36a	42.72c	119.63b	59.49c
	7月	31.61a	59.53a	39.38a	44.07a
	10月	12.23a	37.16a	10.38a	36.62a
栾树	1月	27.22a	39.33a	19.48a	32.48a
	4月	47.83a	148.40a	89.43a	160.68a
	7月	15.86a	25.31a	94.10a	61.58a
	10月	21.24a	28.40ab	36.19ab	61.37b
马褂木	1月	33.64ab	21.64a	29.53ab	35.77b
	4月	323.75a	116.72ab	58.10b	227.23ab
	7月	35.07a	33.88a	48.38ab	75.36b
	10月	28.96a	18.22a	36.90a	46.44a

字母表示同月份处理间是否显著差异,字母相同两者无显著差异,反之则有($P<0.05$,one-way ANOVA,LSD)

通过分析翌年10月各树种土壤PAHs浓度可知,经过1a实验,各树种L1、L2处理土壤中的PAHs浓度已与对照土壤相当,说明低、中处理土壤中PAHs已实现完全降解;L3处理各树种土壤中PAHs情况为马褂木>栾树>广玉兰>樟树,樟树土壤中PAHs浓度已降至9.04 mg/kg,虽然樟树组在实验初期土壤中PAHs降解速率较低,但在其后时间中均保持了较高的降解速率。

