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Host species and geographic location shape microbial diversity and functional potential in the conifer needle microbiome

Robert M. Bowers^{1*} , Shayna Bennett², Robert Riley¹, Juan C. Villada¹, Iolanda Ramalho Da Silva², Tanja Woyke^{1,2} and A. Carolin Frank^{2,3*}

Abstract

Background The aerial surface of plants, known as the phyllosphere, hosts a complex and dynamic microbiome that plays essential roles in plant health and environmental processes. While research has focused on root-associated microbiomes, the phyllosphere remains comparatively understudied, especially in forest ecosystems. Despite the global ecological dominance and importance of conifers, no previous study has applied shotgun metagenomics to their phyllosphere microbiomes.

Results This study uses metagenomic sequencing to explore the microbial phyllosphere communities of subalpine Western conifer needle surfaces from 67 trees at six sites spanning the Rocky Mountains, including 31 limber pine, 18 Douglas fir, and 18 Engelmann spruce. Sites span ~1,075 km and nearly 10° latitude, from Glacier National Park to Rocky Mountain Biological Laboratory, capturing broad environmental variation. Metagenomes were generated for each of the 67 samples, for which we produced individual assemblies, along with three large coassemblies specific to each conifer host. From these datasets, we reconstructed 447 metagenome-assembled genomes (MAGs), 417 of which are non-redundant at the species level. Beyond increasing the total number of extracted MAGs from 153 to 294, the three coassemblies yielded three large MAGs, representing partial sequences of host genomes. Phylogenomics of all microbial MAGs revealed communities predominantly composed of bacteria ($n = 327$) and fungi ($n = 117$). We show that both microbial community composition and metabolic potential differ significantly across host tree species and geographic sites, with site exerting a stronger influence than host.

Conclusions This dataset offers new insights into the microbial communities inhabiting the conifer needle surface, laying the foundation for future research on needle microbiomes across temporal and spatial scales. Variation in functional capabilities, such as volatile organic compound (VOC) degradation and polysaccharide metabolism, closely tracks shifts in taxonomic composition, indicating that host-specific chemistry, local environmental factors, and regional microbial source pools jointly shape ecological roles. Moreover, the observed patterns of mobile genetic elements and horizontal gene transfer suggest that gene exchange predominantly occurs within microbial lineages,

*Correspondence:

Robert M. Bowers
rmbowers@lbl.gov

A. Carolin Frank
cfrank@ucmerced.edu

Full list of author information is available at the end of the article



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with occasional broader transfers dispersing key functional genes (e.g., those involved in polysaccharide metabolism), which may facilitate microbiome adaptation.

Keywords Microbial ecology, Phyllosphere, Conifer, Metagenome, Mobile genetic elements

Background

Coniferous forests, which dominate temperate and boreal ecosystems, provide critical ecosystem services such as carbon sequestration [97], regulation of water cycles [11], soil erosion control [99], and habitat for diverse plant and animal species. However, these forests are increasingly under threat from climate change [115]. Current perspectives on forest management often overlook the significance of forest tree microbiomes. These microbiomes comprise ectomycorrhizal (ECM) fungi [47] alongside other fungal and bacterial species adapted to forest vegetation and soil [4]. A better understanding of forest microbiomes is essential due to their role in maintaining forest health, resilience, and biodiversity. A significant portion of this biodiversity resides on the aerial surfaces of plants, also known as the phyllosphere, one of the largest microbial habitats on Earth [75, 124]. Microbes that reside on leaves are vital for nutrient cycling, plant growth, and mitigating both biotic and abiotic stress [75], yet while agricultural and model plant phyllospheres have been extensively studied [66, 72], the phyllospheres of forest trees remain understudied.

The phyllosphere hosts a community of airborne generalists [14] that is shared among plants of different species [104, 124]. Leaf surface microbes are dispersed via aerosols and dust particles, and wind facilitates their movement over short and long distances. While the phyllosphere can act as a passive aerosol sampler [43], persistent microbial communities are maintained through plant–microbe interactions and adaptation to leaf environments [122]. The leaf community of a given plant is influenced by plants growing in the immediate vicinity but also with additional microbial signatures from more distant plant surfaces [81]. Conifer forests provide a vast and enduring reservoir of phyllosphere microbes. Unlike the ephemeral leaves of many agricultural plants, conifer needles offer a long-lived surface for microbial colonization, with individual needles persisting for years to decades [37]. The trees themselves can live for centuries or even millennia, sustaining these microbial communities over extended timescales. Studies of other evergreen plants, such as sagebrush [48], demonstrate that persistent communities of leaf-associated microbes, including at least 20 fungal genera, are maintained over time and are influenced by both weather and leaf age. Similarly, conifers likely provide stable habitats and significant reservoirs for phyllosphere-associated microbial

communities, supporting interactions across both nearby and distant habitats and plant ecosystems.

For example, in boreal forests, the composition of the microbial community living on nitrogen-fixing mosses depends on both the moss species and the surrounding canopy structure [56]. A higher proportion of conifers in the overstory is associated with greater α -diversity in moss-associated microbiomes, likely because conifers modify the forest floor environment (e.g., through needle litter, pH, and moisture), creating conditions that support a more diverse microbial community [107, 109]. While microbial dispersal was not directly assessed in [107, 109], conifer-derived microbes, such as those from needle surfaces, may contribute to moss colonization and influence community assembly alongside environmental filtering. Thus, the presence of conifers and the sharing of microbial communities among plant species can enhance microbial diversity and stability in forest ecosystems. Moreover, the ability of conifers to host diverse microbial communities, including nitrifiers that significantly contribute to nitrogen cycling, further underscores their ecological importance as habitats for important phyllosphere communities [44]. Additionally, coniferous trees often endure extreme environmental conditions, such as high UV radiation, low temperatures, and nutrient-poor soils, making them ideal for studying stress tolerance mechanisms in phyllosphere communities. Conifer species exhibit diverse needle characteristics that potentially influence the taxonomic and functional composition of microbial communities on their leaf surfaces. Secondary metabolites like terpenes and phenolic compounds in needles create unique chemical environments [34], selecting for specific microbial taxa that are tolerant of, or potentially capable of metabolizing, these compounds [61].

In parallel, polysaccharide decomposition is another critical microbial function in the phyllosphere with broader implications for forest carbon cycling. Conifer needle surfaces contain complex plant polymers such as cellulose, pectin, and hemicellulose derived from cuticles and cell walls. Among the microbes that inhabit these surfaces, members of the Bacteroidetes phylum are common colonizers [124] and are well equipped to degrade such polymers due to their diverse repertoires of carbohydrate-active enzymes (CAZymes) [6]. Recent work suggests that phyllosphere microbial communities influence ecosystem-level processes, including the

“home-field advantage” in litter decomposition, where microbes accelerate decomposition of their host’s own litter relative to foreign litter sources [39]. This advantage could arise because early colonization and metabolism of polysaccharides by phyllosphere organisms creates priority effects, influencing microbial succession and subsequent litter breakdown in soils. However, the prevalence and genomic mechanisms underlying polysaccharide decomposition specifically in conifer phyllosphere microbiomes remain largely unexplored.

Bacterial communities on conifer needles have been implicated in nitrogen fixation and growth promotion [7, 84], both of which contribute to stress resilience. Additional mechanisms by which phyllosphere microbes may enhance conifer stress tolerance include protection against extreme temperatures via heat shock and antifreeze proteins [57], desiccation resistance through biofilm formation or production of extracellular polysaccharides that retain moisture [106], and the synthesis of protective pigments such as carotenoids that absorb or mitigate UV radiation [58]. A recent genome-centered study of switchgrass and miscanthus phyllosphere communities revealed that these microbes harbor genes for osmoprotectants, compatible solutes, and antioxidative enzymes like catalases and peroxidases, which detoxify reactive oxygen species generated under environmental stress [51]. Both conifers and grasses are exposed to similar abiotic stresses, such as drought temperature extremes, and oxidative stress, which can select for analogous stress tolerance functions in their leaf-associated microbiomes [122]. Thus, similar microbial mechanisms may be at work in the conifer phyllosphere. In addition to these adaptations, phyllosphere microbes may also influence trace gas dynamics, including methane oxidation [15], although the extent and mechanisms of methane cycling in conifer needle microbiomes remain poorly understood. Beyond abiotic stress mitigation, phyllosphere microbes, including both bacteria and fungi, play critical roles in defending their host plants against biotic stress. Leaf surface communities can directly suppress pathogens and herbivores through competitive exclusion [75], production of antimicrobial and antiherbivore compounds [85], and induction of systemic resistance. For instance, fungal endophytes in conifer needle tissues have been shown to reduce infection severity by pathogenic fungi and enhance resistance to insect herbivory [3, 22], while bacterial communities further contribute to pathogen suppression by competing for nutrients and space and producing antibiotics, thereby shaping plant community dynamics and improving overall plant fitness [54]. Despite these promising roles, targeted studies on microbial-driven

biotic stress tolerance in conifer phyllospheres remain relatively sparse, underscoring the need for further investigation into these complex interactions.

Furthermore, mobile genetic elements (MGEs), including phages, prophages, plasmids and transposons, may facilitate microbial adaptation to environmental stressors and host defenses through horizontal gene transfer (HGT) [65, 112]. Although most research on MGEs has focused on soil and rhizosphere microbiomes, plant associated habitats such as the phyllosphere also harbor MGEs and antibiotic resistance genes (ARGs) that contribute to microbial functional plasticity [52]. Interestingly, large-scale metagenomics comparisons suggest that phyllosphere-associated bacteria may be relatively depleted in MGEs compared to other environments [71], potentially reflecting distinct ecological constraints on horizontal gene transfer in this habitat [10]. Nevertheless, those MGEs that persist may contribute to stress response, chemical defense, or metabolic flexibility, underscoring the need to better characterize their roles in conifer needle microbiomes.

Studies using 16S rRNA-based profiling of bacterial needle communities, including work by Carper et al. [20] and Carrell et al. [21], have shown that the subalpine conifer phyllosphere harbors diverse bacterial populations shaped by a complex interplay between selection and dispersal, with local site factors influencing communities more than host species identity or time across the growing season. However, the functional potential of forest tree phyllosphere communities remains understudied, particularly with respect to key processes such as polysaccharide decomposition, the role of mobile genetic elements (MGEs) in adaptation, and the potential for methane cycling. To our knowledge, no shotgun metagenomics studies of the needle surface exist to date. To address this gap, we sequenced the metagenomes of needle microbiomes from three species of subalpine conifers – limber pine, Engelmann spruce, and Douglas fir – from six sites in the Rocky Mountains, USA, ranging from Glacier National Park, MT (48.70°N) to Rocky Mountain Biological Laboratory, CO (38.96°N) and spanning 1,075 km. We generated 67 metagenomes, where each was assembled and binned into Metagenome Assembled Genomes (MAGs), but we also utilized three large coassemblies specific to each host conifer species, creating a combined, dereplicated set of MAGs that was used to assess overall genome-level abundance, diversity, and functional potential within the conifer needle microbiomes. By generating the first broad-scale metagenomic survey of conifer-needle microbiomes spanning six Rocky Mountain sites and three host species, this study establishes a critical baseline for future work on phyllosphere ecology and function, providing an important

foundational resource for understanding the genomic diversity and functional potential of these unique phyllosphere communities. Examining the long-lived, aerial surfaces of conifers, key reservoirs for microbial dispersal across landscapes, this work offers insight into microbial connectivity, persistence, and influence beyond the immediate leaf surface, shaping broader forest and ecosystem processes.

