Investigating Roadside Soil Microbiomes: Metagenomic Analyses to Identify Taxa Driving Rubber Degradation

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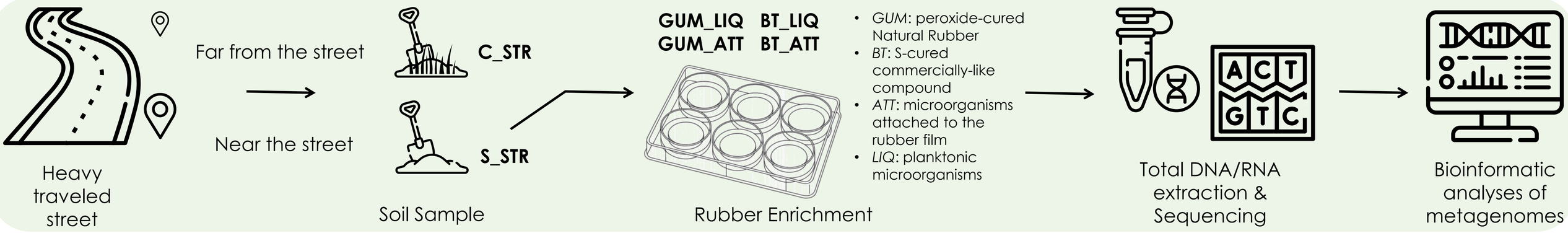
Background & Rationale

Tire and road wear particles (TRWPs) represent a massive, recalcitrant environmental pollutant, yet their biodegradation remains significantly under-researched compared to plastics. Current studies focus on isolated microbial strains, overlooking the complex synergistic interactions within consortia required to break down the resilient rubber matrix. This study employs a dual metagenomic approach - 16S rRNA gene sequencing and Shotgun metagenomics - combined with selective enrichment from high-traffic roadside soils to map the rubber-degradative potential of both culturable and non-culturable taxa. By shifting the focus from single strains to functional microbial communities, we provide novel insights into the taxonomic shifts driven by rubber as a sole carbon source, identifying key players for future bioremediation strategies.



16S rRNA gene sequencing

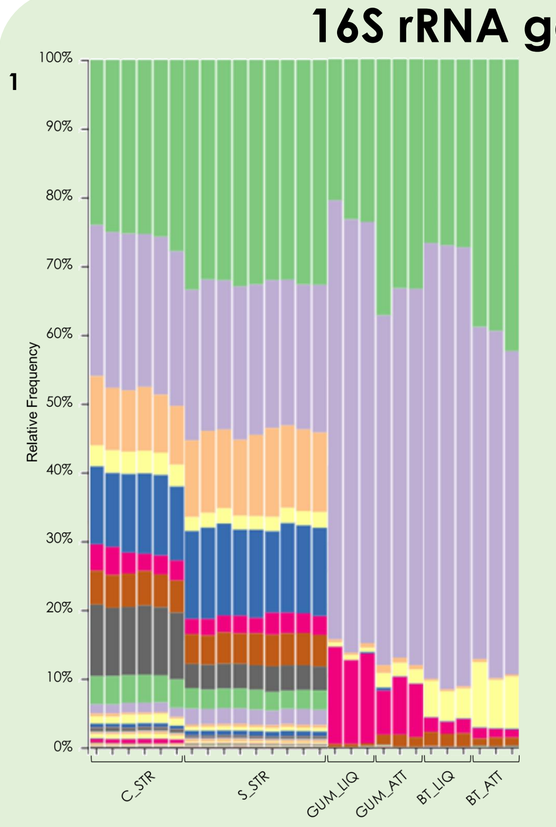


Figure 1: Taxonomic profiles of the soil and liquid samples at phylum level. The profiles include samples collected far from the street (C_STR), near the street (S_STR), and those derived from the soil enrichment experiment. The last differentiate between attached (ATT) and planktonic (LIQ) microorganisms grown on either GUM or BT (Tread Compound) rubber films (GUM_ATT, GUM_LIQ, BT_ATT, BT_LIQ).

