Functional biodiversity of microbial communities in the rhizospheres of hybrid larch \((Larix\ eurolepis)\) and Sitka spruce \((Picea\ sitchensis)\)

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Summary The diversity of microorganisms associated with trees and their different functional capabilities is thought to be a consequence of variation in carbon compounds in the rhizosphere. We used the Biolog\textsuperscript{®} system (Biolog Inc., Hayward, CA), a redox-based test, to construct sole carbon source utilization profiles (metabolic fingerprints) of microbial communities from the rhizospheres and rhizoplanes of hybrid larch \((Larix\ eurolepis\ A.\ Henry)\) and Sitka spruce \((Picea\ sitchensis\ Bong.\ Carr.)\) taken from a farm woodland site and two second-rotation plantation forest sites. Canonical variate analysis (CVA) of carbon utilization data differentiated among the microbial communities from the three forest sites, with the greatest discrimination between the farm woodland and the two second-rotation forest sites. Carbohydrates and carboxylic acids were the substrates responsible for this discrimination. Carbon profiles of the microbial communities from the rhizospheres of the two tree species also clustered when evaluated by CVA, as a result of differences in utilization of carboxylic acids and amino acids, suggesting that these tree species differ in the exudates they produce. Isolation and enumeration of organisms confirmed that there were qualitative and quantitative differences in the culturable populations of microorganisms at the different sites and between tree species. We conclude that Biolog is a useful technique for evaluating the functional diversity of microbial communities; however, to interpret the results accurately, they must be assessed in conjunction with the actual carbon substrates available in the particular ecosystem under study.

Keywords: Biolog, carbon utilization profiles, metabolic fingerprints, root exudates.

Introduction

Trees are grown for timber in a wide variety of soil types and systems (e.g., coppice plantations, agroforestry and farm woodland on former agricultural land). Because of increasing emphasis on low-input sustainable production systems, nutrient availability is a key factor governing tree growth (Mahendrappa et al. 1986). Soil microorganisms can increase nutrient availability through mineralization of soil organic matter and the solubilization of soil minerals (Lee and Parkhurst 1992, Sparling 1994). Although microbial growth in soil is carbon limited (Wardle 1992), the presence of high concentrations of carbon in the rhizosphere, as a result of rhizodeposition, makes it an area of high microbial activity (Lynch and Whipp 1990). It has been hypothesized that the diversity of microorganisms present in different plant rhizospheres is due to variation in the compounds exuded by plants (Curl and Truelove 1986, Bowen and Rovira 1991, Bolton et al. 1992). Because soil microorganisms differ in their potential to perform nutrient transformations and other beneficial functions (e.g., antagonism of pathogens), the composition of the microbial community in the rhizosphere will have important consequences for tree growth (Grayston et al. 1996). However, there has been little research on the nature of tree root exudates (Leyval and Berthelin 1993) or on the diversity of microorganisms in tree rhizospheres (Rambelli 1973, Malacziuk and McComb 1979, Linderman 1988).

The Biolog\textsuperscript{®} system is a commercially available redox-based sole carbon source utilization test (Biolog Inc., Hayward, CA) that is used to make metabolic fingerprints and hence enable identification of pure cultures of microorganisms (Biolog 1993). Recently, the Biolog system has been used to assess differences in microbial communities from diverse habitats (Garland and Mills 1991), soil types (Winding 1994) and grasslands (Zak et al. 1994) and to quantify the impact of heavy metals on microbial diversity (Campbell et al. 1995). In all of these studies, multivariate analysis of the carbon substrate utilization profiles facilitated classification of microbial communities based on their metabolic abilities. The technique is, therefore, an ecologically relevant method to measure biodiversity, because it determines differences in community utilization of carbon, a key factor governing microbial growth in soil. The community approach to measuring biodiversity may provide more information than measuring the presence of individuals in the population, which may not relate to the function of the community as a whole.

The objective of this study was to determine the taxonomic and metabolic diversity of microbial communities from the rhizospheres and rhizoplanes of two tree species, hybrid larch \((Larix\ eurolepis\ L.\ Henry)\) and Sitka spruce \((Picea\ sitchensis\ Bong.\ Carr.)\) growing at three different forest sites, two second-rotation forest plantations and a farm woodland. We tested the hypothesis that microbial communities from the rhizospheres of different tree species and different sites vary in their rate of
utilization of C sources because of differences in community composition.

