ABSTRACT

The soil harbors an extensive community of microorganisms comprised of bacterial, fungal, and archaeal species. The microbial diversity of a soil microbial community can influence the environmental conditions and ecosystem services provided by the soil. To explore microbial diversity and antibiotic resistance in soil, we performed the phylogenetic analysis of 60 soil isolates from the UCLA Botanical Garden using the 16S rRNA gene sequences. Soil samples were collected from a total of nine sites (nine soil samples) across the UCLA Botanical Garden. An average of 87% of the isolates were classified using environmental databases, and the remaining isolates were characterized through the GenBank database. The 16S rRNA gene sequences were analyzed for antibiotic resistance using the National Institute of Allergy and Infectious Diseases (NIAID) antibiotic database.

RESULTS

1. The soil isolates were sequenced and compared to the GenBank 16S rRNA gene database. The isolates were classified into five major phylogenetic groups: Gammaproteobacteria, Alphaproteobacteria, Actinobacteria, Bacteroidetes, and Firmicutes.

2. Four of the 60 isolates produced antibiotics against the Gram-positive indicator bacteria Micrococcus luteus (Table 1). Two of these isolates were sequenced, and one was characterized as an antibiotic producer.

3. Three of the 23 sequenced isolates were resistant to erythromycin: one Bacillus (Clone 35) and two Bacillus (Bacterium C22 and Bacillus pumilus) (Table 2). All of these isolates were sequenced, and only one was characterized as an antibiotic producer.

4. Test the 23 isolates for antibiotic resistance (Fig. 4, Table 2).

OBJECTIVES

1. Generate a 16S rRNA phylogenetic tree to illustrate the microbial diversity within the soil isolates.

2. Perform preliminary characterization of the soil isolates.

3. Test the 23 isolates for antibiotic resistance (Fig. 4, Table 2).

4. Complete daptomycin resistance demonstrated by isolate 42 (MIC < 0.1 μg/mL) (Fig. 3).

5. Three isolates have no phylogenetic affiliation with any of the major groups typically represented in culture-independent surveys. The phylogenetic analysis indicates enrichment bias likely obtained in current study.

6. Nested hierarchy, which suggests differences between phylogenetic and taxonomic classification systems for some classes within the phyla Proteobacteria, Bacteroidetes, Firmicutes, Chloroflexi and Planctomycetes are detected in 25–75% of the culture-independent studies.

7. Assess the total phylogenetic diversity within soil samples and test the limitations of the current method of analysis by performing culture-independent molecular surveys using PCR-mediated amplification of the SSU rRNA gene sequences from DNA extracted directly from soil.

8. Test the 23 isolates for antibiotic resistance (Fig. 4, Table 2).

9. Complete daptomycin resistance demonstrated by isolate 42 (MIC < 0.1 μg/mL) (Fig. 3).

10. Three isolates have no phylogenetic affiliation with any of the major groups typically represented in culture-independent surveys. The phylogenetic analysis indicates enrichment bias likely obtained in current study.

11. Nested hierarchy, which suggests differences between phylogenetic and taxonomic classification systems for some classes within the phyla Proteobacteria, Bacteroidetes, Firmicutes, Chloroflexi and Planctomycetes are detected in 25–75% of the culture-independent studies.

12. Assess the total phylogenetic diversity within soil samples and test the limitations of the current method of analysis by performing culture-independent molecular surveys using PCR-mediated amplification of the SSU rRNA gene sequences from DNA extracted directly from soil.

13. Test the 23 isolates for antibiotic resistance (Fig. 4, Table 2).

14. Complete daptomycin resistance demonstrated by isolate 42 (MIC < 0.1 μg/mL) (Fig. 3).

15. Three isolates have no phylogenetic affiliation with any of the major groups typically represented in culture-independent surveys. The phylogenetic analysis indicates enrichment bias likely obtained in current study.

16. Nested hierarchy, which suggests differences between phylogenetic and taxonomic classification systems for some classes within the phyla Proteobacteria, Bacteroidetes, Firmicutes, Chloroflexi and Planctomycetes are detected in 25–75% of the culture-independent studies.

17. Assess the total phylogenetic diversity within soil samples and test the limitations of the current method of analysis by performing culture-independent molecular surveys using PCR-mediated amplification of the SSU rRNA gene sequences from DNA extracted directly from soil.

18. Test the 23 isolates for antibiotic resistance (Fig. 4, Table 2).

19. Complete daptomycin resistance demonstrated by isolate 42 (MIC < 0.1 μg/mL) (Fig. 3).

20. Three isolates have no phylogenetic affiliation with any of the major groups typically represented in culture-independent surveys. The phylogenetic analysis indicates enrichment bias likely obtained in current study.

