

Environmental and Agricultural Metagenomics: Crops Perspective

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Around 40% of crops worldwide are lost to pests and diseases and, even using modern farming techniques that include the use of pesticides and herbicides, this figure can reach 15-20% in Europe. However, over the next 5 years the use of pesticides and herbicides is set to reduce under new legislation. New and improved methods of crop protection are thus needed to maintain current food supplies and increase them into the future. Microbials, the use of microorganisms in crop production, is one area that is being actively pursued as a replacement for chemicals (including fertilizers to assist plant growth). We know that some microbes act together in what are called suppressive soils to reduce disease incidence of the growing crop. Amplicon sequencing of specific sections of nucleic acid within a microbe's genome (e.g. ribosomal RNA) can provide information about the different microbes present in a soil; groups that can then, in some cases, be isolated and tested for their suppressive abilities. This method can also be used to identify different groups of microbes on a range of plant parts, allowing us to investigate a variety of factors, including pathogen spread. While amplicon sequencing has allowed us to understand the makeup and distribution of microbial communities in the plant environment, there is the potential for much more information to become available through the use of metagenomics. Metagenomics examines nucleic acids from whole genomes of microbes within a community, and allows us to study changes in gene function in addition to microbial community composition. As well as crop protection and plant growth enhancement, such an approach has many other potential applications on plants. For example, it is being used to investigate changes in microbial communities, together with gene function related to metabolic processes, involved in the fermentation of rice and grapes. Investigating microbial populations and their cognate gene functions provides new possibilities for studying microbial communities on plants, and is set to allow rapid progress towards improved, chemical free, crop production.