Methods

Conifer needle sampling and DNA extraction

Conifer needles were collected from each of the three conifer tree species at each of the six different sampling locations. For each tree, approximately 10 g of tissue (a twig with needles) was collected at breast height from the north side of the tree using sterile razor blades and placed into sterile bags. The samples were then placed on ice and shipped overnight to the University of California, Merced. Two 1-g samples were placed in 50 mL tubes, immersed in 15 mL of PBS-S buffer, vortexed for 15 s, and then sonicated for 5 min. Samples were transferred to a new tube and centrifuged for 15 min at 3200 g. The resulting pellet, consisting of needle surface microbes (bacteria and microbial eukaryotes), was resuspended in 1.5 mL of PBS, transferred to a 2 mL tube, centrifuged for 5 min at 10000 g, and frozen at -80°C until extraction. A CTAB protocol described in Carper et al. [20] was used to extract DNA. This protocol was designed to exclude cells from inside the needle tissue.

Metagenomic DNA sequencing

Illumina libraries were prepared using standard JGI protocols, i.e. following the protocols described in [12]. Briefly, the Nextera XT kit (Illumina) was used with 2 ng of DNA that was fragmented and adapter ligated. Ligated DNA fragments were PCR amplified and purified using SPRI beads (Beckman Coulter). Library concentrations were determined with quantitative PCR (qPCR) using a LightCycler 480 real-time PCR instrument (Roche). Sequencing was performed on the HiSeq 2500 platform, generating 150 bp paired-end reads.

Metagenome assembly and annotation

Paired end reads were trimmed and screened according to BBTools documentation [5] and corrected using BFC [73] version r191. Reads without a mate pair were removed. Following trimming and error correction, reads were assembled using metaSPAdes [91]. The filtered read set was mapped to the final assembly where coverage statistics were generated with BBMap version 38.22 using default parameters. Coassemblies were generated for each host tree species (Engelmann spruce, $n=18$, limber pine, $n=31$, and douglas fir, $n=18$) with

MetaHipMer2 [50] using default settings. It is worth noting that an attempt was made to create a coassembly of all 67 metagenomes, however, all attempts failed, which prompted us to perform coassemblies of metagenomes within each tree species. Small contigs, less than 500 bp were removed, and coverage information was generated internally in MetaHipMer2 during post assembly processing. For individual assemblies, coverage information was generated using BBTools version 38.79 (pileup.sh using default parameters). Functional annotation of the assembled contigs was performed using the IMG annotation pipeline [25] and eggNOG-mapper v2 [17]. CRISPR elements were predicted within IMG via a modified version of CRT-CLI version 1.2 [8]. rRNA genes (5S, 16S, 23S) were identified by comparing the contigs against the Rfam version 13.0 database [86] via cmsearch from the Infernal version 1.1.3 package [87]. Prediction of tRNAs was performed using tRNAscan-SE [23] version 2.0.8. A combination of GeneMarkS-2 version 1.05 [78] and Prodigal version 2.6.3 [53] were used to predict protein-coding genes.

MAG production and quality control

Metagenome binning was performed using MetaBAT2 [59] with default parameters, using both composition and coverage to generate the MAGs analyzed in this study. All MAGs were quality assessed using CheckM2 [27], and completeness and contamination estimates for each genome are provided in the Supplementary Excel Table. To ensure consistency across both bacterial and eukaryotic MAGs, we adopted the numerical cutoffs from the bacterial minimal information about metagenome-assembled genome (MIMAG) standards [13] rather than specifically assigning HQ/MQ/LQ labels, which were not defined for eukaryotes at the time of publication, including categorization into MIMAG standards [13]. Genes were called and annotated using the Integrated Microbial Genomes (IMG) system at the DOE Joint Genome Institute (JGI) [26]. Furthermore, all genomes were subject to a combined pairwise genomic ANI analysis using fastANI [55] with a 95% identity and 70% alignment threshold to define species-level clusters. Genomes were then clustered into species-level groups using MCL [123] version 14–137 with an inflation parameter of 1.5.

Phylogenomics of bacterial MAGs

A 56 single copy concatenated marker gene tree was constructed by combining a set of reference genomes spanning the bacterial domain together with the individually assembled and coassembled MAGs. To generate a phylogenetically broad yet non-redundant set of references, we clustered all publicly available IMG isolate bacterial genomes using CD-HIT [76], based

on the RNA polymerase gene (*rpoB*) at 80% sequence identity. This clustering produced a reduced set of reference genomes, roughly unique at the genus to family taxonomic levels (see also Supplementary Fig. 1). The MAGs were dereplicated by grouping them into species-level groups using Mash [96] version 2.0 at a cut-off distance of 0.05, followed by clustering with MCL [123] version 14–137 with an inflation parameter of 1.5. This dereplicated set of MAGs and the reduced set of bacterial reference genomes were passed through the SGTREE version 0.0.10 pipeline (<https://github.com/NeLLi-team/sgtree>). Briefly, this pipeline extracts sets of marker genes from the query and reference genomes using *hmmsearch* [82] version 3.1b2, performs alignments of each marker with *MAFFT* [60] version v7.490 (2021/Oct/30) using the *mafft-linsi* option, trims alignments with *trimAl* version 1.4 [18], and removes sites when more than 90% of taxa contain a gap. Due to various levels of MAG completeness, not all MAGs are included in the bacterial phylogeny (Fig. 2A; specifically, MAGs with less than 20% completeness were excluded, resulting in the omission of 10% of MAGs from the tree). Finally, individual protein alignments were concatenated, followed by maximum likelihood tree construction with *IQ-TREE* [89] multicore version 1.6.1 using the WAG substitution model and ultrafast bootstrap with 1,000 replicates [49]. Trees were visualized with *ggtree* v3.2.1 [130].

Phylogenomics of eukaryotic MAGs

To place the eukaryotic MAGs from the conifer needle phyllosphere into a concatenated marker gene tree, we used BUSCO_Phylogenomics (https://github.com/jamie-mcg/BUSCO_phylogenomics). This is a pipeline that relies on extracted BUSCO [116] marker genes. To create a reference dataset, we ran BUSCO on the full set of eukaryota_odb10 reference genomes to obtain a BUSCO profile for each reference. We then ran BUSCO on all eukaryotic MAGs with BUSCO completeness scores greater than 50%. These MAGs were defined as eukaryotic based on the identification of Eukaryotic contigs with EukRep [127]. EukCC [113] was then run to further assess quality. The full set of BUSCO generated output consisting of the eukaryota_odb10 reference database and our query MAGs was dereplicated into species clusters at a Mash [96] version 2.0 distance of 0.05. The dereplicated eukaryotic MAGs together with the eukaryotic reference set were then passed to the BUSCO_Phylogenomics pipeline, which uses *IQ-TREE* applying the WAG substitution model and ultrafast bootstrap with 1,000 replicates [49]. Trees were visualized with *ggtree* v3.2.1 [130].

MAG abundances

To assess the taxonomic composition of the conifer phyllosphere, we determined the relative abundance of microbial taxa by mapping metagenomic reads to the set of representative MAGs described above. Metagenomic reads from each sample were then mapped to this reference set of dereplicated MAGs using *BBSplit* from the *BBMap* suite (v38.90), which allows for unambiguous assignment of reads to the most similar reference genome.

Host-derived MAGs were identified and excluded from microbial community analyses. For community-level composition, we expressed the number of reads assigned to each microbial MAG as a proportion of all mapped reads within that sample. Taxonomic classifications were assigned to each MAG based on its placement in a reference phylogeny (See Phylogenomics of MAGs above). The resulting abundance data was processed in R (v4.2.0) [103] to visualize taxonomic composition across host plants and sampling sites. Hierarchical clustering of samples was performed using Bray–Curtis dissimilarity on abundance data rarefied to the minimum sample sum (i.e., the lowest total count across samples) using the *rrarefy()* function from the *vegan* R package [93]. Dendrograms were constructed to visualize relationships between metagenomes from different host plants and collection sites. Abundance profiles are displayed as stacked bar plots showing the relative abundance of major taxonomic groups, with taxa contributing less than 1% relative abundance grouped into an "Other" category. This approach allowed us to examine the influence of both host plant species and geographical location on microbial community structure in the conifer phyllosphere. Taxa enrichment was determined using DESeq2 [79], a differential abundance testing framework based on the negative binomial distribution that is specifically designed for raw count data. Raw reads assigned to each taxon were used directly for DESeq2 analysis, while filtering out low-abundance taxa that had either fewer than 100 total reads across all samples or fewer than 10 reads in at least 3 samples. For each host species or site, a binary contrast was established comparing the target group against all others. *P*-values were adjusted using the DESeq2 built-in procedures to control for false discovery rate (FDR). For statistical analyses and tabular presentation, taxa were considered significantly enriched or depleted if $FDR < 0.01$. For visualization purposes (Supplementary Fig. 2), a relaxed threshold of $FDR < 0.5$ was applied to provide a broader view of potential enrichment patterns. Log₂ fold change was calculated directly by DESeq2, representing the log-ratio of normalized counts between target and other groups. The size of points in the supplementary figures represents $-\log_{10}(FDR)$, allowing

visual distinction between highly significant and marginally significant results.

To assess differences in community composition among samples, we performed non-metric multidimensional scaling (NMDS) and permutational multivariate analysis of variance (PERMANOVA) using the *vegan* R package [94]. Bray–Curtis dissimilarity matrices were calculated from rarefied abundance tables. NMDS ordinations were generated with the *metaMDS* function (*trymax*=100, *k*=2), and stress values were reported [28]. PERMANOVA was conducted using the *adonis2* function with 999 permutations to test for significant effects of host species and site on community structure [2]. Ordination plots were visualized with *ggplot2* [128], including convex hulls for group separation, biplot arrows for influential taxa, and annotation of PERMANOVA *p*-values and *R*² statistics.

Orthologue clustering

For gene content comparisons, annotations of individual genes were used in combination with gene family clustering using *OrthoFinder* 2.1.3 [35], and the dereplicated species level MAG collections as input. Only medium quality MAGs and higher were used for orthologue clustering.

