

Stress Associated Microbial Profiling for Crop Plants for Sustainable Agricultural Practices- *In silico* Metagenomic Insight

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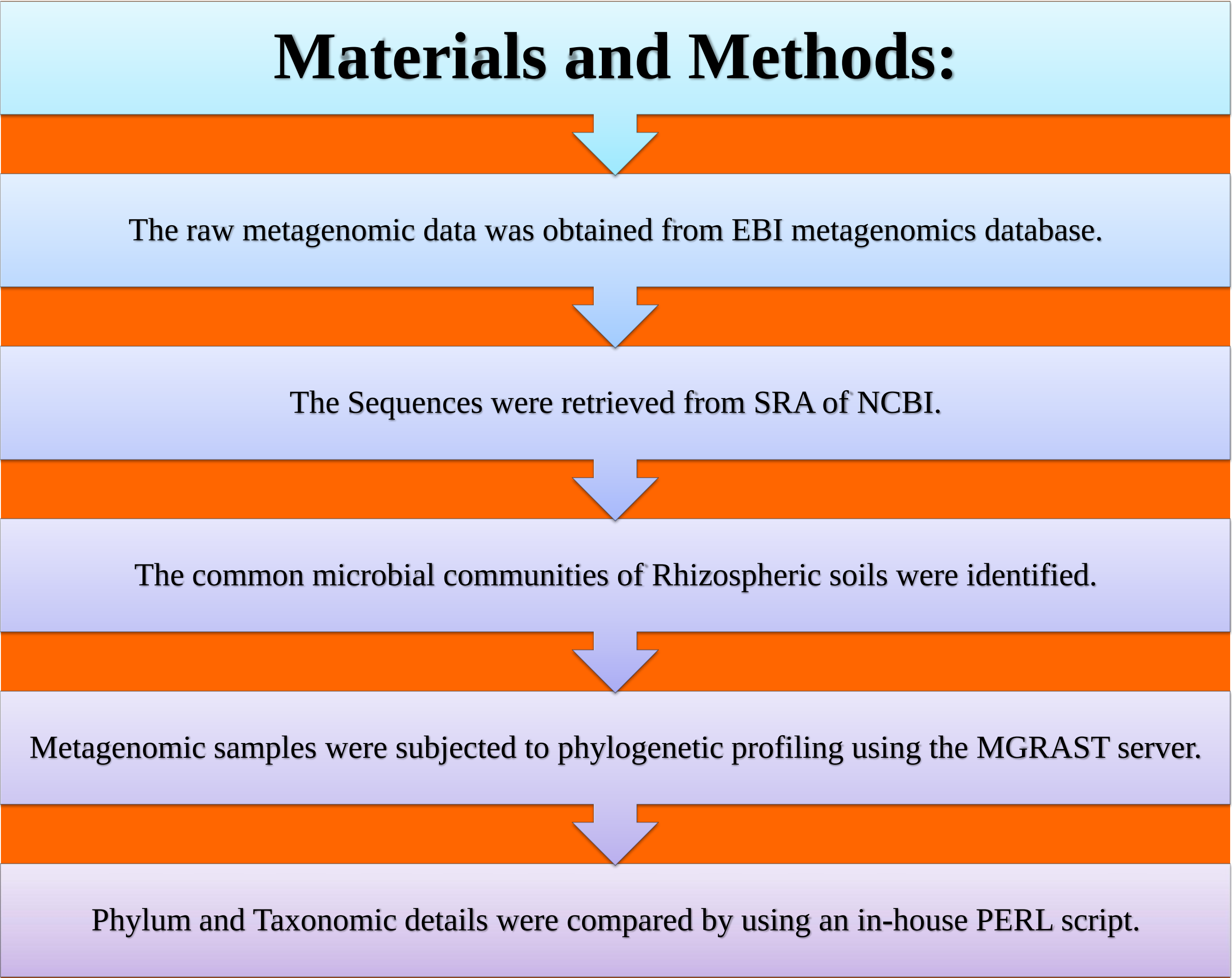
Abstract:

Understanding the earth and its life processes has been the quest of science and with every successful endeavour we inch closer towards the systems level understanding of the various organismic processes that contribute towards life on earth. Climate change, anthropogenic and other factors adversely affect the environment preliminarily and attack the existing microbial community and influence the microcosm of a particular area by creating an imbalance amongst the microflora which in turn affects the primary consumers and in turn affect the entire food chain of the place. Environmental Genomics approaches have enabled the rapid identification of the various microbial population that contribute towards the microflora of a particular geographical or environmental niche. Metagenomics approach has enabled us to get an insight into the segment or group of microorganisms which could not be cultured in vitro, thus opening up new vistas into the understanding of form and function of that community. Sustainable agriculture in India is faced with constant land use issues and hence the crop plantations all around the country are facing abiotic stress environments resulting in yield loss.

