Increasing phytoremediation efficiency and reliability using novel omics approaches

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Phytoremediation is a cost-effective green alternative to traditional soil remediation technologies, but has experienced varied success in practice. The recent omics revolution has led to leaps in our understanding of soil microbial communities and plant metabolism, and some of the conditions that promote predictable activity in contaminated soils and heterogeneous environments. Combinations of omics tools and new bioinformatics approaches will allow us to understand integrated activity patterns between plants and microbes, and determine how this metaorganism can be modified to maximize growth, appropriate assembly of microbial communities, and, ultimately, phytoremediation activity. Here we provide an overview of how new omics-mediated discoveries can potentially be translated into an effective and reliable environmental technology.

The challenge of harnessing plants for soil remediation

Phytoremediation is a cost-effective green alternative to traditional soil remediation technologies such as excavation followed by chemical processing. There are also additional benefits to this approach: biomass from plants grown in a contaminated area may be harvested for use as biofuel or, alternatively, plants may continue to grow on site, potentially acting as pioneer species for ecosystem regrowth, increasing local biodiversity, and contributing to atmospheric CO_2 fixation and the restructuring of disturbed soils. Phytoremediation efficiency is the result of synergistic interactions between plants and the surrounding environment, particularly microorganisms. For instance, plants may translocate and sequester compounds such as heavy metals, whereas it is primarily microorganisms that degrade organic contaminants (Box 1).

Despite the enormous promise of phytoremediation, it has yet to gain traction as a viable remediation alternative,

mainly because of its variable effectiveness. The uncertainty of full and rapid site remediation is cited as a major impediment to investment in phytoremediation technologies [1]. For example, organic phytoremediation efficiency has varied depending on the concentration and composition of contaminants [2,3], and initial planting advantages have disappeared after a year or less [3,4]. Tradeoffs can also exist between promoting plant growth (which increases the volume of plant-influenced soil) and microbial remediation efficiency following co-treatments such as nutrient application [5].

Traditional characteristics sought for the ideal phytoremediation plant are exceptional contaminant tolerance, quick growth on degraded land, and rapid biomass production, and work has focused on developing transgenic plants

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Glossary

Endophyte: microorganism, generally a bacterium or fungus, that grows nonpathogenically inside a plant. Endophytes may assist in plant tolerance to contaminants that are taken up into the body of the plant.

Endosphere: term describing the plant interior as a microbial habitat; environment in which endophytes reside. May refer to either the aerial or root components of a plant, or both.

Metabolome: complement of metabolites associated with an individual or mixed-species community (when performed on mixed communities, sometimes termed meta-metabolome). Frequently studied in plants and may be used to assess differences in activity between plant tissues.

Metagenome: as opposed to a single isolated genome, the metagenome represents DNA elements from (ideally) all members of a mixed-species community. This term has often been used in conjunction with mixed microbial communities from which total DNA is extracted from lysed cells.

Metatranscriptome: identical to the definition of metagenome, but represents total extracted RNA. RNA can degrade quickly and expression generally varies on a timescale much shorter than total DNA, so the time of sampling and the preservation method are critical for meaningful comparisons between samples.

Microbiome: all microorganisms inhabiting a specific environment. For instance, the gut microbiome may refer to all microorganisms inhabiting a particular intestinal tract, but the composition of this microbiome can vary substantially between individuals.

Phyllosphere: surface area of the aerial portions of plants. Owing to limited resource availability (e.g., compounds released by plants, airborne compounds, sunlight), microbial diversity in these habitats is generally low relative to the rhizosphere.

Quantitative trait loci: loci that contribute to a trait that is dependent on the combined influence of multiple genes and the environment (also known as polygenic traits). Many plant traits cannot be related directly to single genes, so large data approaches will help in identifying clusters of important genes across populations and different environments.

Rhizosphere: zone in soil that is influenced directly by plant roots. This includes the surface of the roots (rhizoplane) and any external region that is affected by root exudation.

Box 1. Plant and microbial contributions to phytoremediation

The possible fates of soil pollutants following plant introduction are described clearly in a review by Pilon-Smits [69]. Here we show the major contributions of both introduced plants and partner microorganisms in the phytoremediation of mixed contaminant soils (Figure I). Soil microorganisms are the primary agents of organic mineralization in soil, and may also convert contaminants such as heavy metals to stable and/or less toxic forms. Although such microbial activity can occur in bulk soil, introduced plants have the potential to augment microbial contributions to bioremediation in the soil via stimulation of microbial biomass and/or activity in the rhizosphere, although this activity is dependent on which specific microorganisms and activities are promoted. Plant–microbe interactions are complex, and plants may favor microorganisms that promote their growth or provide protection from pathogens if pollutant stress is not sufficiently elevated, whereas opportunistic microorganisms that do not contribute to phytoremediation may also capitalize on plant-produced compounds.