Materials and methods

Sample collection

Rhizosphere soil samples were collected from three sites in the Grampian Region in northeastern Scotland. Samples were taken from monoculture stands of two tree species, hybrid larch (Larix eurolepis) and Sitka spruce (Picea sitchensis) at two second-rotation plantation forest sites, Durris (NO 772917, 2°22′32″ W 57°0′58″ N, Countesswells Series) and Midmar (NJ 695005, 2°30′14″ W 57°8′22″ N, Countesswells Series), and a farm woodland site at Lower Affleck (NJ 864239, 2°13′33″ W 57°18′20″ N, Thistlyhill Series). All tree species were of the same age (7 years) and had been planted four years previously. Trees at the forest site were planted at 2,500 stems ha⁻¹, whereas trees at the farm forest at Lower Affleck were planted at a density of 4,000 stems ha⁻¹. The ground vegetation consisted of grasses and herbs. At each site, triplicate soil and root samples were collected to a depth of 15 cm with a soil corer (5 cm in diameter) and bulked for each of three replicates for each tree species.

Carbon utilization profiles

Rhizosphere communities were extracted by shaking 10 g of rhizosphere soil (soil adhering to roots) in 100 ml of 0.25-strength Ringers solution (Oxoid, Unipath Ltd., Basingstoke, U.K.) for 10 min. In a sequential process, the rhizoplane communities were then extracted by shaking 5 g of the washed roots in 50 ml of Ringers solution containing glass beads (20 g) on a wrist action shaker for 10 min. Biolog GN microplates (Biolog Inc., Hayward, CA) were used to determine the metabolic diversity of the microbial communities from these samples. The 96-well microtiter plate contained 95 different carbon sources and a control well with no carbon source (Biolog 1993). Each well also contained a redox indicator dye, tetrazolium violet, and nutrients in dehydrated form, which were rehydrated on addition of the sample (Bochner 1989). A 50-ml aliquot of a 10⁻⁴ dilution of each rhizosphere and rhizoplane sample was centrifuged at 750 g for 10 min to remove any soil or root particles that might introduce extraneous carbon into the wells. The 10⁻⁴ dilution was chosen to minimize background color in the inoculum and was consistent for all samples to reduce confounding effects on rates of color development caused by different inoculum densities (Garland and Mills 1991). A 150-μl aliquot of the supernatant from the centrifuged samples was added to each of the 96 wells in the GN microplate. Plates were incubated at 25 °C and color development was measured as absorbance at 590 nm every 24 h for 120 h with an optical density (OD) plate reader.

The data were evaluated by canonical variate analysis (CVA) to differentiate samples based on the overall pattern of carbon utilization and to identify which carbon sources influenced the discrimination. Previous studies (Garland and Mills 1991, Winding 1994) noted a correlation between inoculum cell density and rate of color development that was corrected for, when data were transformed, by dividing each well OD by the average well color development (AWCD) for that sample (Garland and Mills 1991). The AWCD of different carbon substrate groups (e.g., carbohydrates, carboxylic acids, amino acids, amides, polymers and miscellaneous compounds) was calculated (as defined by Zak et al. 1994) and treatment effects assessed by a three-way ANOVA. Canonical variate analysis (CVA) and ANOVA were performed using Genstat 5.3 (Copyright 1992, Lawes Agricultural Trust, Rothamsted Experimental Station, U.K.).

Plate counts of microbial populations

The same rhizosphere and rhizoplane community samples used in the carbon utilization profiles were serially diluted and 0.1 ml suspensions spread, in duplicate, on the following selective media: Tryptone Soy agar (Oxoid, 0.1 strength) plus cycloheximide (50 mg l⁻¹) for enumeration of bacteria and actinomycetes; Pseudomonas Isolation agar (Oxoid), which is selective for populations of pseudomonads; and Rose Bengal agar (Oxoid) for enumeration of yeasts and fungi. The plates were incubated at 25 °C and colonies counted after 4 days for pseudomonads and fungi and after 14 days for bacteria and actinomycetes. An ANOVA was used to determine statistically significant treatment differences according to the F-test, and the LSD for the 95% confidence interval (LSD₀.₀5) value was used in multiple comparisons. Isolates from the Pseudomonas Isolation agar were identified using the Biolog® system (Biolog 1993). Microlog software (Biolog Inc.) was used to identify cultures based on their metabolic profiles.