Keywords: Metagenomics, Climate, microcosm, Sustainable agriculture

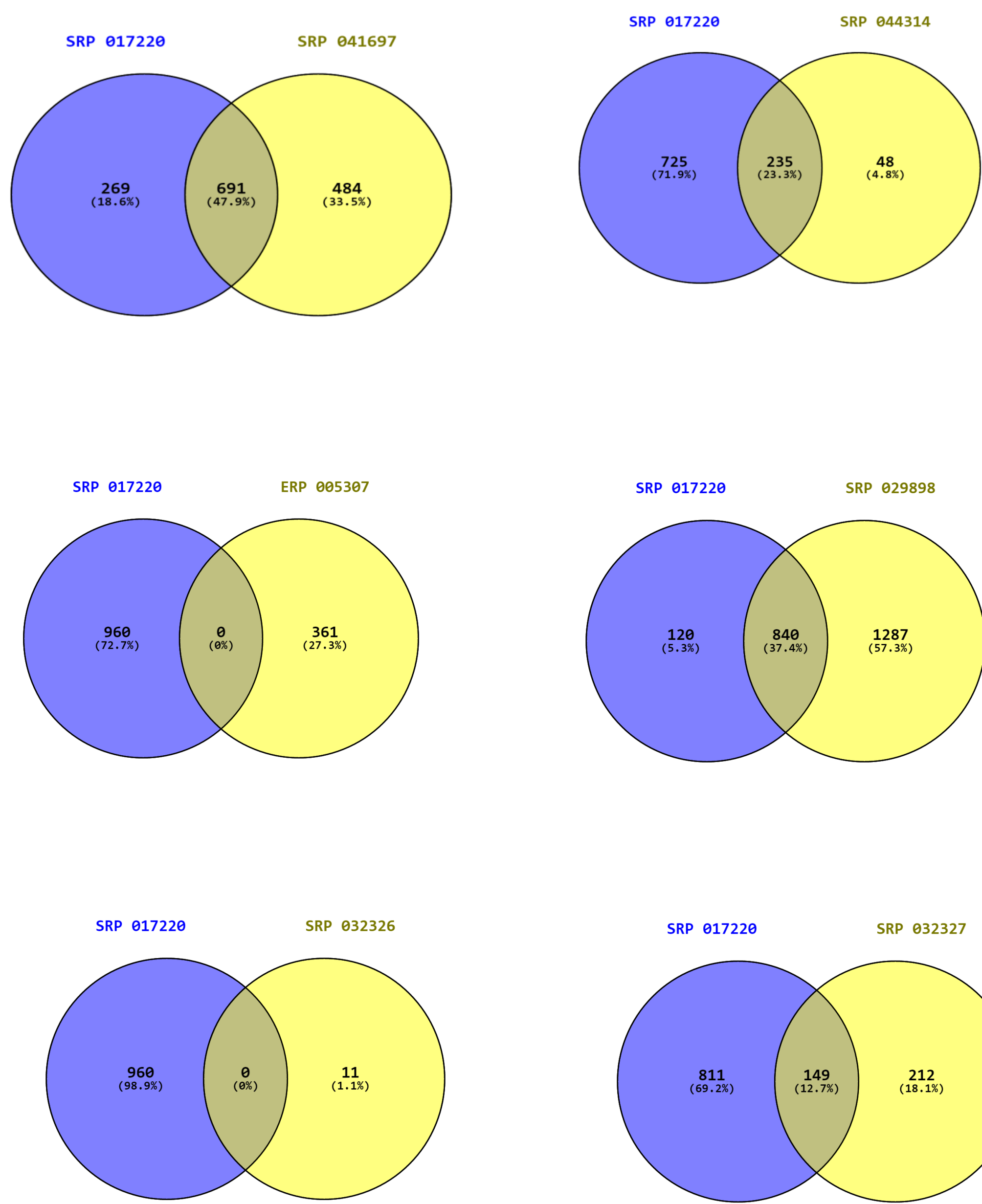
SRP017220	Soil microbe Metagenome;	Forest soil (Biome)
SRP041697	Grassland 16S amplicons;	Grassland (Biome)
SRP044314	Bamboo soil bacterial community with different elevation Metagenome;	Soil (Biome)
ERP005307	Microbial Community of Mobilong Acid Sulfate Soil depth profile using Metagenomics;	Grassland (Biome)
SRP029898	Wetland peat Targeted Locus (Loci);	Rhizosphere (Biome)
SRP032326	Monsoon bacterial diversity of pneumatophore-rhizosphere of <i>Avicennia Marina</i> in vellar estuarine Metagenome;	Rhizosphere (Biome)
SRP032327	Monsoon bacterial diversity of pneumatophore-rhizosphere of <i>Avicennia Marina</i> in vellar estuarine Metagenome;	Rhizosphere (Biome)

