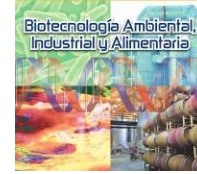


Poster



Metagenomic and metabarcoding analysis of microbial populations in agricultural soils using 16S ribosomal sequencing and database development

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ABSTRACT

Motivation: Metagenomic and metabarcoding analyses of microbial populations present in agricultural soils using 16S ribosomal region sequencing and processing technology are performed to understand the microbial diversity and their role in crop productivity, as well as to identify possible environmental impacts.

Methods: A bioinformatic analysis is carried out involving taxonomic assignment of the sequences to different microbial groups. This analysis is performed by comparing the obtained sequences with public databases containing information on the diversity of 16S gene sequences. A data filtering and purification process is carried out to eliminate low-quality sequences. The methodology used involves the use of three taxonomic assignment methods: 1. a classical method of taxonomical assignment using a generalist database of public use, 2. a single assignment step using a specific database with a predictive algorithm, and 3. two-step method of taxonomical assignment involving different algorithms using a specific database. A comparison is made between the three methods to determine which is the most effective in taxonomic identification. Additionally, statistical tools can be used to determine the abundance of different microbial taxa present in soils. Finally, work is done on improving the specific database by expanding its information to obtain more accurate results.

Results: The results obtained show that the use of a specific database for agricultural soils produces more accurate results in taxonomic identification. This is because the databases contain general information on a wide variety of samples, which can introduce noise and make it difficult to accurately identify the microbes present. By expanding the specific database, an improvement in the accuracy of the results is observed.

Conclusions: In conclusion, metabarcoding is an important tool for understanding microbial diversity. The characteristics of the database used in taxonomic identification have a great impact on the taxonomic results. It can be affirmed that the use of different databases has a significant impact on the identification of the most abundant taxa. Additionally, the improvement and maintenance of databases are essential to obtain more accurate results and should be continued to be researched and updated to maintain the effectiveness of the technology used.

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