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Genome-Resolved Metagenomics Recovers 109 Prokaryotic Genomes from Driftwood Ecosystems

Environment * Climate Change * Atmospheric Physics

Submerged and stranded woody biomass represents one of the most chemically recalcitrant carbon reservoirs entering aquatic and coastal ecosystems. In a data descriptor published in Scientific Data on November 18, 2026, Arunmozhi Bharathi Achudhan, Rajnish Narayanan, Honglae Sohn, and Thirumurthy Madhavan released a genome -resolved microbiome collection comprising 109 prokaryotic genomes reconstructed directly from driftwood metagenomes. Rather than relying on laboratory cultivation -- which systematically misses slow-growing, syntrophic, and obligate biofilm -forming lineages -- the collection applies de novo metagenomic assembly and differential-coverage binning to recover metagenome-assembled genomes (MAGs) from wood-associated bacterial and archaeal communities.

From a systems-microbiology perspective, driftwood acts as both an ecological island and a biogeochemical reactor. Transported across watersheds, estuaries, and littoral zones, woody detritus carries terrestrial organic polymers into brackish and marine waters characterized by fluctuating salinity , steep oxygen gradients, and severe dissolved- nitrogen limitation. Resolving the genomic repertoire of the prokaryotes colonizing these substrates provides a direct window into the metabolic division of labor governing aquatic lignocellulose turnover, halotolerant biocatalysis, and coastal carbon export.

Biophysical Architecture of Lignocellulosic Driftwood Substrates

To understand why driftwood selects for specialized prokaryotic consortia, it is necessary to examine the macromolecular architecture of secondary xylem. Terrestrial wood is composed primarily of three tightly interlinked polymers: crystalline cellulose (typically 40% to 50% of dry mass), branched heteropolysaccharide hemicelluloses (20% to 35%), and aromatic lignin (15% to 35%). Cellulose microfibrils consist of linear beta-1,4-linked D-glucan chains stabilized by dense intra- and intermolecular hydrogen -bonding networks that exclude bulk water and resist spontaneous hydrolysis.

These microfibrils are embedded in a matrix of xylan-, glucomannan-, and arabinogalactan-rich hemicelluloses, which are in turn covalently cross-linked via ferulate and ester bridges to lignin -- a heterogeneous, non-hydrolyzable polymer synthesized through radical coupling of p -coumaryl, coniferyl, and sinapyl alcohols. In terrestrial forests, white-rot and brown-rot basidiomycete fungi dominate initial lignin oxidation using extracellular class II peroxidases and Fenton chemistry. Once wood enters waterlogged sediments or marine littoral zones, however, low dissolved oxygen and elevated ionic strength restrict filamentous fungal proliferation, shifting the burden of polymer deconstruction onto specialized bacterial, archaeal, and marine-fungal biofilms.

Within a single piece of waterlogged driftwood, physical transport processes

establish steep millimeter-scale physicochemical gradients. The outer millimeter experiences episodic wave oxygenation, photic exposure, and tidal salinity swings, favoring aerobic and facultatively anaerobic heterotrophs. Just beneath the surface, oxygen consumption outpaces molecular diffusion , creating microaerophilic and strictly anoxic microniches dominated by fermentative bacteria , sulfate-reducing lineages, and methanogenic or syntrophic archaea . Consequently, driftwood metagenomes capture multiple redox regimes simultaneously within a compact spatial footprint.

Genome-Resolved Metagenomics and De Novo Binning Mechanics

Early environmental surveys of wood-fall microbiomes relied primarily on PCR-amplified 16S rRNA gene metabarcoding. While amplicon sequencing maps taxonomic presence and relative abundance, it cannot link functional pathways -- such as glycoside hydrolase arrays, nitrogenase operons, or respiratory electron-transport chains -- to specific uncultivated organisms, nor can it resolve strain-level metabolic plasticity. Genome-resolved metagenomics overcomes this limitation by shotgun-sequencing total community DNA, assembling short or long reads into contiguous scaffolds via de Bruijn or overlap-layout-consensus graphs, and clustering those scaffolds into discrete population genomes.

Accurate binning of driftwood-derived contigs presents distinct computational challenges. Biofilms growing on porous wood matrices often harbor closely related strains within the same genus, producing high microdiversity that fragments de Bruijn graphs at conserved loci such as ribosomal RNA operons and mobile genetic elements. Modern binning algorithms mitigate these assembly breaks by combining two orthogonal signals: intrinsic sequence composition -- typically normalized tetranucleotide frequency (TNF) vectors reflecting genome-wide codon and dinucleotide bias -- and differential read coverage across multiple samples or spatial fractions.