Table 1: Showing Different accession number with their biomes used in this study

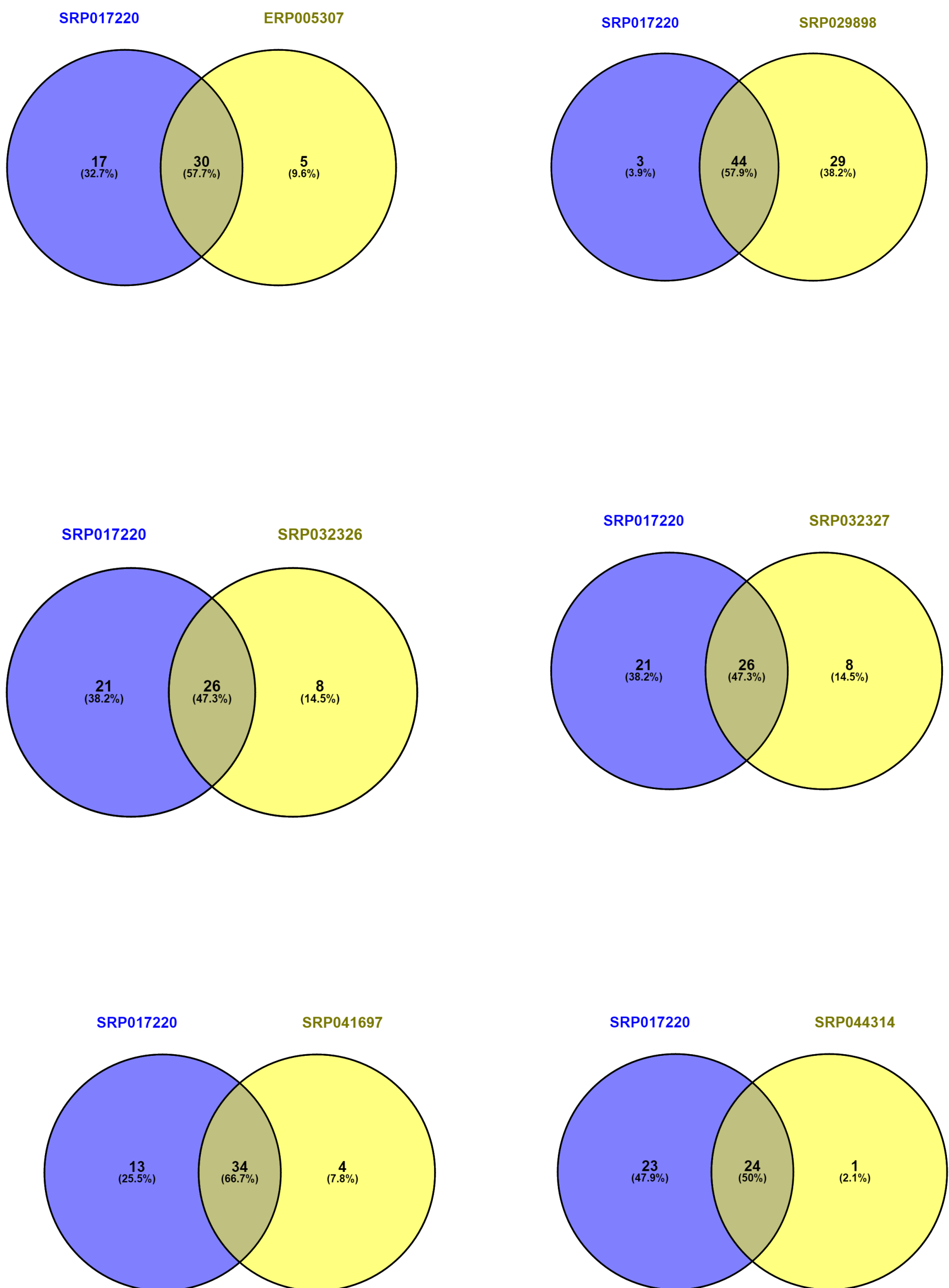


Results:

I. Based on Taxonomy



II. Based on Phylum



Discussion:

Results indicate that several rhizospheric communities share numerous microbial members which can be explored further for classifying and identifying stress specific microbial biomarkers which will enable sustainable agricultural practices across the country.

Acknowledgment:

The authors acknowledge Principal of Bangabasi Evening College and West Bengal Department of Science and Technology sanction number: 933(Sanc.)/ST/P/S&T/1G - 17/2016 for funding.

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