Identification of genes potentially relevant to volatile organic compound degradation

To assess the potential for conifer microbes to degrade common volatile organic compounds (VOCs), we searched the annotations of all MAGs for indicators of common VOC compound degradation such as alpha-pinene, methanol, among others. See Supplemental Excel Table for a full list.

Identification and characterization of carbohydrate-active enzyme gene families

To identify and classify carbohydrate-active enzyme (CAZyme) gene families, we utilized *dbCAN3* [131], a widely used tool for the annotation of CAZymes based on the CAZy database [77]. Predicted protein sequences from all MAGs were screened against the *dbCAN3* database using *HMMER* [100] version 3.3.2. Hits were filtered based on a stringent *e*-value cutoff (<1e-15) and coverage threshold (>35%) to ensure high confidence in CAZyme identification. The outputs from *dbCAN3* were further corroborated by cross-referencing annotations generated through the *IMG* pipeline [26]. To characterize the functional diversity and potential ecological roles of CAZymes, we categorized identified genes into functional groups, including glycoside hydrolases (GHs), glycosyltransferases (GTs), carbohydrate esterases (CEs), polysaccharide lyases (PLs), and auxiliary activities

(AAs). Each group was analyzed for their distributions across the MAGs. Substrate utilization profiles were analyzed by mapping CAZyme annotations to their associated substrate types based on the *dbCAN3* database. CAZyme families annotated with multiple substrate preferences were counted in all relevant substrate categories, such that each enzyme was included in the normalized count for every substrate it is predicted to target. For each taxonomic group, we calculated the normalized count of substrate-degrading enzymes per genome to account for differences in sampling depth across taxa. The normalized count represents the average number of enzymes targeting each substrate type that would be found in a typical genome from that taxonomic group.

Detection of mobile genetic elements and their host associations

To identify MGEs, including viruses and plasmids, from both the individual assemblies and coassemblies, contigs were screened with *geNomad* version 1.1.0 [16] and *VirSorter2* version 2.2.4 [45], taking the union of both results as the full set. MGE completeness was assessed with *CheckV* version 1.0.1 (database version 1.4) [88]. MGEs were then clustered into OTUs using *skani* [117] with a 90% sequence identity and a 70% alignment fraction. Hosts were assigned to MGEs if they were either binned directly into a MAG or were assigned to a host based on the host prediction tool, *iPhoP* [110]. To complement the automated prediction of MGEs we also searched for a small set of common phage, conjugative and non-conjugative plasmid and genes within the annotations. The full set of genes used in these searches are available in the Supplemental Excel Table.

Detection of horizontally transferred genes

Horizontal gene transfer (HGT) was analyzed among all dereplicated MAGs using *MetaCHIP* [119], a pipeline designed to detect HGT events in microbial genomes by assessing phylogenetic incongruence and taxonomic discrepancies. All dereplicated MAGs were used as input, and the pipeline was run with default parameters to ensure consistency and reproducibility. *MetaCHIP* begins by identifying candidate HGT genes through sequence similarity searches and taxonomic classification. Genes are flagged as potential HGT candidates if their predicted taxonomy differed significantly from that of the host MAG. To validate these candidates, *MetaCHIP* constructs phylogenetic analyses, generating gene trees for each candidate and comparing them to the species tree constructed from single-copy marker genes (Fig. 2A). Significant topological discrepancies between the gene trees and the species tree were flagged as evidence of HGT. To reduce false positives, additional

filters were applied, including minimum alignment coverage and sequence identity thresholds. Confirmed HGT events were classified into donor-recipient pairs based on taxonomic relationships and the predicted functions of the transferred genes.

Results & discussion

Study sites, tree species, and dataset overview

This study builds on prior 16S rRNA gene amplicon based research investigating bacterial communities of limber pine and co-occurring conifers across the limber pine species range, spanning sites from California to Colorado and New Mexico to Montana [20]. For the current study, we chose a subset of samples from this broader dataset to apply shotgun metagenomics, allowing deeper insights into microbial community composition and functional potential than previously possible with amplicon sequencing. These samples were collected from six sites spanning the Rocky Mountains, from Glacier National Park, MT in the north to the Rocky Mountain Biological Laboratory (RMBL), CO in the south. At each site, three distinct conifer species, limber pine (*Pinus flexilis*), Douglas fir (*Pseudotsuga menziesii*), and Engelmann spruce (*Picea engelmannii*), representing distinct genera within the family Pinaceae, were sampled, with minor exceptions: Engelmann spruce was not sampled at Glacier National Park or RMBL. Despite these gaps, each site contained limber pine and Douglas fir samples, ensuring robust coverage across the latitudinal gradient (Fig. 1A). Corresponding climate data [20] from each site (Fig. 1B) highlight environmental gradients present across sites.

Our metagenomic dataset includes 67 conifer needle surface samples collected from individual trees across three conifer species: 31 from limber pine, 18 from Douglas fir, and 18 from Engelmann spruce. Each sample yielded a unique shotgun metagenome, resulting in 67 metagenomes, each with a corresponding individual assembly (Fig. 1C, Supplementary Table 1). Additionally, we generated three large-scale coassemblies, one for each host species, to enhance the recovery of low-coverage sequences [31]. The individual assemblies averaged 342 Mb, while the coassemblies spanned an average total size of 19.3 Gb, offering a valuable resource for exploring both taxonomic and functional diversity within the conifer phyllosphere microbiome.

MAG extraction, domain-level classification and quality assessment

To further characterize the microbial communities identified in these metagenomes, we extracted metagenome-assembled genomes (MAGs) to analyze the taxonomic

and functional diversity within the conifer needle microbiome. From 67 conifer needle metagenomes we recovered a total of 447 MAGs, three of which were very large (average 3.7 Gb), host-derived MAGs reflecting conifer nuclear genome contamination, and seven insect MAGs, including those from *Ixodes scapularis* (tick, average 23 Mb) and *Copidosoma floridanum* (parasitic wasp, average 66 Mb), alongside 437 microbial genomes. Despite the challenges of assembling eukaryotic genomes from metagenomes [114], the host-derived MAGs provide valuable context for understanding sequence read origins, especially given that conifer genomes are notoriously large (typically 20–30 Gb [92]). The host MAGs underscore the difficulty of assembling highly repetitive eukaryotic genomes from metagenomes, as they averaged only 40.1% completeness by EukCC [113] and 8% by BUSCO [116], with BUSCO's lower estimate likely reflecting a more accurate representation of assembly gaps. These host-derived MAGs offer useful insights into host sequence contamination, a common challenge in phyllosphere microbiome studies described previously [51]. Our analysis revealed that contamination from host sequences was substantial, with a mean of $90.7\% \pm 2.0\%$ SEM of mapped reads aligning to contaminant MAGs across samples, highlighting the significant challenge of separating microbial biomass from host material in phyllosphere studies. In contrast, the mean percentage of reads mapping to microbial MAGs (bacterial and eukaryotic combined) was $9.3\% \pm 2.0\%$ SEM. It is also worth noting that chloroplast MAGs were not recovered, a common result given organellar circularity, lower effective coverage, and high sequence similarity that lead to fragmented or unbinned contigs [125].

The 447 MAGs (including the 10 contaminant MAGs) were clustered into 417 species-level MAGs after dereplication, and then partitioned into bacterial and eukaryotic sets. Bacterial MAGs were taxonomically assigned with GTDB-Tk [24] and refined by custom phylogenetic analyses (Fig. 2A). Completeness and contamination estimates, from CheckM2 for bacteria and EukCC for eukaryotes (Supplementary Excel Table), were then used to assign quality based on the numerical cutoffs of the bacterial MIMAG standards [13], applied uniformly since formal HQ/MQ/LQ labels do not yet exist for eukaryotic MAGs. Of 327 bacterial MAGs, 40 met the $\geq 90\%$ completeness $\leq 5\%$ contamination threshold, 102 met $\geq 50\%$ completeness $\leq 10\%$ contamination threshold, and 185 were $< 50\%$ complete. Of 117 eukaryotic MAGs, 7 met the $\geq 90\%$ completeness $\leq 5\%$ contamination threshold, 55 met the $\geq 50\%$ completeness $\leq 10\%$ contamination threshold, and 58 were $< 50\%$ complete (Fig. 1D).