Because each prokaryotic population exhibits a characteristic GC content and k-mer signature alongside a coherent abundance trajectory across metagenomic libraries, multi-sample covariance clustering separates co-occurring genomes even when their taxonomic affinities are novel. Nevertheless, horizontal gene transfer of plasmid-borne catabolic islands or integrative conjugative elements can distort local TNF profiles, requiring post-binning refinement to prevent chimeric contamination.

Quality Benchmarking Under MIMAG and GTDB-Tk Frameworks

To ensure that a 109-genome collection serves as a reliable reference resource for downstream comparative genomics, recovered bins must be rigorously audited against community-wide completeness and contamination thresholds. Under the Minimum Information about a Metagenome-Assembled Genome (MIMAG) specification established by the Genomic Standards Consortium (Bowers et al., 2017), single-copy marker gene inventories -- most commonly evaluated using lineage-specific hidden Markov models -- partition MAGs into three formal quality tiers.

| Standard / Framework | | Tier or Criterion | | Quantitative Thresholds & Diagnostic Markers |

| MIMAG High-Quality Draft | | Genome Completeness & Integrity | | >90% completeness, <5% contamination, plus 23S, 16S, 5S rRNA genes and >=18 tRNAs |

| MIMAG Medium-Quality Draft | | Genome Completeness & Integrity | | >=50% completeness, <10% contamination (rRNA completeness not strictly required) |

| MIMAG Low-Quality Draft | | Genome Completeness & Integrity | | <50% completeness and <10% contamination (typically excluded from core metabolic claims) |

| GTDB-Tk v2 Placement | | Species-Level Demarcation | | Average Nucleotide Identity (ANI) >=95% to reference genome over aligned fraction |

| GTDB-Tk v2 Placement | | Higher-Rank Novelty | | Relative Evolutionary Divergence (RED) normalized across concatenated bac120 / ar53 markers |

As summarized in the benchmarking table above, achieving the High-Quality MIMAG tier is notoriously difficult with short-read assemblies alone because multi-copy rRNA operons frequently collapse into unbinned, high-coverage unitigs. Even Medium-Quality drafts (>=50% completeness, <10% contamination), however, provide robust statistical power for metabolic pathway reconstruction and phylogenomic placement when evaluated across a multi-genome collection.

Taxonomic assignment of novel driftwood MAGs relies on the Genome Taxonomy Database Toolkit (GTDB-Tk v2; Chaumeil et al., 2022). Rather than depending on single-gene 16S rRNA similarity thresholds -- which suffer from variable evolutionary rates and primer bias -- GTDB-Tk places candidate genomes into a standardized bacterial or archaeal reference tree built from concatenated single-copy marker proteins (120 bacterial markers or 53 archaeal markers). Species boundaries are adjudicated via fast Average Nucleotide Identity (ANI) comparisons against representative genomes using a 95% ANI demarcation, while deeper taxonomic novelty at the genus, family, or order level is calibrated through Relative Evolutionary Divergence (RED).

Enzymatic Depolymerization and CAZyme Repertoires

Across genome-resolved wood-associated microbiomes, metabolic reconstruction consistently centers on Carbohydrate-Active Enzymes (CAZymes) encoded in co-regulated polysaccharide utilization loci (PULs) or secreted multi-domain complexes. Complete deconstruction of driftwood polysaccharides requires coordinated action across four complementary biochemical classes:

First, glycoside hydrolases (GHs) cleave glycosidic bonds via retaining or inverting acid-base catalysis. Endoglucanases (commonly distributed across families such as GH5, GH9, and GH44) hydrolyze internal amorphous regions of cellulose chains, exposing reducing and non-reducing chain ends for processive exoglucanases (cellobiohydrolases, e.g., GH6 and GH48) and beta-glucosidases (GH1 and GH3) that release fermentable D-glucose monomers. Parallel suites of endoxylanases (GH10, GH11) and beta-xylosidases dismantle the hemicellulose sheath.