Results

Carbon utilization profiles

Color development in the Biolog wells generally followed a sigmoidal curve with incubation time but varied for different groups of carbon sources (Figure 1). The order of highest utilization after 120 h was carbohydrates > amino acids > miscellaneous compounds > polymers > amides > carboxylic acids. The AWCD for each group of carbon compounds showed that there was significantly greater utilization of carbohydrates by microbial communities in rhizosphere soil compared with those on the rhizoplane (Table 1). Microbial communities from the farm woodland site at Lower Affleck tended to have greater rates of utilization of all six groups of C sources than microbial communities taken from either of the two second-rotation forest sites at Durris and Midmar (Table 1). The two tree species exhibited differences in carbon utilization. At the Durris site, there was significantly higher utilization of amino acids by the microbial communities from the larch rhizosphere and rhizoplane than from the Sitka spruce rhizosphere and rhizoplane (Table 1).

Multivariate analysis was performed on all data from each incubation time to identify patterns of response among samples. The results presented are those after 24 h of incubation because this incubation time resulted in the greatest discrimination among treatments. The different soils had distinct patterns of carbon utilization (Figure 2). The most distinctive
patterns were obtained with samples from the farm woodland site at Lower Affleck, which had lower coordinate values on canonical variate (CV)-1 (which explained 38.5% of the variance in the data) than the two second-rotation forest sites at Midmar and Durris. The two forest sites showed some separation on the CV-2 axis (which explained 15% of the data variance) with Midmar samples possessing a lower canonical score than Durris samples (Figure 2). The samples from larch at Durris were most distinct, being separated mainly on CV-1, but with clear separation of the rhizosphere and rhizoplane on CV-2 as well (Figure 2). The ANOVA of the AWCD of the carbon compounds responsible for discrimination of CV indicated that microbial communities in the farm woodland had significantly greater utilization of several carboxylic acids. In addition, microbial communities from Durris showed significantly greater utilization of cellobiose than those from Midmar.

In addition to separation among the forest sites, there was also clear clustering of samples between different tree species and root sample zones (Figure 2). On CV-2, the separation of microbial communities (e.g., Durris larch rhizosphere and rhizoplane) was the result of differences in utilization of several carbohydrates (N-acetyl glucosamine, adonitol, cellobiose and xylitol), carboxylic acids (β-galactonic acid lactone, itaconic acid and succinic acid) and the amide 2-amino-ethanol.

The discrimination between larch and Sitka spruce was mainly a result of differences in utilization of some carboxylic acids and amino acids (Table 2). Differences in utilization of carbon sources between rhizosphere and rhizoplane samples from the same tree species were only found at Midmar, where microbial communities from the larch rhizoplane had significantly lower utilization of all carbon compounds listed in Table 3 than microbial communities from the larch rhizosphere.

**Microbial populations**

Rhizosphere and rhizoplane samples from the farm woodland at Lower Affleck contained significantly higher populations of all microorganisms than samples from the second-rotation forest sites at Durris and Midmar (Figure 3). There were no significant quantitative differences between populations of microorganisms associated with the different tree species, but there were clear trends in associations (Figure 4). For example, Sitka spruce had higher populations of fungi in its rhizosphere and on its rhizoplane than larch, except for rhizoplane samples from Midmar (Figure 4). There were more bacteria in the rhizosphere and on the rhizoplane of larch than of Sitka spruce, except for rhizosphere samples at Midmar. In addition to quantitative differences in microorganisms between the two tree species at the different sites, there were also qualitative differences. At Lower Affleck, there were significantly greater numbers and species of pseudomonads than at the two other sites (Figure 5) and these pseudomonads constituted a high proportion of the bacterial population. The Sitka spruce rhizosphere soils and rhizoplane contained significantly higher populations of pseudomonads than those of larch at every site except for the rhizosphere samples at Durris (Figure 5). Cultures of these pseudomonads included a mixture of fluorescent (P. fluorescens Type G., P. corrugata, P. putida) and non-fluorescent species (P. cepacia) from the Sitka spruce rhizosphere and rhizoplane, whereas non-fluorescent species dominated in the larch rhizosphere.

