

Biolog for the determination of diversity in microbial communities

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Abstract

Diversity and dynamics of microbial communities have been analysed by culture-dependent methods, which exclude the majority of fastidious microbes due to the selective nature of the media. Molecular methods have been used to determine diversity of microbial communities, but indicate the genetic complexity within a community. An alternative approach is to examine components of functional biodiversity (i.e. substrate utilisation), for which there exists a reasonable chance of detecting patterns, which could be related to the functional diversity of the species present in the community. In this study, different carbon source profiles were generated by inoculating Biolog GN and GP microtitre plates, with different dilutions of microbial communities. The high number of substrates utilised at the lower dilutions (10^{-1} and 10^{-2}) indicated a high functional diversity in the communities tested. This, however, did not necessarily reflect the evenness of the functionality. Functional evenness of each species was reflected upon further dilution. Our results indicated differences in the functional diversity of the microbial communities amongst some of the natural environments studied. The results indicated that evenness and dominance can be demonstrated by mixtures of cultures as well as in natural environments.

Introduction

The majority of micro-organisms in their natural habitat cannot be cultured and remain unidentified (Cloete et al., 1992; Haldeman and Amy, 1993; Wagner et al., 1993). This has led to a lack of knowledge of microbial community composition and function. Recently, molecular techniques have been used in microbial ecology studies in an attempt to overcome the limitations of culture techniques (Pace et al., 1986; Wagner et al., 1993; Amann et al., 1995; Muyima et al., 1997). These techniques require a high level of expertise and sophistication and are often tedious (Schwieger and Tebbe, 1998). The techniques are qualitative and not quantitative (Muyima et al., 1997). Hence, there is a need for techniques that characterise microbial communities without the reliance on selective culturing and which are less complex than molecular techniques.

Microbial communities can be considered to be systems containing information (data), which is related primarily to microbial diversity. The higher the diversity, the more the information. By employing molecular techniques, it is currently attempted to translate this information into meaningful data. Molecular techniques rely on information in a microbial community which are extracted as molecules from the genome of the different members of the community (Torsvik et al., 1990). This would indicate genetic complexity, which could, in turn, be attributed to microbial diversity in the system. A more simplistic and effective method is, however, required to achieve this translation and interpretation of data.

In any given system one or more species exists, each performing a certain function. The more species, the more functions related to their metabolism. It can be said that a specific microbial community has a specific metabolic capacity. Functional diversity can be determined in terms of the presence, absence or rate of substrate utilisation (Griffiths et al., 1997). Griffiths et al. (1997) indicated

that there could be changes in microbial community structure with no changes in function, but that function was affected below a certain level of species diversity (microbial capacity). One of the objectives of this study was to determine the microbial capacity of the community to utilise certain selected substrates to functional diversity. The hypothesis is that the more substrates utilised, the higher the diversity, due to the collective action of individual species.

Any one organism will not necessarily utilise all the available substrates in a system, nor does the utilisation of some of the substrates suggest that this is the complete set of substrates which a particular organism can use because of:

- competition, which might suppress the activity of a particular organism;
- dominance where one organism utilises all the substrates in such a way that the contribution of other organisms to substrate utilisation is overshadowed and goes unnoticed;
- substrates which might not match the metabolic activity of a particular organism (meaning that it will not show up on the analysis);
- the system that might be selective, i.e. it would only allow the metabolic activities of aerobic or facultatively anaerobic, heterotrophic and copiotrophic micro-organisms which are capable of growing at sufficient rates on the substrates;
- dependence on the abundance of each species, i.e. the organisms present in higher numbers will be able to utilise the carbon sources easier than organisms present in low numbers;
- inoculum density which has an influence on the tempo and occurrence of colour development due to the growth rates of organisms on different substrates;
- incubation time that influences substrate utilisation of a community due to individual growth rates of the micro-organisms on different substrates (Wünsche et al., 1995);
- antagonistic interactions between organisms, where one organism inhibits another organism's growth and therefore its

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