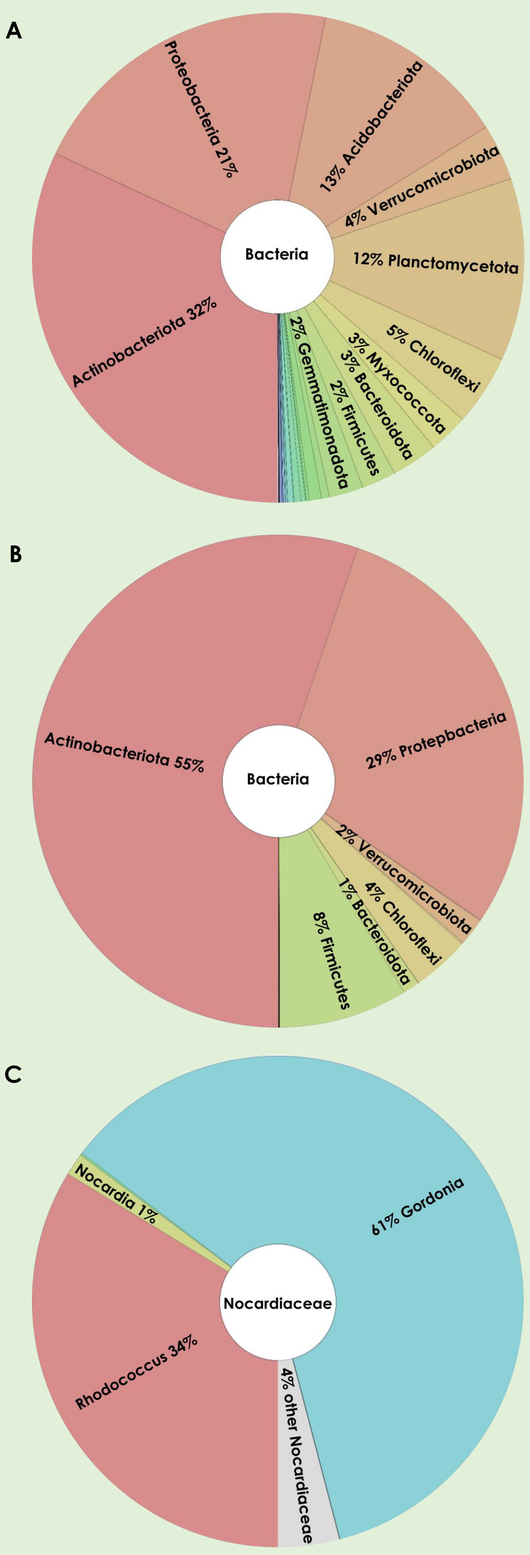


Figure 2: Krona charts of single metagenomes show each metagenome represented as concentric rings in a circular form, with each ring corresponding to a taxonomic rank. The white rings in each figure represent the bacteria which in this study is 100% of the population. The area of each ring reflects its abundance in the sample. Krona chart of S_STR (A) and BTL_ATT (B & C). The taxonomic classification goes from phylum (A & B) to genus level (C).