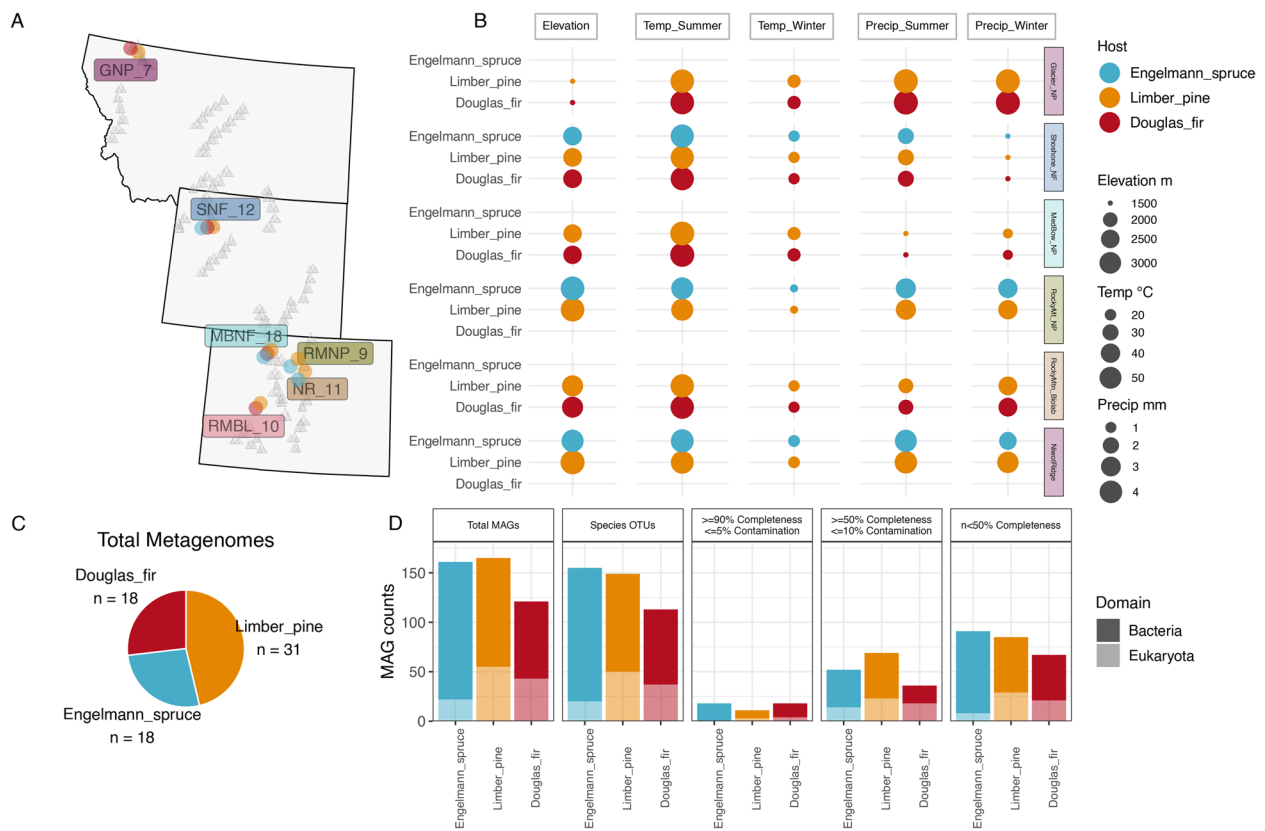


Fig. 1 Geographic distribution of sampling sites, their environmental characteristics, and the resulting metagenomic data obtained from three conifer host species. **A** Map showing the sampling sites distributed across the Rocky Mountains, from central Colorado to northern Montana. Site codes (GNP = Glacier National Park, SNF = Shoshone National Forest, MBNF = Medicine Bow National Forest, RMNP = Rocky Mountain National Park, NR = Niwot Ridge, RMBL = Rocky Mountain BioLab) are shown with the total number of samples collected at each location. Circle sizes on the map are uniform and serve as markers for sampling locations. **B** Environmental parameters (elevation, temperature, and precipitation) for each sampling site and host species combination. The size of each circle reflects the underlying metadata value for that site-host combination. Engelmann spruce samples were not collected at GNP, MBNF, and RMBL; Douglas fir samples were not collected at RMNP and NR. **C** Total metagenome distribution by host species, with Limber pine representing the largest sample group ($n = 31$). **D** Counts of bacterial and eukaryotic metagenome-assembled genomes (MAGs) categorized by host species and quality. Species-level OTUs were defined using a 95% average nucleotide identity (ANI) threshold. Completeness and contamination thresholds follow the bacterial MAG criteria of Bowers et al. [13] ("MIMAG" standards [13]). Because MIMAG quality categories (high/medium/low) are currently not defined for eukaryotic MAGs at the time of publication, we use these explicit numerical thresholds for all MAGs rather than the HQ/MQ/LQ labels

Host species and geographic site shape the diversity of conifer-associated microbiomes

The microbial diversity observed in our MAG dataset is consistent with previous findings from amplicon-based studies on limber pine and co-occurring species [20], as well as other investigations into conifer-associated microbiomes, including those on limber pine, lodgepole pine [21], and Monterey pine [1]. While prior studies focused on bacterial communities using amplicon sequencing, our metagenomic approach enables a more comprehensive analysis of both bacterial and fungal communities across multiple hosts and geographic locations.

Bacterial communities in the conifer needle microbiome were dominated by phyllosphere-associated taxa, particularly members of Alphaproteobacteria, Bacteroidota, and Gammaproteobacteria [104]. Less abundant

groups included Actinomycetota, Armatimonadota, Acidobacteriota, and Myxococcota. Within Alphaproteobacteria, Acetobacteraceae were the most prominent, with additional representation from Burkholderiaceae, Sphingomonadaceae, and Pseudomonadaceae. Hymenobacteraceae dominated among the Bacteroidota, along with smaller contributions from Sphingobacteraceae and Spirosomaceae (Fig. 2A and B and Supplementary Fig. 1A). Additionally, the presence of Rickettsiaceae in the phyllosphere is intriguing given their typical role as obligate intracellular parasites. Among the eukaryotic MAGs, we recovered bins assigned to Ixodes ticks, which are well-known reservoirs of Rickettsia endosymbionts [64]. The co-occurrence of Rickettsiaceae MAGs with the arthropod MAGs suggests that the bacteria originate from endosymbionts harbored by arthropods incidentally

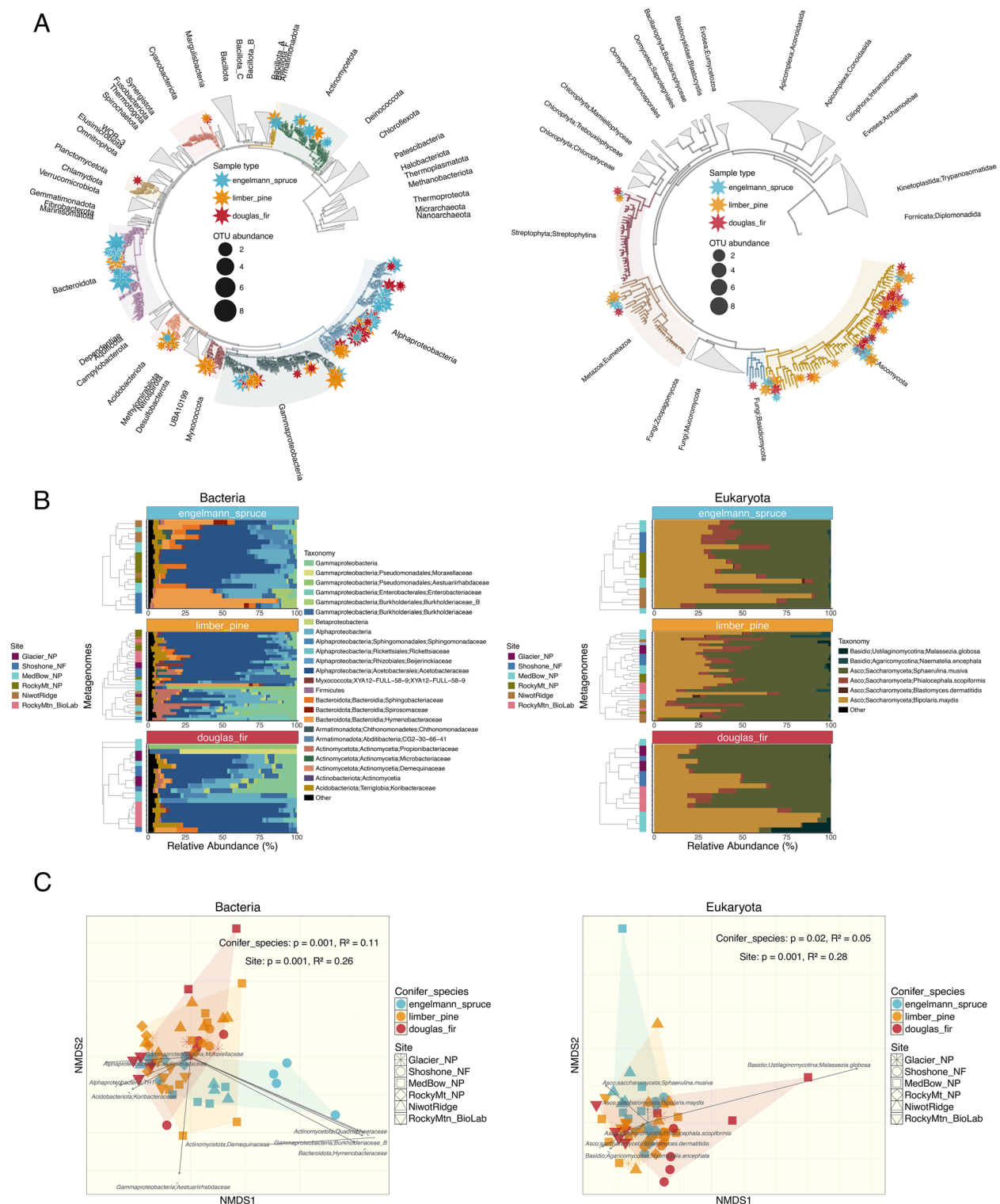


Fig. 2 Analysis of bacterial (left-hand panels) and eukaryotic (right-hand panels) metagenomic data: **A** Phylogenetic relationships among recovered MAGs. The bacterial phylogeny is constructed from 56 concatenated marker genes, while the eukaryotic phylogeny is based on the complete set of eukaryotic BUSCO markers. **B** Relative abundances of microbial taxa across different conifer species. Abundances represent the proportion of reads mapped to each MAG, normalized by the total number of reads for the corresponding domain. **C** Community composition visualized through NMDS ordination based on Bray–Curtis dissimilarities (stress values: Bacteria=0.11, Eukarya=0.14). Ordinations use species-level dereplicated sets of MAGs for each domain. Host-associated MAGs, including conifer and insect genomes, are excluded from the Eukarya relative abundance and ordination panels to focus on microbial taxa

collected with the needles, rather than from free-living rickettsiae or protistan associations. Significant differences in bacterial community composition were detected across host species and sampling sites (PERMANOVA, $p=0.0001$; Fig. 2C). Community composition was significantly influenced by both site and host species, with site-level variation explaining a slightly larger proportion of the variation in bacterial communities ($R^2=0.26$; Fig. 2C) compared to host species ($R^2=0.11$; Fig. 2C). Site-level variation likely integrates multiple environmental factors, including climate and microbial dispersal from surrounding habitat, with our prior 16S analysis of a larger set of samples from a wider geographic range showing that land cover exert a stronger influence than climate alone on conifer needle communities [20]. To further quantify these patterns of microbial enrichment across hosts and sites, we performed differential abundance analysis, which revealed 67 significant site and/or host-microbe associations (Table 1, FDR < 0.01).

Engelmann spruce communities exhibited distinct taxonomic profiles, with significant enrichment of Bacteroidota (Spirosomaceae, Hymenobacteraceae), Actinomycetota (Microbacteriaceae, Propionibacteriaceae), Alphaproteobacteria (Sphingomonadaceae), and Armatimonadota (Chthonomonadaceae) compared to other hosts. The enrichment of Sphingomonadaceae is particularly noteworthy as members of this family are known for their ability to metabolize recalcitrant aromatic compounds [54, 124], potentially providing adaptation to the complex phytochemistry of spruce needles. In contrast, limber pine samples showed significant depletion of several bacterial families including Bacteroidota (Spirosomaceae, Hymenobacteraceae), Gammaproteobacteria (Moraxellaceae) and Alphaproteobacteria (Sphingomonadaceae), suggesting a more selective microbiome. Douglas fir was characterized by elevated levels of Gammaproteobacteria (Moraxellaceae) while showing depletion of several Bacteroidota and Armatimonadota families. The interplay between host and site effects was evident across all sampling locations. At Glacier National Park, Myxococcota (XYA12-FULL-58–9) was significantly enriched, a group rarely reported in phyllosphere studies but known for predatory behavior, including synthesis and secretion of antimicrobial compounds, nutrient cycling via microbial cell lysis, and biofilm modulation through extracellular polymer production [74, 83]. Medicine Bow National Park showed enrichment of several Gammaproteobacteria families (Aestuariirhabdaceae, Enterobacteriaceae, Moraxellaceae) and Alphaproteobacteria (Caulobacteraceae), while Niwot Ridge showed enrichment of Armatimonadota (Chthonomonadaceae). Hymenobacteraceae, which emerged as one of the most prominent bacterial families in our analysis, showed a complex pattern, enriched in Engelmann spruce

but depleted in limber pine, Douglas fir, Glacier NP, and Niwot Ridge. This pattern highlights the context-dependent nature of these host-microbe and site-microbe associations [21, 104]. Notably, these taxonomic abundance and enrichment patterns agree with the taxonomic vectors displayed in the ordination plots (Fig. 2C), where the arrows point in the direction of maximum change in abundance for each bacterial family, with their length proportional to the correlation with the ordination axes ($p < 0.05$), revealing the taxa most strongly associated with community differences across sites and hosts.