Twenty fungal species were isolated from the three forest sites. Nine species were present at Lower Affleck, one of which was site specific. Sixteen species were found at the Durris site, five of which were not isolated from the other sites. Twelve species of fungi were present in the Midmar samples; three were site specific. All sites appeared to have the same dominant fungal genera: Trichoderma sp., Penicillium sp., Fusarium sp., Mucor sp., Rhizopus sp. and Aspergillus sp. At all sites, Trichoderma and Penicillium species dominated the rhizosphere of larch, and Aspergillus species dominated the rhizosphere of Sitka spruce.

Thirteen species of yeast were isolated from the three sites, eleven from Lower Affleck, three of which were not found at the other sites. Nine species were found at Durris, of which two were site specific. Eight species were found at Midmar, all of which were present at the other sites. In addition, two yeast species were specific to larch and two were specific to Sitka spruce.
Discussion

We found quantitative and qualitative differences in the microbial populations of the rhizospheres of hybrid larch and Sitka spruce. These populations also varied depending on the soil type where the trees were grown. We demonstrated that the Biolog system can be used as a rapid screening technique to discriminate among microbial communities from different tree species and habitats based on metabolic profiles. The use of differential utilization of a range of carbon compounds to assess microbial diversity is an ecologically relevant method for measuring diversity, because carbon is one of the main influences on microbial growth in soil (Wardle 1992). However, the technique can only elucidate the causal relationship in conjunction with information about what exudates are produced by trees. We found that the microbial communities from the farm woodland system at Lower Affleck exhibited more rapid utilization of all six groups of carbon compounds contained in the Biolog plate than the microbial communities from the two second-rotation forest systems, indicating different metabolic profiles between the farm woodland and second-rotation forest systems. The plate counts also confirmed that there were qualitative and quantitative differences in the microbial communities between the forest sites.

<table>
<thead>
<tr>
<th>Carbon compound</th>
<th>Forest site</th>
<th>Hybrid larch</th>
<th>Sitka spruce</th>
<th>LSD (0.05)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Rhizoplane</td>
<td>Rhizosphere</td>
<td></td>
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<tr>
<td>Carbohydrates</td>
<td>Lower Affleck</td>
<td>0.715</td>
<td>0.739</td>
<td>0.789</td>
</tr>
<tr>
<td></td>
<td>Durris</td>
<td>0.654</td>
<td>0.857</td>
<td>0.485</td>
</tr>
<tr>
<td></td>
<td>Midmar</td>
<td>0.244</td>
<td>0.567</td>
<td>0.326</td>
</tr>
<tr>
<td></td>
<td>Mean (all sites)</td>
<td>0.537</td>
<td>0.721</td>
<td>0.533</td>
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<tr>
<td>Carboxylic acids</td>
<td>Lower Affleck</td>
<td>0.535</td>
<td>0.497</td>
<td>0.584</td>
</tr>
<tr>
<td></td>
<td>Durris</td>
<td>0.378</td>
<td>0.469</td>
<td>0.325</td>
</tr>
<tr>
<td></td>
<td>Midmar</td>
<td>0.239</td>
<td>0.405</td>
<td>0.310</td>
</tr>
<tr>
<td></td>
<td>Mean (all sites)</td>
<td>0.384</td>
<td>0.457</td>
<td>0.407</td>
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<td>0.666</td>
<td>0.769</td>
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<td></td>
<td>Durris</td>
<td>0.464</td>
<td>0.675</td>
<td>0.370</td>
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<td></td>
<td>Midmar</td>
<td>0.232</td>
<td>0.414</td>
<td>0.343</td>
</tr>
<tr>
<td></td>
<td>Mean (all sites)</td>
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<td>0.585</td>
<td>0.494</td>
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<tr>
<td>Amides</td>
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<td>0.427</td>
<td>0.332</td>
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<tr>
<td></td>
<td>Durris</td>
<td>0.238</td>
<td>0.256</td>
<td>0.131</td>
</tr>
<tr>
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<td>Midmar</td>
<td>0.082</td>
<td>0.210</td>
<td>0.169</td>
</tr>
<tr>
<td></td>
<td>Mean (all sites)</td>
<td>0.249</td>
<td>0.266</td>
<td>0.248</td>
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<tr>
<td>Polymers</td>
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<td>0.546</td>
<td>0.523</td>
<td>0.497</td>
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<td></td>
<td>Durris</td>
<td>0.416</td>
<td>0.364</td>
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<tr>
<td></td>
<td>Midmar</td>
<td>0.209</td>
<td>0.349</td>
<td>0.260</td>
</tr>
<tr>
<td></td>
<td>Mean (all sites)</td>
<td>0.390</td>
<td>0.412</td>
<td>0.361</td>
</tr>
<tr>
<td>Miscellaneous</td>
<td>Lower Affleck</td>
<td>1.101</td>
<td>1.051</td>
<td>1.050</td>
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<td></td>
<td>Durris</td>
<td>0.815</td>
<td>1.067</td>
<td>0.680</td>
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<tr>
<td></td>
<td>Midmar</td>
<td>0.347</td>
<td>0.546</td>
<td>0.304</td>
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<tr>
<td></td>
<td>Mean (all sites)</td>
<td>0.754</td>
<td>0.888</td>
<td>0.678</td>
</tr>
</tbody>
</table>