Shotgun metagenomics

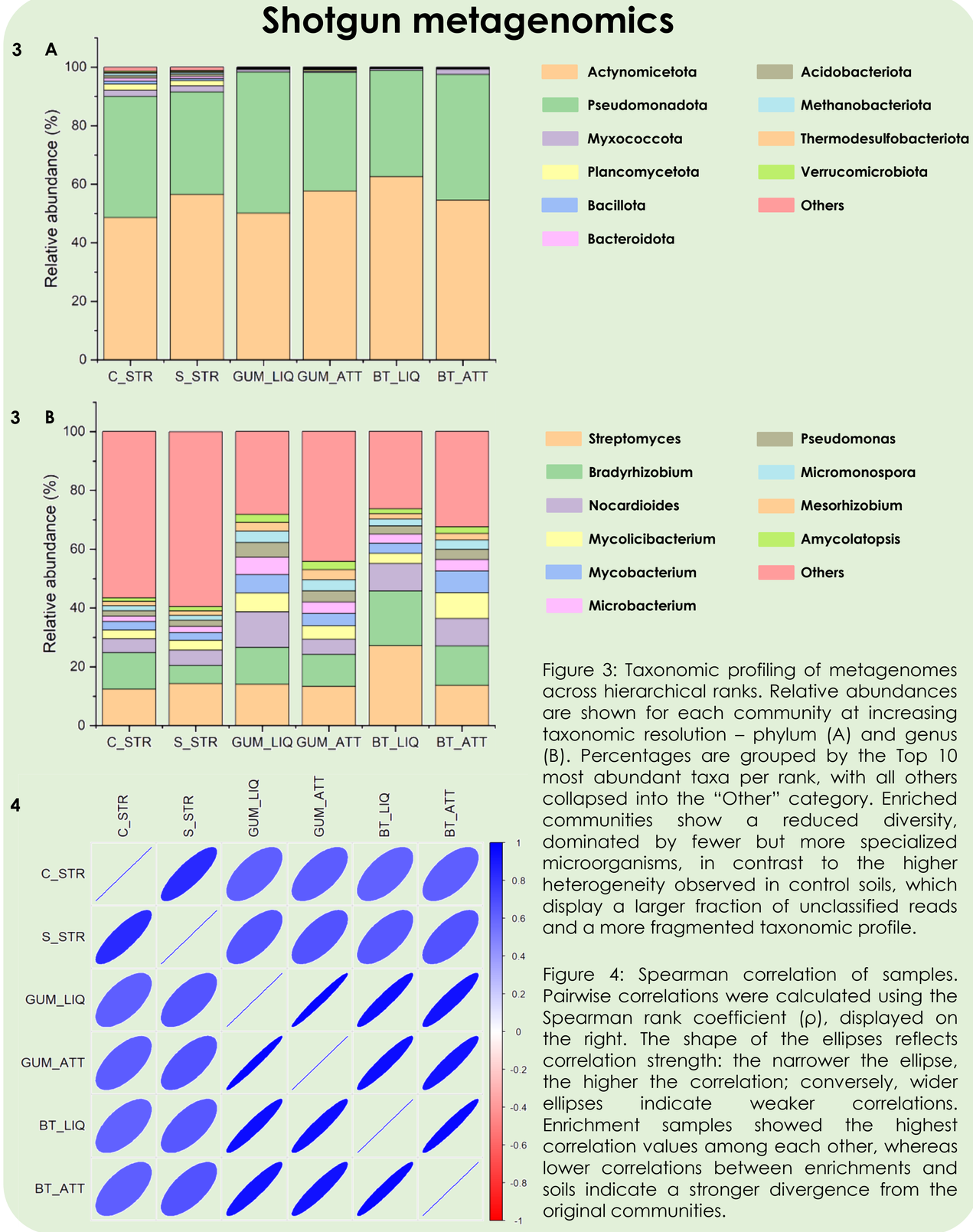


Figure 3: Taxonomic profiling of metagenomes across hierarchical ranks. Relative abundances are shown for each community at increasing taxonomic resolution – phylum (A) and genus (B). Percentages are grouped by the Top 10 most abundant taxa per rank, with all others collapsed into the "Other" category. Enriched communities show a reduced diversity, dominated by fewer but more specialized microorganisms, in contrast to the higher heterogeneity observed in control soils, which display a larger fraction of unclassified reads and a more fragmented taxonomic profile.

Figure 4: Spearman correlation of samples. Pairwise correlations were calculated using the Spearman rank coefficient (ρ), displayed on the right. The shape of the ellipses reflects correlation strength: the narrower the ellipse, the higher the correlation; conversely, wider ellipses indicate weaker correlations. Enrichment samples showed the highest correlation values among each other, whereas lower correlations between enrichments and soils indicate a stronger divergence from the original communities.

Conclusions & Perspectives

Comparative metagenomic analyses reveal significant community shifts driven by selective pressure, providing novel insights into how environments respond to rubber pollutants. These results characterize microbial communities potential for breakdown, establishing a foundational framework for future TRWPs bioremediation, sustainable waste management and a taxonomic identification pipeline.

CONTACT ME !

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