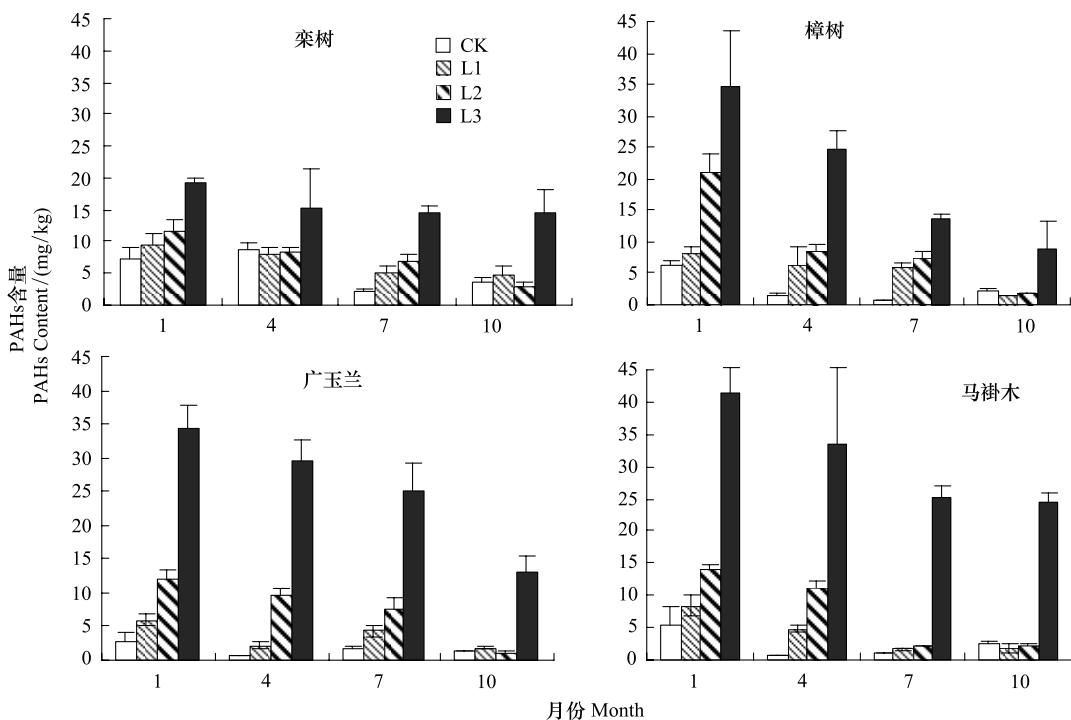


图2 土壤中PAHs含量的变化

Fig. 2 Changes of PAHs content in soils

3.3 土壤微生物与PAHs的相关性分析

樟树幼苗土壤中真菌数量与PAHs初始浓度极显著负相关(表3),表明污染初期PAHs对樟树土壤中真菌的繁殖产生了一定的抑制作用,但真菌与PAHs含量呈显著负相关,则表明在PAHs浓度降低过程中,真菌数量在随之增大。广玉兰幼苗土壤情况与樟树相似,PAHs初始浓度、PAHs含量与真菌数量显著相关(表4),放线菌数量与PAHs初始浓度极显著负相关,表明在PAHs污染初期,真菌、放线菌受PAHs抑制作用较强,这与沈国清等^[5]的研究结果是一致的。栾树幼苗土壤微生物数量与PAHs之间的相关性不强(表5)。马褂木幼苗土壤放线菌数量与PAHs初始浓度有显著负相关关系(表6)。上述结果表明在PAHs污染初期,放线菌、真菌更易受到抑制,而细菌则受影响较小。

表3 樟树幼苗土壤微生物和PAHs的相关性

Table 3 Correlations between soil microbes and PAHs of *Cinnamomum camphora* seedlings

项目 Item	PAHs 含量 PAHs concentration	PAHs 初始浓度 Initial concentration of PAHs	PAHs 去除率 Removal rate of PAHs	细菌 Bacteria	真菌 Fungi	放线菌 Actinomycetes
PAHs 初始浓度 Initial concentration of PAHs	0.670 **	1				
PAHs 去除率 Removal rate of PAHs	-0.266	0.242	1			
细菌 Bacteria	-0.221	-0.269	-0.193	1		
真菌 Fungi	-0.316 *	-0.405 **	-0.109	0.662 **	1	
放线菌 Actinomycetes	-0.091	-0.170	-0.403 **	0.361 *	0.478 **	1
微生物总数 Total microbe	-0.223	-0.280	-0.232	0.993 **	0.696 **	0.468 **

* * 代表相关性极显著($P<0.01$, Pearson Correlation, 2-tailed), * 代表相关性显著($P<0.05$, Pearson Correlation, 2-tailed)

表4 广玉兰幼苗土壤微生物和PAHs的相关性

Table 4 Correlations between soil microbes and PAHs of *Magnolia grandiflora* seedlings

项目 Item	PAHs 含量 PAHs concentration	PAHs 初始浓度 Initial concentration of PAHs	PAHs 去除率 Removal rate of PAHs	细菌 Bacteria	真菌 Fungi	放线菌 Actinomycetes
PAHs 初始浓度 Initial concentration of PAHs	0.742 **	1				
PAHs 去除率 Removal rate of PAHs	-0.304	0.174	1			
细菌 Bacteria	0.119	0.025	0.077	1		
真菌 Fungi	-0.339 *	-0.388 *	0.181	0.188	1	
放线菌 Actinomycetes	-0.294	-0.501 **	-0.225	0.219	0.293	1
微生物总数 Total microbe	0.071	-0.042	0.060	0.993 **	0.254	0.321 *

表5 栾树幼苗土壤微生物和PAHs的相关性

Table 5 Correlations between soil microbes, enzymes and PAHs of *Koelreuteria bipinnata* seedlings

项目 Item	PAHs 含量 PAHs concentration	PAHs 初始浓度 Initial concentration of PAHs	PAHs 去除率 Removal rate of PAHs	细菌 Bacteria	真菌 Fungi	放线菌 Actinomycetes
PAHs 初始浓度 Initial concentration of PAHs	0.726 **	1				
PAHs 去除率 Removal rate of PAHs	0.128	0.558 **	1			
细菌 Bacteria	0.244	0.299	0.178	1		
真菌 Fungi	-0.145	-0.131	0.033	0.341 *	1	
放线菌 Actinomycetes	-0.161	-0.170	0.100	0.274	0.640 **	1
微生物总数 Total microbe	0.212	0.264	0.182	0.992 **	0.417 **	0.389 *

表6 马褂木幼苗土壤微生物和PAHs的相关性

Table 6 Correlations between soil microbes, enzymes and PAHs of *Liriodendron chinense* seedlings

项目 Item	PAHs 含量 PAHs concentration	PAHs 初始浓度 Initial concentration of PAHs	PAHs 去除率 Removal rate of PAHs	细菌 Bacteria	真菌 Fungi	放线菌 Actinomycetes
PAHs 初始浓度 Initial concentration of PAHs	0.798 **	1				
PAHs 去除率 Removal rate of PAHs	-0.307	0.074	1			
细菌 Bacteria	0.103	0.099	0.112	1		
真菌 Fungi	0.146	0.244	0.042	0.145	1	
放线菌 Actinomycetes	-0.215	-0.383 *	-0.221	0.015	0.055	1
微生物总数 Total microbe	0.093	0.082	0.098	0.998 **	0.175	0.078