21. Nested hierarchy, which suggests differences between phylogenetic and taxonomic classification systems for some classes within the phyla Proteobacteria, Bacteroidetes, Firmicutes, Chloroflexi and Planctomycetes are detected in 25–75% of the culture-independent studies.

22. Assess the total phylogenetic diversity within soil samples and test the limitations of the current method of analysis by performing culture-independent molecular surveys using PCR-mediated amplification of the SSU rRNA gene sequences from DNA extracted directly from soil.

23. Test the 23 isolates for antibiotic resistance (Fig. 4, Table 2).

24. Complete daptomycin resistance demonstrated by isolate 42 (MIC < 0.1 μg/mL) (Fig. 3).

25. Three isolates have no phylogenetic affiliation with any of the major groups typically represented in culture-independent surveys. The phylogenetic analysis indicates enrichment bias likely obtained in current study.

26. Nested hierarchy, which suggests differences between phylogenetic and taxonomic classification systems for some classes within the phyla Proteobacteria, Bacteroidetes, Firmicutes, Chloroflexi and Planctomycetes are detected in 25–75% of the culture-independent studies.

27. Assess the total phylogenetic diversity within soil samples and test the limitations of the current method of analysis by performing culture-independent molecular surveys using PCR-mediated amplification of the SSU rRNA gene sequences from DNA extracted directly from soil.

28. Test the 23 isolates for antibiotic resistance (Fig. 4, Table 2).

29. Complete daptomycin resistance demonstrated by isolate 42 (MIC < 0.1 μg/mL) (Fig. 3).

30. Three isolates have no phylogenetic affiliation with any of the major groups typically represented in culture-independent surveys. The phylogenetic analysis indicates enrichment bias likely obtained in current study.

31. Nested hierarchy, which suggests differences between phylogenetic and taxonomic classification systems for some classes within the phyla Proteobacteria, Bacteroidetes, Firmicutes, Chloroflexi and Planctomycetes are detected in 25–75% of the culture-independent studies.

32. Assess the total phylogenetic diversity within soil samples and test the limitations of the current method of analysis by performing culture-independent molecular surveys using PCR-mediated amplification of the SSU rRNA gene sequences from DNA extracted directly from soil.

33. Test the 23 isolates for antibiotic resistance (Fig. 4, Table 2).

34. Complete daptomycin resistance demonstrated by isolate 42 (MIC < 0.1 μg/mL) (Fig. 3).

35. Three isolates have no phylogenetic affiliation with any of the major groups typically represented in culture-independent surveys. The phylogenetic analysis indicates enrichment bias likely obtained in current study.

36. Nested hierarchy, which suggests differences between phylogenetic and taxonomic classification systems for some classes within the phyla Proteobacteria, Bacteroidetes, Firmicutes, Chloroflexi and Planctomycetes are detected in 25–75% of the culture-independent studies.

37. Assess the total phylogenetic diversity within soil samples and test the limitations of the current method of analysis by performing culture-independent molecular surveys using PCR-mediated amplification of the SSU rRNA gene sequences from DNA extracted directly from soil.

38. Test the 23 isolates for antibiotic resistance (Fig. 4, Table 2).

39. Complete daptomycin resistance demonstrated by isolate 42 (MIC < 0.1 μg/mL) (Fig. 3).

40. Three isolates have no phylogenetic affiliation with any of the major groups typically represented in culture-independent surveys. The phylogenetic analysis indicates enrichment bias likely obtained in current study.

41. Nested hierarchy, which suggests differences between phylogenetic and taxonomic classification systems for some classes within the phyla Proteobacteria, Bacteroidetes, Firmicutes, Chloroflexi and Planctomycetes are detected in 25–75% of the culture-independent studies.

42. Assess the total phylogenetic diversity within soil samples and test the limitations of the current method of analysis by performing culture-independent molecular surveys using PCR-mediated amplification of the SSU rRNA gene sequences from DNA extracted directly from soil.

43. Test the 23 isolates for antibiotic resistance (Fig. 4, Table 2).

44. Complete daptomycin resistance demonstrated by isolate 42 (MIC < 0.1 μg/mL) (Fig. 3).

45. Three isolates have no phylogenetic affiliation with any of the major groups typically represented in culture-independent surveys. The phylogenetic analysis indicates enrichment bias likely obtained in current study.

46. Nested hierarchy, which suggests differences between phylogenetic and taxonomic classification systems for some classes within the phyla Proteobacteria, Bacteroidetes, Firmicutes, Chloroflexi and Planctomycetes are detected in 25–75% of the culture-independent studies.