Identification of Bacterial Species Using 16S rRNA Microarray Technology

Bioinformatics Program, University of the Sciences in Philadelphia

Abstract

The goal of this project was to develop DNA-based microarray technology that could be used to identify unknown bacteria. To this end, we have successfully developed a PCR-based culture-free system for the identification of unknown bacterial species. By targeting the 16S ribosomal RNA (rRNA) gene region of the bacterial genome, we have been able to design and synthesize DNA probes that can hybridize to the 16S rRNA of many different bacterial species. These probes are then used to identify unknown bacterial species by hybridizing to a microarray slide. The microarray slide is then scanned with a fluorescence intensity scanner, and the resulting signal is analyzed to determine which bacterial species were present in the sample.

Introduction

Microarray technology has become an important tool in microbiology for the identification of large sets of nucleic acids (DNA and RNA) and proteins. The use of microarrays in our exercise is based on the recent discovery of DNA microarrays that can be used to identify unknown bacterial species. These microarrays are based on the 16S rRNA gene, which is the predominant ribosomal RNA gene. The 16S rRNA gene is used to identify bacteria because it is highly conserved across different bacterial species.

Methods

16S Microarray Construction

The 16S rRNA microarray was constructed by synthesizing DNA probes that are complementary to the 16S rRNA gene. The DNA probes were then labeled with either Cy3 or Cy5 fluors. The labeled DNA probes were then hybridized to the microarray slide, and the resulting signal was analyzed to determine which bacterial species were present in the sample.

Results

Figure 1: Graphical representation of the 16S rRNA microarray results. The x-axis represents the bacterial species, and the y-axis represents the fluorescence intensity. The color of the bar represents the relative fluorescence intensity. The bacterial species are ordered by the level of fluorescence intensity, with the highest intensity shown in red and the lowest intensity shown in green.

Conclusions

We have developed a DNA-based microarray technology that can be used to identify unknown bacterial species. This technology is based on the recent discovery of DNA microarrays that can be used to identify unknown bacterial species. The 16S rRNA gene is used to identify bacteria because it is highly conserved across different bacterial species. The DNA microarrays are based on the 16S rRNA gene, which is the predominant ribosomal RNA gene. The DNA microarrays are used to identify unknown bacterial species by hybridizing to a microarray slide. The microarray slide is then scanned with a fluorescence intensity scanner, and the resulting signal is analyzed to determine which bacterial species were present in the sample.

References


Figure 1: Graphical representation of the 16S rRNA microarray results. The x-axis represents the bacterial species, and the y-axis represents the fluorescence intensity. The color of the bar represents the relative fluorescence intensity. The bacterial species are ordered by the level of fluorescence intensity, with the highest intensity shown in red and the lowest intensity shown in green.