Microorganisms can also facilitate the uptake of pollutants such as heavy metals by plant roots, which are then translocated (absorbed and relocated) to other components of the plant. Plants can store many contaminants in biomass that can later be harvested, but some compounds are volatilized from the aerial portions of the plant. However, volatilization without prior transformation may simply release toxic compounds into the air. Microorganisms that reside on or within aerial plant tissue can help to stabilize and/or transform contaminants that have been translocated, which may limit the extent of volatilization. Microorganisms that form direct associations with either the above-ground or below-ground portions of plants can positively (for a review on plant-growth-promoting bacteria, see [70]) or negatively influence plant growth and fitness, which alters the ability of a plant to directly remediate and/or stimulate associated organisms.
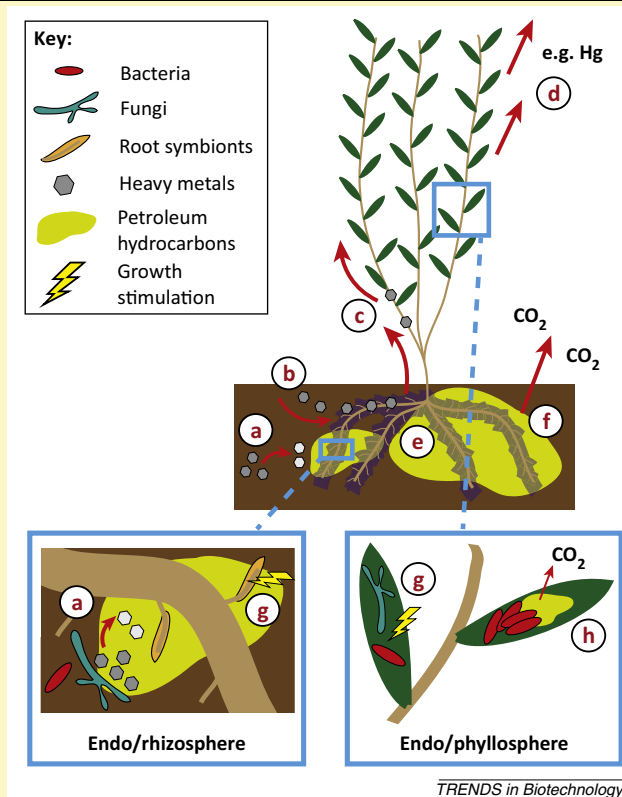

Figure I. Primary contributions of plants and associated microorganisms to phytoremediation in mixed contaminant soils. Metals may be (a) transformed by microorganisms in the rhizosphere, (b) taken up by the plant, (c) translocated to plant tissue, and/or (d) volatilized. Microbial activity can be stimulated directly by plants through (e) root exudate release, which may be particularly important for promoting (f) microbial degradation of hydrocarbons. Through a variety of mechanisms, microorganisms also influence (g) plant growth and can be involved in (h) pollutant transformation in the aerial parts of plants.

with increased tolerance to contaminants and/or enhanced contaminant uptake abilities [6,7]. It was recently shown that the composition of plant-recruited microbial communities can be independent of these characteristics and should also be considered in plant selection [8]. Microbial contributions to phytoremediation have been challenging to target, because they depend on the interactive activities of the plant and potentially thousands of microbial taxa with varying capacities for pollutant degradation and/or transformation.

Next-generation sequencing technologies appeared on the market in 2005 and have led to an explosion in our understanding of plants, microbes, and plant–microbe interactions. Large omics data sets are already being translated into usable technologies in the health sector (Box 2), and the ever-decreasing cost of sequencing now makes it possible to apply omics to environmental issues such as soil contamination. In this review, we discuss how new high-throughput molecular approaches have advanced our understanding of plant and microbial responses to pollutants and of plant–microbe interactions, and how phytoremediation strategies can be directed by omics data sets to harness the functional potential of introduced plants and their associated microbes. Although we focus

on phytoremediation, omics probing of plant–microbe assemblages will likely guide the next generation of strategies for managing invasive species, restoring disturbed sites, and optimizing crop production.

Microbial omics: enhancing predictability and community modification

A frequently cited roadblock in the study of natural microbial communities is that over 99% of microbial taxa are yet to be cultured and can only be characterized using culture-independent methods [9]. Omics technologies now permit analysis of microbial community composition and activity while preserving the fingerprint of biotic and abiotic factors that shaped these communities *in situ*. These omics approaches can be applied at several scales that are relevant to phytoremediation (Box 3).

Metagenomics

Metagenome analysis of plant-dependent environments such as the rhizosphere, endosphere (see Glossary), or phyllosphere, whether through shotgun sequencing or amplicon-targeting of specific genes, can be used to probe plant-associated microbial communities. High-throughput sequencing of bacterial 16S rDNA has shown that