4 讨论

(1) 4个树种土壤微生物区系组成以细菌占优势,放线菌次之,真菌最少。土壤细菌、真菌、放线菌是土壤生态系统中微生物区系的主要组成部分,但不同植物之间在根系分泌物组成和含量上都存在较大的差异^[36],而且同一植物的分泌物在不同生育期也有变化,因此根区微生物表现出与植物种类、土壤及其他环境条件有关的特异性,并随植物生育期不同而呈现数量和优势种群的交替变化^[37]。在本研究中所有树种各处理土壤中微生物区系组成以细菌最多,放线菌次之,真菌最少。

(2) 4个绿化树种对照土壤中微生物总数随时间的变化都是从10月到翌年4月逐渐增加,4月到10月不断减少。污染处理下土壤微生物总数因为树种的差异及PAHs污染胁迫等级的不同表现为峰值提前或滞后现象,主要出现在1月或7月。亚热带地区4月份气候湿热,非常利于微生物生长,此时也是植物旺盛生长的季节有利于改善根系周围的土壤环境,促进微生物数量的增加,因此一般土壤中4月份微生物数量最多^[15],这与本实验研究结果相同。

研究表明,微生物遭受污染胁迫时其数量和生物量通常会受到抑制^[38-39],随着时间推移,对PAHs具有耐受性和降解性能的微生物将会逐渐增多,并对污染进行降解。本研究中,樟树、广玉兰和马褂木PAHs处理土壤中微生物总数在实验前期均低于对照,表明污染对微生物存在抑制作用,而栾树则高于对照,原因在于栾树根系能更快的促进土壤微生物种群的改变,使具有PAHs降解能力的微生物更快的适应污染并加速其降解过程,翌年1月栾树土壤中、高污染处理组中低浓度的PAHs也证实此点,表明此时栾树土壤微生物已经适应PAHs的初期抑制效应,并利用PAHs进行代谢,故PAHs处理微生物数量多于对照,而栾树的优良抗污、修复性能在锰矿尾渣废弃地修复中也有很好体现^[40]。

经过1a实验期后,在实验初期PAHs降解表现较差的樟树、广玉兰组对高污染处理中的PAHs降解效果最好,原因可能在于这两种树种对污染的初期适应能力较差,但由于两者均为常绿树种,其在1a中多数时间均有较好生长条件,而栾树、马褂木为落叶树种,其生长受季节、温度变化影响较大,所以其降解能力在跨季节时表现较差。

(3) 为了探讨土壤PAHs降解的控制因素,对4个树种PAHs降解率及细菌、真菌、放线菌进行了主成分分析,共获得了2个因子,分别解释了39.17%和73.82%的变量(表7)。因子1主要是由细菌组成,而PAHs降解率在该因子上的得分为负值,显示细菌与PAHs降解没有明显的正相关。因子2主要是由PAHs降解率和真菌组成,这说明真菌是控制PAHs降解的一个重

表7 土壤PAHs因子载荷及贡献率

Table 7 The component matrix and cumulative percent of PAHs in soils

项目 Item	因子 Factors	
	1	2
PAHs 降解率 Removal rate of PAHs	-0.789	0.481
细菌 Bacteria	0.853	0.078
真菌 Fungi	0.464	0.600
放线菌 Actinomycetes	-0.038	-0.888
因子贡献率 Factor contribution/%	39.17	73.82

要因素,在分析中还表明放线菌与PAHs降解的关系不大。土壤微生物是陆地生态系统中最活跃的成分,是污染物降解的驱动力^[16]。许多细菌、真菌可以降解PAHs,放线菌则鲜见于报道,本研究中真菌为降解PAHs重要因素。PAHs污染胁迫下,真菌虽然PAHs的降解能力,但其数量却没有表现出明显的增加,可能是因为经过适应后,虽然PAHs专性降解菌生长会因为大量的碳源得到刺激,但其他菌种会受到污染抑制,导致总数上没有明显增加。

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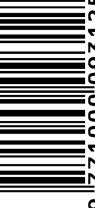
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