Abstract
The soil being the most heterogeneous substance hosts the dynamic environments for diverse micro-organisms. Traditional techniques are limited to explore only few portion of massive unknown soil microbial world due to their well-known biasness in detecting microbial genetic and functional diversity. With this respect, Omics targets the powerful genomics, metagenomics, transcriptomics, proteomics, and metabolomics tools to explore the vast microbial community, new biomolecules, novel pathways to better understand toxicity mechanisms, predict the risks associated with environmental toxicity and bio-prospecting of value added products. These new approaches will be useful to establish the linkage between structure and function of soil microbial community to get better insight in ecological processes in the environment with special emphasis on plant-microbe ecosystems. Application of genomics, proteomics, and transcriptomics provides better understanding of the catabolic reactions of organic and inorganic compounds. The vision about the different -omic tools that provide information in the microbes involved in soil bioremediation and their metabolic reactions. The present review will give an overview of the application of the advanced molecular tools as well as their potentials and limitations in studying the soil microbial ecology for their potential application in bioremediation.

Keywords: Omics; soil, bacteria, genomics, proteomics, transcriptomics, metabolomics bioremediation

Fig.1. Classification of soil contamination

Fig. 2. Conventional methods for treatment of soil contamination

Fig. 3. Application of Omic tools in soil bioremediation: A conceptual framework

Table 1. Application of Omic tools in soil bioremediation

Table 2. Traditional vs advanced tools for soil decontamination
Advancement of omics: Future prospects for bioremediation of contaminated soils

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What is soil Pollution?

SOIL POLLUTION IS DEFINED AS THE CHANGE IN PHYSICAL, CHEMICAL AND BIOLOGICAL CONDITIONS OF THE SOIL THROUGH MAN’S INTERVENTION RESULTING IN DEGRADATION IN QUALITY.
Sources of Soil Pollution:

- Urban runoff
- Agricultural runoff
- Mining
- Industrial operations
- Atmospheric deposition
- Contaminated groundwater
Remediation Techniques:

**Chemical**
- Benzene (toxic/Carcinogenic)
- Naphthalene (Toxic/ non-carcinogenic)
- PAHs (vary depending on type but can be both Toxic and Carcinogenic)

**Physical**
- Air sparging/ Soil Vapor Extraction (AS/SVE)
- Monitored Natural Attenuation (possible phyto-remediation to be used in future)

**Bioremediation**
Bioremediation

**In situ**
- At the site
- Treatment of contaminated material in place
- Ex – Benzene, Toluene, TNT, 2,4-D
- Only certain types of soils can be bioremediated in-situ
- Complete degradation is often difficult to achieve

**Ex Situ**
- Away from site
- Techniques involve physical removal of the contaminated material for treatment process
  - Ex- Bio-piles, soil treatment unit, Compost pile, Windrows etc.
  - Use of bioreactors to process the material in a highly controlled environment.
Why???
Application of Meta-genomics:

Figure 1: Essential steps to explore and exploit the genomic diversity of soil microbial communities by metagenomics. Shown is a flow diagram of the main steps in the construction of a metagenomic DNA library from a soil sample. Soil DNA is recovered through separation of cells from soil particles followed by cell lysis and DNA recovery, or through direct lysis of cells contained within soil and recovery of DNA. Recovered soil DNA is fragmented and ligated into the linearized cloning vector of choice which might be a plasmid, cosmid, fosmid or BAC (bacterial artificial chromosome). Following the introduction of the recombinant vectors into a suitable bacterial cloning host, screening strategies can be designed to identify those clones which might contain new and useful genes.
Different molecular techniques used in partial community analysis approaches

- Microautoradiography
- Clone library
- Genetic fingerprinting
- Raman FISH
- DNA/RNA stable isotope probing
- Microbial lipid analysis
- DNA microarrays
- qPCR
Different molecular techniques used in whole community analysis

- Metatranscriptomics
- DNA De novo Reassociation
- GC Fractionation
- Proteogenomics
- Metaproteomics
- Metagenomics
- Whole genome sequencing
- Next generation techniques
Case study 1

Comparative study of As tolerant and sensitive plants

At the level of

Genome (QTL)

Transcriptome

Proteome

Metabolome

Mathematical modeling

Identification of key-regulators

Knowledge generated can be used for development of safer crops with low grain As level
Case study-II

Heavy metals/metalloids Exposure

DNA Sequencing, Structural and functional analysis
RNA Sequencing, Expression Profiling and regulation
Protein Identification, Quantification, Expression profiling
Metabolite Profiling, Hormones and Signaling molecules
Morphological, Biochemical and Physiological Characterization

Genomics

Transcriptomics

Proteomics

Metabolomics

Phenomics

Identification of candidate genes/Regulators

Transgenic Cisgenic

Gene-stacking

Pathway Engineering

Genome Editing TALENs, CRISPR-Cas9

Developing plants for phytoremediation

Engineered Hyperaccumulator Plant
Future perspectives:

- Exploration of soil microbial community structure and function
- Screening of Novel value added product from soil microbiome using Omics tools
- Combination of advance genome editing tools with Omics
- Integrating Omics with System Biology
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My Research Team
THANK YOU