Second, lytic polysaccharide monooxygenases (LPMOs) , classified within Auxiliary Activity (AA) families such as AA9 and AA10, catalyze oxidative cleavage of crystalline cellulose surfaces in the presence of molecular oxygen (or hydrogen peroxide) and a copper-histidine brace active site. By introducing nicks directly into flat, recalcitrant crystalline faces, LPMOs create new entry points that

dramatically accelerate subsequent GH hydrolysis.

Third, carbohydrate esterases (CEs) remove O-acetyl and feruloyl substituents from hemicellulose backbones, stripping steric hindrance that otherwise blocks glycoside hydrolase binding. Fourth, lignin-modifying enzymes -- including bacterial dye-decolorizing peroxidases (DyP-type peroxidases), multicopper laccases, and beta-etherases -- depolymerize or demethylate accessible phenolic oligomers, generating low-molecular-weight aromatic compounds that enter central catabolic funnels such as the beta-ketoadipate or protocatechuate pathways.

Syntrophic Cross-Feeding and Nitrogen Stoichiometry

A defining constraint of woody biomass is its extreme carbon-to-nitrogen (C:N) molar ratio, which routinely exceeds 200:1 to 500:1 -- far above the roughly 5:1 to 8:1 C:N ratio required to build prokaryotic cellular biomass. Consequently, driftwood-colonizing bacteria and archaea cannot sustain exponential growth or synthesize extracellular enzyme cocktails solely from carbon substrates; they must either scavenge dissolved inorganic nitrogen from surrounding water or fix atmospheric dinitrogen directly.

Genome-resolved analyses of marine and estuarine wood falls repeatedly uncover diazotrophic bacteria encoding nitrogenase structural and cofactor operons (nifHDK and accessory maturation genes) embedded directly within lignocellulolytic biofilms. Because the nitrogenase iron-molybdenum cofactor is irreversibly inactivated by trace oxygen, diazotrophs in surface-exposed wood exploit spatial oxygen depletion generated by neighboring aerobic cellulolytic respirators. In return, fixed ammonium leaks or turns over into the shared biofilm matrix, fueling extracellular enzyme synthesis by non-diazotrophic primary degraders.

Deeper within anoxic wood cores, primary fermenters convert liberated hexoses and pentoses into acetate, propionate, butyrate, formate, and molecular hydrogen (H 2). Accumulation of H 2 rapidly renders anaerobic fermentation thermodynamically unfavorable unless syntrophic partners -- such as sulfate-reducing Deltaproteobacteria (Desulfobacterota in GTDB nomenclature) in marine waters or hydrogenotrophic methanogenic archaea in freshwater and brackish sediments -- continuously draw down hydrogen partial pressures below roughly 10 Pa. This tight thermodynamic coupling links carbohydrate hydrolysis at the wood surface directly to terminal anaerobic mineralization in the interior.

Thermodynamic Limits and Redox Zonation in Waterlogged Wood

Beyond carbon-to-nitrogen stoichiometry, the spatial partitioning of prokaryotic guilds inside driftwood is governed by the classical redox tower of terminal electron acceptors. At the oxygenated outer rind, aerobic heterotrophs couple glucose and aromatic monomer oxidation to molecular oxygen reduction (E 0 ' ~ +815 mV), capturing the highest free-energy yield per mole of substrate oxidized and funding the metabolically expensive biosynthesis of extracellular cellulases and LPMOs. Immediately below the oxic-anoxic boundary -- often less than two millimeters beneath the biofilm surface in stagnant estuaries -- denitrifying facultative anaerobes switch to nitrate reduction (NO 3 -> N 2 , E 0 ' ~ +740 mV), followed by dissimilatory iron- and manganese-reducing bacteria exploiting mineral oxides

trapped in coastal sediments.

In marine and brackish settings where seawater sulfate (SO 4 2) approaches 28 millimolar, sulfate-reducing bacteria dominate the deeper anaerobic wood matrix (E 0 ' ~ 220 mV). Hydrogen sulfide (HS / H 2 S) generated by dissimilatory sulfate reduction diffuses outward, supporting chemolithoautotrophic sulfide-oxidizing bacteria at the oxic interface and chemically reacting with ferrous iron to precipitate iron monosulfides within xylem tracheids. Notably, elevated sulfide concentrations also inhibit heme-containing oxidative peroxidases while promoting slow abiotic sulfurization of lignin functional groups, creating a chemical feedback that slows anaerobic lignin degradation relative to polysaccharide hydrolysis.