Fungal diversity, while less taxonomically rich than bacterial diversity, showed comparable site and host-associated variation. Most fungal MAGs were classified within Ascomycota, with smaller contributions from Basidiomycota, consistent with the known dominance of ascomycetes in the phyllosphere [108] (Fig. 2A and B and Supplementary Fig. 1B). Fungal community composition was also significantly influenced by site (PERMANOVA, $p=0.001$; Fig. 2C), with site-level variation ($R^2=0.28$; Fig. 2C) explaining more of the observed differences than host species ($R^2=0.05$; Fig. 2C). Several dominant fungal clades included potential pathogens, such as *Bipolaris maydis* and *Sphaerulina musiva*, which are known to cause southern corn leaf blight [121] and poplar cankers [33], respectively. While neither is documented as a conifer pathogen, their presence on needle surfaces likely reflects airborne dispersal, as both produce wind-borne spores capable of widespread transport. Alternatively, their presence highlights potential gaps in current fungal reference databases, underscoring the need for expanded genomic resources in fungal ecology. Among less dominant fungal taxa, *Phialocephala scopiformis* stood out as a known mutualistic foliar endophyte in conifers. This fungus, which provides protection against spruce budworm [40], was detected across all host species and sites, suggesting it is a generalist capable of colonizing diverse conifer hosts. Its widespread distribution raises intriguing questions about its ecological role and potential protective benefits across varying environmental conditions. Although fungal community composition also varied across hosts and sites, these patterns were less pronounced than those observed for bacterial communities and appeared driven by a few outlier samples. Given the limited phylogenetic diversity of fungal MAGs at broader taxonomic levels (i.e., the dominance of Ascomycota), the remainder of this manuscript focuses on the functional dynamics of bacterial communities.

Volatile organic compound metabolism: adaptation to conifer chemistry

Trees emit a variety of volatile organic compounds (VOCs), including monoterpenes such as α -pinene,

Table 1 Host and Site-specific enrichment of microbial taxa based on differential abundance analysis. DESeq2 [79] was used to identify significantly enriched or depleted taxa (FDR < 0.01) based on raw read counts. For each host species or site (rows), the table shows the number of significant taxa and their enrichment status, with the most abundant taxa listed. Min. FDR indicates the strongest statistical significance observed for each comparison. Host and site comparisons are distinguished by background colors (blue: hosts, green: sites). All host species and site locations showed significant differential abundance patterns, with a total of 67 significant host-microbe and site-microbe associations detected

Category	Variable	Total_Significant	Enriched	Depleted	Top_Enriched	Top_Depleted
Host	engelmann_spruce	13	6	7	Bacteroidota; Spirosomaceae, Bacteroidota; Hymenobacteraceae, Actinomycetota; Microbacteriaceae, Alphaproteobacteria; Sphingomonadaceae, Actinomycetota; Propionibacteriaceae, Armatimonadota; Chthonomonadaceae	Gammaproteobacteria; Aestuariirhabdaceae, Gammaproteobacteria; Moraxellaceae, Gammaproteobacteria; Unknown, Gammaproteobacteria; Enterobacteriaceae, Alphaproteobacteria; Rickettsiaceae, Myxococcota; XYA12-FULL-58-9, Alphaproteobacteria; Caedimonadaceae
Host	limber_pine	4	0	4	None	Bacteroidota; Spirosomaceae, Bacteroidota; Hymenobacteraceae, Gammaproteobacteria; Moraxellaceae, Alphaproteobacteria; Sphingomonadaceae
Host	douglas_fir	6	1	5	Gammaproteobacteria; Moraxellaceae	Bacteroidota; Spirosomaceae, Bacteroidota; Hymenobacteraceae, Armatimonadota; CG2-30-66-41, Actinomycetota; Microbacteriaceae, Armatimonadota; Chthonomonadaceae
Site	Glacier_NP	6	1	5	Myxococcota; XYA12-FULL-58-9	Gammaproteobacteria; Aestuariirhabdaceae, Bacteroidota; Spirosomaceae, Bacteroidota; Hymenobacteraceae, Bacteroidota; Sphingobacteriaceae, Gammaproteobacteria; Burkholderiaceae
Site	Shoshone_NF	8	3	5	Bacteroidota; Spirosomaceae, Bacteroidota; Hymenobacteraceae, Actinomycetota; Propionibacteriaceae	Acidobacteriota; Koribacteraceae, Gammaproteobacteria; Aestuariirhabdaceae, Alphaproteobacteria; Beijerinckiaceae, Alphaproteobacteria; Caedimonadaceae, Myxococcota; XYA12-FULL-58-9
Site	MedBow_NP	7	4	3	Gammaproteobacteria; Aestuariirhabdaceae, Gammaproteobacteria; Enterobacteriaceae, Gammaproteobacteria; Moraxellaceae, Alphaproteobacteria; Caulobacteraceae	Bacteroidota; Hymenobacteraceae, Alphaproteobacteria; Acetobacteraceae, Actinomycetota; Propionibacteriaceae
Site	RockyMt_NP	5	0	5	None	Bacteroidota; Spirosomaceae, Gammaproteobacteria; Aestuariirhabdaceae, Bacteroidota; Hymenobacteraceae, Armatimonadota; CG2-30-66-41, Actinomycetota; Microbacteriaceae
Site	NiwotRidge	4	1	3	Armatimonadota; Chthonomonadaceae	Gammaproteobacteria; Aestuariirhabdaceae, Bacteroidota; Hymenobacteraceae, Gammaproteobacteria; Burkholderiaceae
Site	RockyMtn_BioLab	14	3	11	Alphaproteobacteria; Caedimonadaceae, Acidobacteriota; Koribacteraceae, Alphaproteobacteria; Acetobacteraceae	Gammaproteobacteria; Aestuariirhabdaceae, Gammaproteobacteria; Moraxellaceae, Bacteroidota; Spirosomaceae, Bacteroidota; Hymenobacteraceae, Actinomycetota; Demequinaceae, Gammaproteobacteria; Enterobacteriaceae, Actinomycetota; Microbacteriaceae, Actinomycetota; Propionibacteriaceae, Gammaproteobacteria; Unknown, Alphaproteobacteria; Caulobacteraceae, Armatimonadota; Chthonomonadaceae

which play important roles in stress adaptation, defense against herbivores and pathogens, and communication between plants [42, 46]. In conifers, VOC emissions are a major component of needle chemistry and may influence the composition and functional capabilities of associated microbial communities. To investigate whether phyllosphere bacteria interact with these host-emitted

compounds, we analyzed microbial genes associated with VOC degradation across the needle-associated metagenomes. Among VOC-degradation genes, those targeting α -pinene, a monoterpene abundantly produced by conifers as a chemical defense compound, were the most prevalent (Fig. 3A). Within our dataset, pinene

degradation genes were primarily associated with bacterial families including Acetobacteraceae, Sphingomonadaceae, and Burkholderiaceae. These taxa likely play key roles in both utilizing these compounds as carbon sources and mitigating their antimicrobial properties, allowing them to thrive on the conifer needle surface. Acetobacteraceae and Sphingomonadaceae showed the highest abundance of genes associated with pinene degradation, suggesting a selective advantage in metabolizing conifer-derived VOCs; a capability that may explain their dominance in the phyllosphere communities we observed across sampling sites. Burkholderiaceae, although less abundant overall, also contributed significantly to VOC degradation potential, underscoring its ecological relevance in specific niches. This pattern of metabolic specialization likely reflects bacterial adaptation to metabolizing the chemical defenses produced by their hosts [75, 124]. The prevalence of pinene-degradation genes suggests that these bacteria not only adapt to the chemical environment of conifer needles but may also contribute to shaping this environment, with implications for tree health, herbivore defense, and climate regulation. Pinene serves multiple ecological roles: it acts as a chemical defense against herbivores and pathogens, deters competing plants, and facilitates communication

between trees by signaling threats [62]. In the atmosphere, pinene is highly reactive and plays a crucial role in secondary organic aerosol formation, influencing cloud formation and rainfall patterns [38]. Bacterial communities on needle surfaces may therefore influence pinene's persistence, breakdown, and atmospheric fate.

In contrast, genes targeting other VOCs, such as methanol, geraniol, and phenol, were relatively scarce, indicating limited specialization for these pathways within the sampled bacterial communities. While we did not detect genes associated with methanol oxidation, genes for methane oxidation were identified in known methane-oxidizing taxa, particularly the genus *Methylocystis* within the family Beijerinckiaceae (Supplementary Fig. 3). This finding aligns with previous work reporting methane oxidation potential within conifer-associated microbiomes [101]. However, the sporadic presence of methane oxidation genes in other bacterial families (e.g., Acetobacteraceae and Burkholderiaceae) suggests these taxa likely lack complete functional capabilities for methane oxidation. We also detected near-complete nitrogen-fixation (*nif*) gene sets, most prominently in three of the five MAGs that were again classified as *Methylocystis* (Beijerinckiaceae), a well-established diazotroph [29, 120]. Additionally, partial nitrogen fixation pathways