1 Values are means of three replicate samples.
in arable farming systems, likely removed any nutrient limitation to microbial growth in the soil. In addition, annual herbaceous plants exude more of their assimilated carbon into the soil than trees (Leyval and Berthelin 1993, Grayston et al. 1996) and also exude a different spectrum of compounds (Grayston et al. 1996), which would influence microbial community structure. The second rotation forest soils also had a lower pH than the farm woodland system. An increase in pH has been shown to increase root exudation in grasses (Meharg and Killham 1990). In addition, bacteria prefer more neutral soil conditions and therefore the low pH of the second-rotation forest soils would select against these microorganisms.

The Biolog system assesses the metabolic diversity of the culturable bacteria only, because fungal growth is too slow to have an influence on the profile (Garland and Mills 1991). Heuer et al. (1995) recently demonstrated that species of Enterobacter were mainly responsible for the color development in Biolog wells by using 16S rRNA probes, after inoculation with microbial communities from the phyllosphere and rhizosphere of potato plants. At Lower Affleck, a high proportion of the bacterial population consisted of Pseudomonas species, which likely accounts for the higher utilization of the carbon sources in the Biolog plate by the microbial communities from this site compared with those from the second-rotation forest sites.

Another factor that could have influenced exudation patterns and hence microbial diversity is the presence of different mycorrhizal symbionts (Molina et al. 1992). Native mycorrhizal

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Table 3. Average well color development in the Biolog GN plates by microbial communities from a farm woodland site (Lower Affleck) and two second-rotation forest sites (Durris and Midmar).  

<table>
<thead>
<tr>
<th>Carbon compound</th>
<th>Forest site</th>
<th>Lower Affleck</th>
<th>Durris</th>
<th>Midmar</th>
<th>LSD (0.05)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Carbohydrates</td>
<td>N-Acetyl galactosamine</td>
<td>0.95</td>
<td>0.69</td>
<td>0.68</td>
<td>0.27</td>
</tr>
<tr>
<td></td>
<td>N-Acetyl glucosamine</td>
<td>1.18</td>
<td>0.74</td>
<td>0.52</td>
<td>0.28</td>
</tr>
<tr>
<td></td>
<td>Cellobiose</td>
<td>1.11</td>
<td>0.78</td>
<td>0.46</td>
<td>0.19</td>
</tr>
<tr>
<td>Carboxylic acids</td>
<td>d-Galacturonic acid lactone</td>
<td>0.36</td>
<td>0.27</td>
<td>0.30</td>
<td>0.06</td>
</tr>
<tr>
<td></td>
<td>d-Glucoronic acid</td>
<td>1.25</td>
<td>1.01</td>
<td>0.87</td>
<td>0.24</td>
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<tr>
<td></td>
<td>d-Galacturonic acid</td>
<td>1.36</td>
<td>0.66</td>
<td>0.74</td>
<td>0.24</td>
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<td></td>
<td>γ-Hydroxybutyric acid</td>
<td>0.80</td>
<td>0.53</td>
<td>0.46</td>
<td>0.12</td>
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<td>Malonic acid</td>
<td>0.91</td>
<td>0.73</td>
<td>0.69</td>
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<tr>
<td></td>
<td>Itaconic acid</td>
<td>1.06</td>
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<td>0.38</td>
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<tr>
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<td>Succinic acid</td>
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<td>0.28</td>
<td>0.28</td>
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<td>Amino acids</td>
<td>Serine</td>
<td>1.14</td>
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<td></td>
<td>γ-Aminobutyric acid</td>
<td>0.65</td>
<td>0.38</td>
<td>0.37</td>
<td>0.10</td>
</tr>
</tbody>
</table>