Where sulfate becomes diffusion-limited -- such as in freshwater rivers or deeply buried terrestrial driftwood -- terminal electron flow shifts to syntrophic acetogenesis and methanogenesis (CO 2 -> CH 4 , E 0 ' ~ 240 mV). Because the Gibbs free energy change (DeltaG) of syntrophic propionate or butyrate oxidation is positive under standard conditions, these reactions proceed in vivo only when hydrogenotrophic methanogens maintain dissolved H 2 near nanomolar thresholds, operating within a narrow thermodynamic window of roughly 10 to 20 kJ per mole of substrate -- barely above the minimum quantum of energy required to translocate a proton or sodium ion across a cytoplasmic membrane for ATP synthesis.

Dereplication, Lineage-Specific Bias, and Pelagic Catalog Gaps

Integrating a specialized 109-genome driftwood collection into broader microbial dark-matter databases requires careful dereplication and awareness of marker-gene biases. When comparing newly recovered MAGs against existing global repositories, bioinformaticians typically cluster genomes at two ANI thresholds: 95% ANI to define species-level Genome Clusters (SGBs) and 99% ANI to resolve closely related ecotypes or strain-level variants. Even when a driftwood MAG shares a species-level assignment with a known coastal isolate, auxiliary genomic islands -- encoding multidrug efflux pumps, heavy-metal resistance operons, or horizontally acquired GH clusters -- frequently distinguish sessile wood-biofilm ecotypes from free-living bacterioplankton.

Equally important is accounting for systematic completeness underestimation in reduced-genome lineages. Traditional single-copy marker sets used in CheckM can misclassify ultra-small Candidate Phyla Radiation (Patescibacteria) bacteria and DPANN archaea as incomplete because these symbionts and episymbionts have genuinely lost canonical biosynthetic pathways (such as de novo amino acid, nucleotide, and lipid synthesis) over evolutionary time. Machine-learning completeness estimators such as CheckM2 and lineage-calibrated archaeal/bacterial marker profiles help distinguish true assembly fragmentation from evolutionary genome streamlining.

Globally, massive metagenomic surveys such as Tara Oceans and the Ocean Microbiomics Database have overwhelmingly sampled free-living pelagic bacterioplankton collected on 0.22-micrometer filters. While those campaigns transformed our understanding of sunlit-ocean primary production and nutrient cycling, they systematically under-sample particle-attached, benthic, and lignicolous biofilms. Focused genome-resolved collections from driftwood directly address this ecological blind spot, capturing surface-attached degraders, bio-corrosive consortia, and

terrestrial-to-marine transitional taxa that rarely appear in open-ocean water-column libraries.

Biogeochemical Implications and Biotechnological Potential

Expanding reference catalogs with collections such as Achudhan et al.'s 109 driftwood MAGs carries dual significance for Earth-system modeling and industrial biotechnology. Biogeochemically, rivers deliver tens of millions of metric tons of terrestrial woody debris to coastal oceans each year, where sunken logs create localized organic-rich "wood-fall" oases on otherwise oligotrophic seafloors. Quantifying which microbial clades dominate coastal wood degradation -- and how their metabolic rates respond to ocean warming, deoxygenation, and acidification -- improves parameterization of particulate organic carbon (POC) remineralization versus long-term burial in marine carbon budgets.

From an applied bioprocessing standpoint, enzymes evolved in marine or estuarine driftwood microbiomes operate under conditions that frequently mirror industrial pretreatment reactors: elevated ionic strength, broad pH tolerance, and high phenolic inhibitor loads. Mining genome-resolved MAG collections for halotolerant GHs, thermostable LPMOs, and bacterial beta-etherases offers a direct route to heterologously expressed biocatalysts capable of converting agricultural residues and forestry waste into second-generation biofuels, platform chemicals, and biodegradable polymers without freshwater-intensive desalination steps.

By releasing standardized, genome-resolved assemblies from an under-sampled lignocellulosic niche, the 2026 Scientific Data collection strengthens the empirical foundation connecting environmental metagenomic dark matter to quantitative ecosystem biochemistry. As future multi-omic campaigns pair these 109 reference MAGs with metatranscriptomics, metaproteomics, and stable-isotope probing, researchers will be able to resolve not merely which prokaryotes inhabit aquatic driftwood, but precisely how enzymatic fluxes shift across salinity, redox, and seasonal temperature regimes.

References & Primary Sources

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