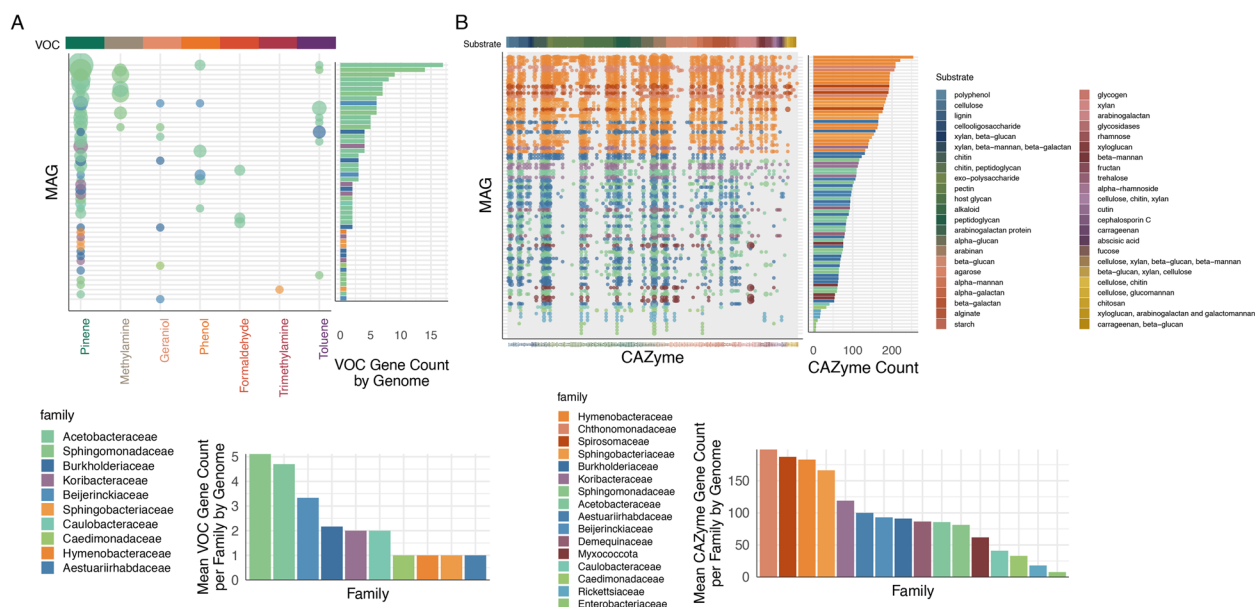


Fig. 3 Functional diversity of bacterial communities in the conifer phyllosphere. **A** VOC degradation genes and abundances. Top: Distribution of VOC degradation genes across phyllosphere MAGs, categorized by substrate type. The predominance of α -pinene degradation genes reflects adaptation to conifer-derived monoterpenes. Bottom: Mean VOC-degradation gene count per genome, normalized by the number of genomes per bacterial family, showing Acetobacteraceae and Sphingomonadaceae with the highest abundance of pinene degradation genes. **B** CAZyme diversity and abundances. Top: Total diversity and abundance of CAZyme genes across MAGs, grouped by substrate type. Bottom: Mean CAZyme gene count per genome, normalized by the number of genomes per family-level group, highlighting the exceptional CAZyme repertoire in Bacteroidetes families (Hymenobacteraceae, Sphingobacteriaceae, and Spirosomaceae) and Chthonomonadaceae. The substrate order follows a biochemical gradient from structural plant polysaccharides (cellulose, xylan) to host-derived glycans and specialized substrates

were detected in a smaller proportion of MAGs from the families Sphingomonadaceae, Burkholderiaceae, and Aestuariirhabdaceae (e.g., *Pseudomonas*). Some of these genera may have been responsible for the nitrigenase activity previously detected in limber pine foliage sampled from Niwot Ridge, CO [7, 84], one of the sites represented in this study. Prior work has demonstrated the presence of nitrogen-fixing *Sphingomonas* isolates in Scots pine needles [7], confirming diazotrophic activity among Sphingomonadaceae in conifer phyllospheres (Supplementary Fig. 3). These findings underscore the potential importance of methane-oxidizing diazotrophs, such as *Methylocystis*, in coupling carbon and nitrogen cycling within the conifer phyllosphere, particularly under nutrient-limited conditions.

Carbohydrate-active enzyme distribution: specialized polysaccharide metabolism

Bacterial communities in the conifer phyllosphere exhibited significant functional potential for polysaccharide metabolism, as evidenced by the distribution of carbohydrate-active enzymes (CAZymes) across MAGs (Fig. 3B). Bacteroidetes as a phylum consistently displayed the highest CAZyme functional potential, with the Hymenobacteraceae, Sphingobacteriaceae, and Spirosomaceae. This pattern agrees with the established role of Bacteroidetes as specialists in complex carbohydrate degradation across diverse environments [6]. Interestingly, we also observed two MAGs belonging to *Chthonomonas calidirosea* (phylum Armatimonadota) with exceptionally high CAZyme gene counts. This finding aligns with previous studies of *C. calidirosea* isolates from geothermal environments, which reported extensive carbohydrate-degrading capabilities in this thermophilic bacterium [68].

The CAZyme profiles were broadly similar across bacterial families, with differences primarily observed in the number of gene copies rather than in their presence or absence. For example, Hymenobacteraceae consistently exhibited high CAZyme gene counts, suggesting potential importance in polysaccharide metabolism, a pattern that may be relevant to the enrichment of Hymenobacteraceae within the Engelmann spruce needles at Shoshone NF (Fig. 2B and C, Table 1). We speculate that their CAZyme repertoire may provide a competitive advantage in this specific host-site combination, though experimental validation would be needed to confirm this relationship. The CAZyme repertoire across families targeted a wide range of carbohydrate substrates, including cellulose, xylan, chitin, pectin, and arabinogalactan (Supplementary Fig. 4). The ability to metabolize diverse polysaccharides likely enhances bacterial ecological flexibility, allowing taxa to occupy multiple niches on

needle surfaces. By breaking down plant-derived polysaccharides, CAZyme-producing bacteria play a key role in recycling carbon, influencing microbial competition, and modulating the availability of nutrients that shape conifer phyllosphere dynamics. Carbon recycling in the phyllosphere is particularly important because this environment is nutrient-limited and subject to fluctuating abiotic stresses (e.g., desiccation, UV exposure) [75, 124]. Efficient degradation and utilization of both labile (easily degradable, e.g., simple sugars and pectins) and recalcitrant (complex, e.g., cellulose and hemicellulose) substrates can provide a competitive advantage under these conditions [70]. The observed CAZyme patterns suggest that many taxa are equipped to access a range of substrates, which may reflect adaptation to stress by maximizing resource acquisition from available plant polymers. This flexibility likely supports microbial persistence and activity during periods of environmental stress, and may favor the utilization of more labile substrates when available, while also enabling the breakdown of recalcitrant compounds as needed. These processes are critical in nutrient-limited phyllosphere ecosystems, where microbial interactions and competition for resources drive community structure and function [124]. Finally, these CAZyme-mediated functions likely extend beyond the living needle. Upon litterfall, phyllosphere microbes may initiate decomposition, shaping microbial succession and influencing nutrient release. Such early conditioning enhances local decomposition efficiency by favoring well-adapted microbial communities [39], linking phyllosphere metabolism to broader ecosystem carbon cycling.

Mobile genetic elements and horizontal gene transfer in the conifer phyllosphere

In the harsh and resource-limited environment of the phyllosphere, the ability of microbes to rapidly acquire new traits can be key to survival. Mobile genetic elements (MGEs) and horizontal gene transfer (HGT) are major engines of microbial adaptation, spreading genes for stress tolerance, metabolism, and competition. To explore how gene mobility shapes conifer needle microbiomes, we analyzed the distribution of MGEs and HGT events across community members. Our analysis revealed distinct patterns of genetic exchange, with MGEs primarily mediating lineage-specific transfers and HGT enabling broader cross-taxa gene flow.

To investigate the prevalence and diversity of MGEs in the pine needle microbiome, we first scanned MAG annotations for hallmark genes associated with phages, conjugative plasmids, and non-conjugative plasmids. This analysis is summarized in Fig. 4A, which displays the distribution and abundance of these hallmark genes across MAGs and distinct taxonomic families, respectively.

To complement the gene-level analysis, we screened for MGE-containing contigs using VirSorter2 [45] and GeNomad [16]. This approach identified 8,956 MGE contigs, including 51 complete phage genomes and 140 high-quality MGEs, with quality assessments performed using CheckV [88]. The results of this contig-level screening are presented as bar charts (Fig. 4A, Right), which summarizes the contig-level screen for each taxonomic family, the mean number of phage and plasmid associated MGEs per genome and viral diversity, expressed as the number of unique viral OTUs per genome (Fig. 4A, Bottom Right).

Altogether, 26% of the identified MGE contigs could be directly linked to a host MAG through binning, while

an additional 0.5% could be linked using iPHoP, which incorporates CRISPR spacer matches and other features for phage-host predictions [111]. The remaining 74% of MGE contigs could not be assigned to a specific host MAG (Supplementary Fig. 5). Nevertheless, nearly all bacterial families hosted at least one MGE, underscoring their ubiquity in the phyllosphere. Based on tetranucleotide ordinations and host-virus interaction networks (Supplementary Fig. 6A and B), we found that the MGEs that could be assigned to a host were predominantly constrained to a single lineage, exhibiting limited host range. For example, MGE sharing was observed between *Falsiroseomonas* and *Commensalibacter*, however both of these lineages fall within the *Acetobacteraceae* family.