1 Values are means of 12 samples.
zal fungi present in the soil are thought to infect tree roots (Bledsoe 1992). Therefore, the lack of previous tree growth at Lower Affleck may have resulted in a poorer and less diverse infection than at the second-rotation forest sites. Mycorrhizae differ in their carbon storage patterns and their conversion of plant sugars to metabolic intermediates (Finlay and Söderstrom 1992), and these differences could result in alterations in the quality and quantity of carbon released from tree roots.

Leyval and Berthelin (1993) showed that beech (*Fagus sylvatica* L.) infected with *Laccaria laccata* exuded more sugars and amino acids and a different range of organic acids than non-mycorrhizal beech or mycorrhizal Scots pine (*Pinus sylvestris* L.). Our results suggest that hybrid larch and Sitka spruce may produce different exudates because the carbon profiles of the microorganisms from the rhizosphere of these two tree species vary, mainly as a result of differences in carboxylic acid and amino acid usage. Previously, we found that utilization of carboxylic acids was highly variable in rhizosphere samples from different tree species growing in the same soil type (Grayston et al. 1994). Although the carbon compounds exuded by hybrid larch and Sitka spruce have not been characterized, it is known that the quantity and character of root exudates released by trees vary considerably among species (see review by Grayston et al. 1996). A wide range of organic acids, which are quantitatively the most important organic component of tree root exudates (Smith 1976), are produced by different tree species. For example, gluconic and malonic acids, which showed differential utilization between larch and Sitka spruce microbial communities (Table 2), are produced by some *Pinus* species, but not by others (Grayston et al. 1996). The types of amino acids exuded are also highly variable; deciduous trees produce cystine and homoserine, whereas these amino acids have not been isolated from exudates of evergreens (Grayston et al. 1996).

Variation in metabolic diversity by microbial communities from the rhizosphere of the two tree species was accompanied
by differences in the culturable populations present. There appeared to be tree- and site-specific bacteria, actinomycetes and yeasts. All the fungal species isolated were present at each site and with both tree species, although the dominant fungal types changed with tree species. However, all the fungal species isolated are prolific spore producers and therefore one must be cautious when interpreting the results of these plate count data. At Lower Affleck, a high proportion of the bacterial population consisted of Pseudomonas species, whereas at the second-rotation forest sites there was a greater diversity of actinomycetes. At every site, the larch rhizosphere contained fewer fluorescent pseudomonads than the Sitka spruce rhizosphere. There have been relatively few studies on microbial diversity in the rhizosphere of trees (Fitter and Garbaye 1994) and none on hybrid larch or Sitka spruce. Studies comparing mycorrhizal and non-mycorrhizal yellow birch (Katznelson et al. 1962), red alder and Douglas-fir (Neal et al. 1968), various coniferous (Oswald and Ferchau 1968) and Eucalyptus species (Malacjzuk and McComb 1979) have shown distinct communities of microorganisms associated with different trees. There is evidence that these rhizosphere microorganisms can enhance tree growth through the production of plant growth regulators (Strelczyk and Pokojska-Burdziej 1984, Strelczyk and Leniarka 1985), nitrogen fixation (Li and Castellano 1987, Li and Hung 1987), solubilization of inorganic phosphates (Leyval and Berthelin 1991) and stimulation of mycorrhization of trees (Garbaye 1994).

Conclusions

We found significant differences in the utilization of various carbon sources by microbial communities from the rhizospheres of larch and Sitka spruce at different sites as a consequence of variation in the species composition of the different microbial populations. The identification of root exudates from these tree species and inclusion of these carbon sources in future utilization tests will improve the resolution of the technique. Measurement of the production of different types of exudates in the tree would allow us to link utilization rates directly with exudation. The beneficial effects of rhizosphere microorganisms on tree growth highlight the need for a greater understanding of microbial community structure and function in the rhizosphere.

Acknowledgments

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References


