ISOLATION OF NUCLEIC ACIDS FROM THE ENVIRONMENT – THE FIRST STEP IN METAGENOME ANALYSIS

Summary

Recently, increasing interest in ecology of microorganisms has been associated with the possibility of direct analysis of microbial community structure due to application of molecular methods based on isolated metagenome DNA. The metagenome approach can provide a cultivation-independent assessment of the largely untapped genetic reservoir of soil or water microbial communities. However, the crucial step in this approach is efficient extraction of high-quality total DNA representing the metagenome of a habitat. The DNA extraction methods for soil habitats are grouped into two major types, i.e. indirect based on the recovery of microbes (e.g. bacterial cells) and their subsequent lysis, and direct lysis of cells in the sample followed by DNA purification. The direct extraction of total DNA from an environmental sample presumably better represents its bacterial or fungal metagenome; hence, this approach has been used more often than the fractionation methods. Although direct extraction of DNA is less labour-intensive and yield more DNA, the recovered DNA fragments are usually smaller than those obtained by the indirect approach are. The fractionation method is advantageous for soil samples containing higher amounts of organic matter or other substances that interfere with DNA isolation. This method is also applied for DNA extraction from water samples. Microbial ecologists currently use different commercially available kits for total DNA isolation from soil or water. However, it would appear that the most efficient method of DNA extraction from environmental samples is still far from being established.