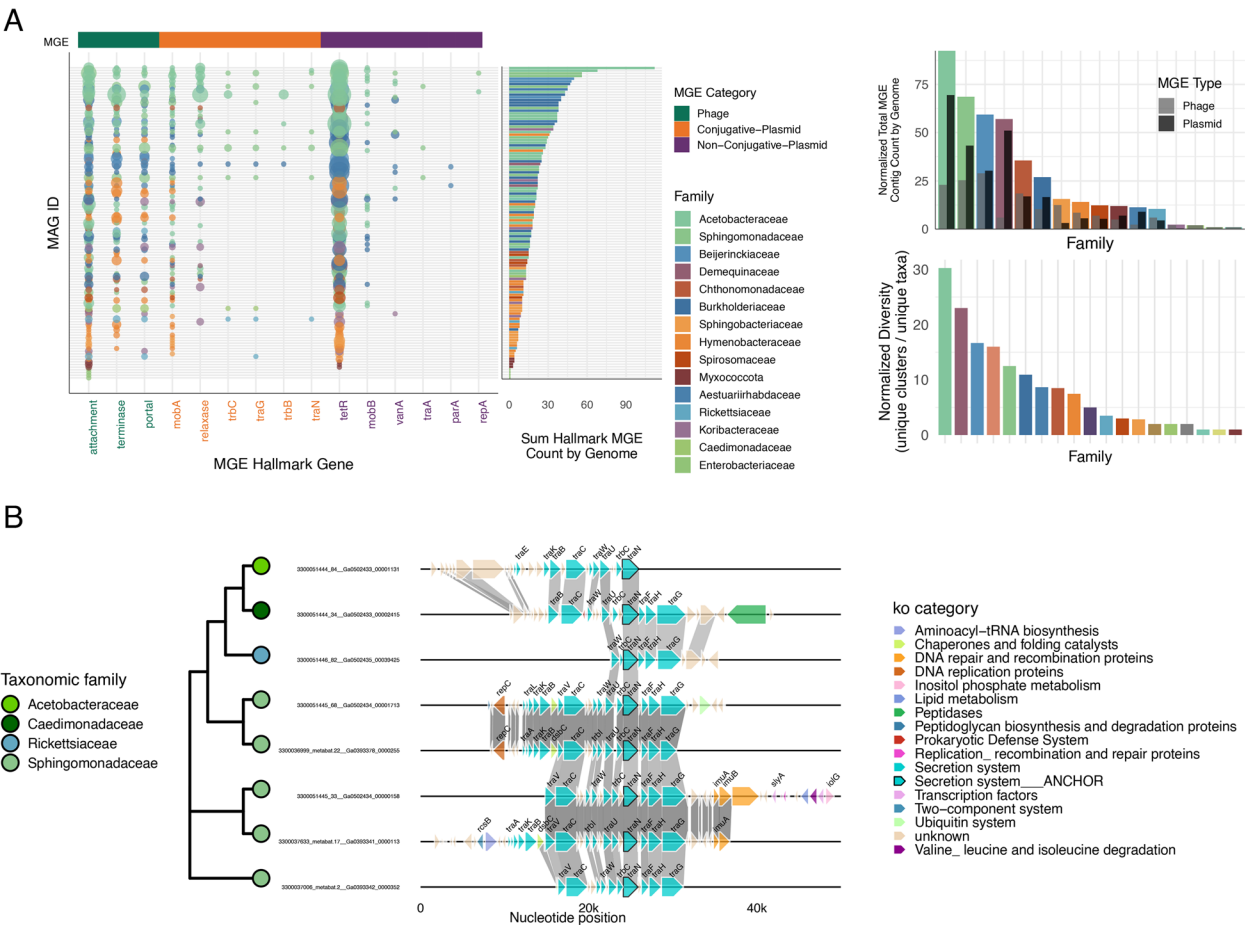


Fig. 4 MGE gene counts in phyllosphere MAGs. **A** Left: Distribution and abundance of major MGE hallmark genes across phyllosphere MAGs, showing their prevalence across bacterial lineages and split by predicted phage (green), conjugative plasmid (orange) and non-conjugative plasmid (purple) gene categories. Top right: Average MGE hallmark gene counts per family-level taxonomic group, normalized by the total number of genomes within each family, highlighting enrichment in Alphaproteobacteria families. Bottom right: Mean MGE count per genome, normalized by the total number of genomes within each family. Inset bars show the normalized counts split into phage and plasmid MGE types. **B** Phylogenetic relationships and synteny analysis of conjugative plasmids. The synteny plot illustrates the genomic organization of potential conjugative plasmids across four Alphaproteobacteria families, ordered by the phylogenetic tree of the *traN* gene, showing conservation of core conjugative machinery genes and variable cargo genes

In contrast, cross-family MGE transfer was rare, with only a few instances detected, such as exchanges involving *Methylocystis* (Beijerinckiaceae) and either *Comensalibacter* or *Roseomonas_A* (Acetobacteraceae). No evidence of widespread cross-lineage MGE exchange was detected, underscoring the lineage-specific nature of MGE-mediated gene flow. MGEs predominantly facilitate gene transfer within closely related taxa, as host specificity is influenced by unique interactions between phage receptor-binding proteins and bacterial surface proteins, which determine the ability of a phage to recognize and infect its host [69, 118]. This pattern aligns with observations in other environments where phage host ranges are typically narrow and constrained by phylogenetic relatedness [32, 63].

In addition to characterizing MGEs at the community level, we identified potential conjugative plasmids within specific bacterial lineages. Using the *traN* gene as an anchor, synteny analysis revealed conserved genomic organization across four Alphaproteobacteria families: Sphingomonadaceae, Acetobacteraceae, Caedimonadaceae, and Rickettsiaceae (Fig. 4B). The *traN* gene encodes a surface-exposed protein that plays a critical role in mating pair stabilization during conjugative transfer, promoting stable contact between donor and recipient cells [80]. Due to its functional importance and relative conservation among conjugative plasmids, *traN* serves as a reliable marker for synteny analyses [67]. Conjugative plasmids are a class of self-replicating mobile genetic elements that carry all of the machinery required for horizontal transfer, namely, a relaxase (e.g., *mobA*), Type IV secretion system components (e.g., *traC*, *traG*, *traA*, *traH*), and coupling factors like *traN* [41]. By shuttling accessory cargo genes (such as *imuA*, *imuB*, and *dnaE2*, which together form a DNA-damage-induced mutasome), conjugative plasmids accelerate microbial adaptation under stress and facilitate the spread of novel traits [36, 126]. We also identified toxin-antitoxin systems such as the Type II TA system RelE-RelB [129] and stress-resistance genes like *czcA*, which encodes a cation efflux system conferring heavy metal resistance [90]. Non-conjugative plasmid-associated MGEs revealed notable enrichment of hallmark genes, particularly the TetR-family regulators (Fig. 4A). Although TetR proteins are traditionally associated with antibiotic resistance in clinical settings, they also broadly mediate microbial responses to diverse environmental stressors, including plant-derived metabolites, oxidative stress, and naturally occurring antimicrobial compounds [30, 102]. The frequent occurrence of plasmid-borne TetR regulators in conifer-associated microbial communities underscores their likely ecological importance, independent

of anthropogenic antibiotic pressures. Supporting this, George et al. [43] detected tetracycline resistance genes, including TetR regulators, in protected forest conifer samples, far removed from agricultural activity. Taken together, the accessory genes we identified on both conjugative and non-conjugative plasmids, suggests that mobile genetic elements may contribute to stress adaptation in the phyllosphere, a habitat characterized by fluctuating conditions such as UV exposure, desiccation, and nutrient limitation [124].

In contrast to the lineage-constrained MGE distributions, horizontal gene transfer (HGT) events displayed greater diversity and frequency, facilitating genetic exchanges across both closely and distantly related taxa. Using MetaChip [119], we identified numerous HGT events spanning diverse bacterial groups within our conifer phyllosphere MAG dataset. The heatmap presented in Fig. 5A highlights the broader scope of HGT, with high abundances of HGT events concentrated in specific taxa, such as Acetobacteraceae and Sphingomonadaceae (Fig. 5B), although the pattern was similar to that of the MGEs, as the total number of HGTs declined with increasing taxonomic distance (Supplemental Fig. 7). This trend suggests that mobile genetic elements (MGEs) play a substantial role in facilitating HGT within certain lineages. However, the widespread occurrence of HGT across diverse taxa suggests that additional exchange mechanisms, beyond MGE activity alone, contribute to horizontal transfer, including recombination and natural DNA uptake [9, 95]. It is likely that some HGT events reflect historical MGE transfers whose direct signatures are no longer detectable [98]. For example, we observed the transfer of CAZyme genes, demonstrating that Acetobacteraceae and Sphingomonadaceae may disperse genes associated with polysaccharide metabolism to other community members (Fig. 5A, C).

The majority of horizontally transferred genes identified in our dataset were associated with phage or transposon-related functions (Fig. 5C) and two of these HGT genes were part of the conjugative plasmid element shown in Fig. 4B. Similar patterns of functional gene transfer have been observed in other plant-associated microbiomes, where genes conferring adaptive advantages in the plant environment show evidence of horizontal transfer [71]. Overall, many of these HGT-associated genes were associated with gene mobility, energy production and conversion, genes of unknown function, and amino acid metabolism and transport, underscoring not only the prevalence of self-propagating genetic elements but also a functional enrichment that has been previously documented in environmental microbiomes [19, 119].

Together, these processes of both MGE infection and HGT illuminate the complex dynamics of genetic

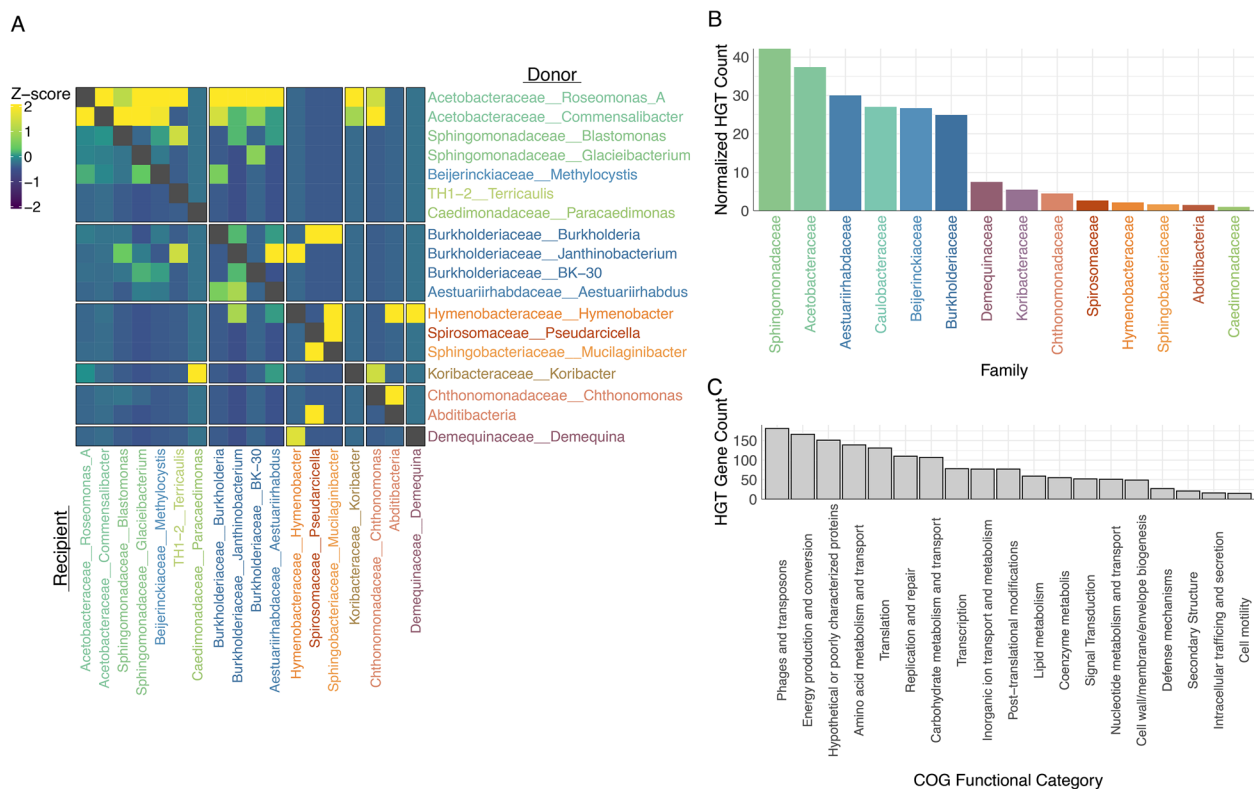


Fig. 5 Horizontal gene transfer (HGT) within the conifer needle microbiome. **A** Heatmap displaying the relative abundance of candidate HGT genes, represented as z-scores and grouped by genus, revealing taxonomic hotspots of gene transfer activity particularly in Acetobacteraceae and Sphingomonadaceae. **B** Normalized HGT gene count per genome, grouped by family-level lineage, highlighting variation in HGT frequency across bacterial taxa. **C** Distribution of HGT gene counts across COG functional categories, showing predominance of mobile genetic element functions, such as the Phages and transposons COG category, and hypothetical proteins among horizontally transferred genes

exchange driving microbial adaptation and functional potential in the conifer phyllosphere. The lineage-specific nature of MGEs likely reinforces ecological niche partitioning among bacterial taxa, while broader HGT events may facilitate adaptive gene sharing across more diverse members of the community. These complementary mechanisms potentially contribute to the resilience and functional stability of the phyllosphere microbiome in the face of environmental fluctuations characteristic of the conifer needle habitat.

Conclusion

This study presents a comprehensive metagenomic analysis of microbial communities associated with conifer needles across a diverse latitudinal gradient in the Rocky Mountains. By leveraging a robust dataset of bacterial MAGs, we uncovered critical insights into the taxonomic and functional diversity of the conifer phyllosphere. Our findings underscore the central role of host-derived compounds, such as volatile organic compounds (VOCs) and complex polysaccharides, in shaping bacterial community structure and driving metabolic adaptations.

Bacterial taxa, particularly members of Acetobacteraceae, Sphingomonadaceae, and Burkholderiaceae, exhibited specialized capabilities for metabolizing dominant monoterpenes like α -pinene, while members of the Bacteroidetes exhibited high potential for breaking down complex carbohydrates such as cellulose and xylan. These metabolic functions underpin their ecological roles, supporting nutrient cycling and microbial community resilience within this unique environment. The spatial patterns observed in community composition, with pronounced host-site interactions exemplified by the Hymenobacteraceae enrichment in Engelmann spruce at Shoshone NF, suggest that host chemistry, local environmental conditions, dispersal rates, and metacommunity structure, all interact to shape the functional potential of needle surface communities.

Predicted MGE contigs were identified as potential mediators of recent and localized gene transfer within closely related bacterial lineages, highlighting their role in short-term evolutionary adaptations. MGEs, including plasmids and phages, were found across nearly all bacterial families, reflecting their ubiquity and contribution

to the genomic plasticity of phyllosphere communities. Notably, MGEs were enriched in alpha- and gamma-proteobacteria compared to other taxa, suggesting that these groups may leverage MGEs to enhance their adaptability and ecological success. However, the constrained nature of MGE-mediated transfers suggests that these elements predominantly facilitate gene exchange within taxonomic lineages, supporting functional redundancy and niche specialization in the phyllosphere. In contrast, horizontal gene transfer (HGT) displayed greater diversity and frequency, potentially facilitating the exchange of metabolic genes across both closely and distantly related taxa. HGT emerged as a significant driver of functional diversification, particularly among Acetobacteraceae, which frequently acted as donors of key metabolic traits, including genes involved in polysaccharide metabolism.

Collectively, our findings illuminate how host species and geographic sites influence the complex dynamics that underpin microbial adaptation and resilience within conifer needle environments. By integrating metagenomic, functional, and evolutionary perspectives, this study advances our understanding of conifer needles as significant microbial reservoirs whose microbial diversity and functional potential are closely intertwined with host characteristics and environmental context. These insights lay a foundation for future research into forest phyllosphere microbiomes, emphasizing their ecological roles and contributions to plant health and broader forest ecosystem function.

Supplementary Information

The online version contains supplementary material available at <https://doi.org/10.1186/s40168-025-02271-y>.

Supplementary Material 1.

Supplementary Material 2: Table 1. MAG counts by genome type, host species and metagenomic assembly type. Co-assemblies were generated with MetaHipMer 2 [105], whereas individual metagenomes were assembled with metaSPAdes [91]. Species-level OTUs were defined using a 95% average nucleotide identity (ANI) threshold, for both bacterial and eukaryotic MAGs. The eukaryotic total counts include MAGs derived from host and insect DNA (10 MAGs total). MAG quality is reported in three numerical categories: $\geq 90\%$ completeness with $\leq 5\%$ contamination, $50\text{--}90\%$ completeness with $\leq 10\%$ contamination, and $< 50\%$ completeness, because no community-endorsed standard yet exists for assigning eukaryotic MAGs to the high-, medium-, and low-quality (HQ/MQ/LQ) categories defined by the bacterial MIMAG guidelines [13].

Supplementary Material 3: Figure 1. Linear representations of bacterial (A, rooted with Archaea) and eukaryotic (B, rooted with Diplomonada) phylogenetic trees. Phyllosphere-derived MAGs are indicated by stars, with size corresponding to the number of MAGs within each species-level group (OTU abundance). Colored clades indicate groups containing at least one phyllosphere MAG. Collapsed clades represent lineages lacking phyllosphere MAGs. Collapsed clades were subsampled to a maximum of 50 tips after phylogenetic inference to highlight relevant clades. The complete phylogenetic analysis was performed using a full dereplicated reference dataset spanning broad diversity across the bacterial and eukaryotic trees. These trees correspond to those depicted in Figure 2, presented here in a linear layout to facilitate more detailed exploration.

Supplementary Material 4: Figure 2. Differential abundance of bacterial taxa across conifer host plants (A) and sampling sites (B) based on DESeq2 analysis. Each panel shows taxa significantly ($FDR < 0.01$) enriched (green bars) or depleted (red bars) in the target host/site compared to all other samples. Bars represent \log_2 fold change, with positive values indicating enrichment and negative values indicating depletion in the target condition. The size of black dots corresponds to statistical significance ($-\log_{10}$ of FDR), with larger dots indicating higher significance. Only the top differentially abundant taxa based on fold change magnitude are displayed in each panel.

Supplementary Material 5: Figure 3. Distribution of methane oxidation and nitrogen fixation genes across bacterial taxa. (A) Methane oxidation gene counts by taxon. Each bar represents the total number of KOs (KEGG Orthologs) for each methane oxidation gene (pmoA, pmoB, pmoC, mmoX, mmoY, mmoZ, mmoB, mmoC, mxaF) within each taxonomic group. Taxa are ordered by gene coverage (proportion of genes present) and total KO count. The number of genomes (n) for each taxon is indicated in parentheses. Colors represent different taxonomic groups. (B) Nitrogen fixation gene counts by taxon. Each bar represents the total number of KOs for each nitrogen fixation gene (nifH, nifD, nifK, nifE, nifN, nifB, nifQ, nifF, nifJ, nifA, nifL, anfG, anfD, anfK, nifM, nifS, nifU, nifV, nifW, nifZ, nifX, nifY) within each taxonomic group. Taxa are ordered by gene coverage and total KO count. The number of genomes (n) for each taxon is indicated in parentheses.

Supplementary Material 6: Figure 4. Distribution of carbohydrate substrate degradation potential across bacterial taxa. The stacked bar plot shows the substrate degradation potential across different bacterial taxonomic groups. Each bar represents a taxonomic group (phylum/family), with Y-axis labels colored by taxonomy. The X-axis shows the normalized count of substrate-degrading enzymes per genome, indicating the average number of enzymes each genome in that taxonomic group possesses for each substrate type. Colors represent different substrate types, ordered from plant cell wall components (blues) through host glycans (greens) to various polysaccharides (reds, oranges, and purples). Taxa are ordered by their total normalized enzyme count, with those at the bottom having the fewest substrate-degrading enzymes and those at the top having the most diverse substrate utilization potential. This visualization reveals substrate specialization patterns across bacterial lineages, highlighting which taxonomic groups are specialized for specific substrate types versus those with broader degradation capabilities.

Supplementary Material 7: Figure 5. Counts of MGEs greater than 5kb, normalized by total assembly size and total number of metagenomes per group. (A) Totals grouped by host and MGE type. (B) Totals grouped by site and MGE type, where shading represents those MGEs observed in a MAG and assigned to a host, those MGEs pulled into a MAG via iPhoP [111], and those MGEs that could not be assigned to a host MAG.

Supplementary Material 8: Figure 6. Mobile genetic element analysis and virus-host network in the phyllosphere microbiome. (A) Principal component analysis (PCA) of tetranucleotide frequencies (TNF) of mobile genetic elements (MGEs) identified from metagenome-assembled genomes (MAGs). The plot illustrates the clustering of MGEs based on nucleotide composition patterns, with axes representing the first two principal components (PC1 and PC2). Each point represents an individual MGE, with colors indicating family level taxonomic identities. (B) Virus-host network visualization depicting predicted relationships between viral populations and their bacterial/archaeal hosts in the phyllosphere. Large colored nodes represent MAG hosts and smaller nodes represent their MGEs including phages, prophages and plasmids.

Supplementary Material 9: Figure 7. Number of cross-taxon Horizontal Gene Transfers (HGTs) across taxonomic ranks. Bar plot showing the total number of inferred cross-taxon horizontal gene transfers (HGTs) identified at five different taxonomic ranks: genus, family, order, class, and phylum. The majority of HGTs occur between closely related taxa (e.g., genus and family), with decreasing numbers observed at higher taxonomic levels.

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Authors' contributions

A.C.F. designed the study. R.M.B. wrote the manuscript together with A.C.F. and T.W. R.M.B. together with S.B., R.R., J.V. and I.R.D.S. processed and analyzed data, generated figures and statistical analyses. All co-authors provided input and edits to the paper.

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Data availability

Metagenome sequence data is available in NCBI's Sequence Read Archive under BioProject accessions ranging from PRJNA712809 to PRJNA712928. The complete list of 67 metagenome BioSample accessions (SAMN18257876 to SAMN18261528) and their corresponding BioProject IDs are provided in the Supplementary Excel Table. High-quality metagenome-assembled genomes (MAGs) have been deposited at NCBI under 62 BioSample accessions (SAMN48921394 to SAMN48921456), also documented in the Supplementary Excel Table. The assembly accessions will be available upon completion of NCBI processing. Additionally, assemblies, contigs, and genes can be browsed using the JGI IMG platform (<https://img.jgi.doe.gov>). All MAGs, regardless of quality, have also been deposited in a Figshare repository (https://figshare.com/articles/dataset/Conifer_Phylosphere_Microbiome_Dataset/29052146), including nucleotide sequences (fna), protein sequences (faa), and Supplemental Data Tables with detailed metadata for each metagenome and MAG, all of which are also included in the manuscript's Supplementary Excel Table. This comprehensive collection of phyllosphere MAGs and accompanying genomic data serves as a valuable resource for future studies investigating microbial dynamics and virus-host interactions on the phyllosphere, particularly on conifer needles. The authors confirm that all data underlying the findings are fully available without restriction.

Declarations

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Competing interests

The authors declare no competing interests.

Author details

¹U.S. Department of Energy, Joint Genome Institute, Berkeley, CA 94720, USA.

²Life and Environmental Sciences, University of California, Merced, CA 95343, USA.

³Sierra Nevada Research Institute, University of California, Merced, CA 95343, USA.

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