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Mini-Review

Global reports on *Glutamicibacter*: a mini review

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Abstract

Glutamicibacter has been recently reclassified from the genus *Arthrobacter* and represents a rare group of actinobacteria with significant biotechnological potential. Based on 16S rRNA signatures and phylogenomic evidence, its species have been discovered in diverse habitats including soils, sediments, wetlands, permafrost, saline coasts, and deserts. Ecologically, they act as endophytes, rhizosphere partners, and pioneers in extreme environments, reflecting exceptional resilience. These rare actinobacteria exhibit distinct biochemical profiles and follow a rod–coccus life cycle dependent on growth phase. Genomic surveys reveal compact genomes containing biosynthetic gene clusters (BGCs) that encode novel metabolites. Functionally, *Glutamicibacter* produces cold-activated and thermoalkaliphilic enzymes, antioxidant exopolysaccharides, uric acid–degrading pathways, and antimicrobial compounds. They have applications in food safety, agriculture, bioremediation, and therapeutics. However, BGCs remain uncharacterized in most species, and mechanisms underlying plant–microbe and insect–microbe interactions are poorly understood. Additionally, the industrial development of their enzymes and metabolites is limited. This review integrates contemporary perspectives on the taxonomy, ecology, morphology, genomics, and metabolism of *Glutamicibacter* and identifies future prospects through genome mining, metabolomics, and synthetic biology.

Keywords: *Glutamicibacter*, Phylogenomics, BGCs, Cold-active enzymes, Uric acid degradation, Antioxidant exopolysaccharides, Bioremediation, Plant-microbe interactions, Synthetic biology.

1. Introduction

Actinobacteria, a group of Gram-positive bacteria, thrive in aquatic and terrestrial ecosystems, including extreme environments [1]. These ubiquitous microorganisms are renowned for producing a wide array of secondary metabolites [2], including enzymes, antibiotics, anticancer agents, antifungals, antimicrobials [3], agroantibiotics or biopesticides [4], antidepressants [5], and quorum-sensing inhibitors that attenuate pathogen virulence without inhibiting growth, thereby preventing the emergence of resistant strains [6, 7].

Several actinobacterial genera, such as *Streptomyces, Rhodococcus, Arthrobacter, Nocardia,* and *Microbacterium*, exhibit substantial bioremediation potential for various pollutants. Members of the genus *Arthrobacter* are noted for their metabolic versatility and capacity to degrade a broad spectrum of environmental xenobiotics [8].

Ongoing reclassification and revision of *Arthrobacter* taxonomy, based on polar lipid profiles, quinone systems, and peptidoglycan composition, have led to the establishment of new genera, including *Glutamicibacter* and *Pseudarthrobacter* [9]. The genus *Glutamicibacter* is widespread in nature, with type strains isolated from both natural biotopes and anthropogenic ecosystems [10].

Interest in *Glutamicibacter* stems from its ecological and biotechnological significance, although research has been largely confined to taxonomic studies and isolated functional reports, in contrast to more extensively studied actinobacterial genera. Recent investigations have revealed gaps in our understanding of *Glutamicibacter*. A comprehensive grasp of its biotechnological potential could facilitate the development of novel drugs, biopesticides, and growth-promoting agents. This review focuses on the diversity of *Glutamicibacter* and the varied applications of its metabolites (Figure 1).

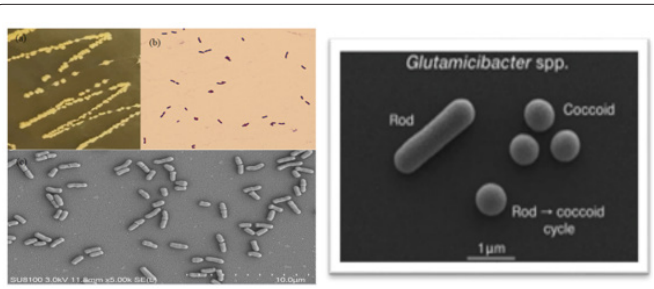


Fig. 1. *Glutamicibacter* adapted from Busse (2016) (Schematic representation of *Glutamicibacter,* reclassified from *Arthrobacter)*

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2. Taxonomy and phylogeny

Following extensive polyphasic revision of the heterogeneous *Arthrobacter* sensu lato group, Busse (2016) formally established the genus *Glutamicibacter* [9]. Integrative analysis using 16S rRNA clustering, chemotaxonomic profiling, and genome-scale studies revealed that several *Arthrobacter* lineages constituted distinct evolutionary clades, warranting their classification as separate genera. Key differentiating markers for *Glutamicibacter* include a glutamic acid interpeptide bridge in the peptidoglycan, predominant menaquinones of the MK-9 family, and specific branched-chain fatty acids [11].

While 16S rRNA gene analysis confirms the monophyletic nature of *Glutamicibacter* and distinguishes it from other *Micrococcaceae*, its high interspecific sequence similarity limits resolution at the species level [12, 9]. Consequently, modern taxonomy heavily relies on genome-based methods such as Average Nucleotide Identity (ANI), digital DNA–DNA hybridization (dDDH), Standardized Percentage of Conserved Proteins (POCP), and Average Amino acid Identity (AAI). Pipelines like Genome Taxonomy Database (GTDB)-Tk and core-gene phylogenies using concatenated single-copy markers have reinforced the genus's monophyly and clarified species relationships [13].

Phylogenomic analyses continue to refine the taxonomy. For instance, genome-scale ANI and dDDH comparisons have resolved *Glutamicibacter nicotianae* and *Arthrobacter mysorens* as heterotypic synonyms [14]. *Glutamicibacter* genomes, typically ranging from 3.4 to 3.9 Mb with G+C contents of 59–65%, demonstrate both taxonomic coherence and ecological diversification [15, 16, 17, 18]. Collectively, taxonomic and phylogenetic data support *Glutamicibacter* as a genomically coherent and ecologically flexible genus within the *Micrococcaceae* family (Figure 2).

3. Ecology and distribution

Glutamicibacter species have been isolated from a remarkably wide range of sources: freshwater sediments, plant-associated niches, food environments, polar ecosystems, and insect hosts. Soils from agronomic, coastal, mangrove, and desert environments are primary reservoirs, harboring strains with stress-resilience genes and diverse catabolic pathways crucial for organic matter turnover and nutrient cycling. For example, cold-shock proteins, oxidative stress regulators, and xenobiotic degradation pathways were identified in *G. mysorens* strains from Asian lakes [18, 8].

A key feature of the genus is its pronounced adaptive capacity. Genomic traits supporting psychrotrophic growth have been reported for *G. halophytocola* from Antarctic sediments [16], while halophyte-associated strains produce exopolysaccharides that confer protection against environmental stressors [19, 20]. Marine environments host species like *G. mishrai* from coral reefs and mangroves, which tolerate wide salinity ranges and exhibit antimicrobial activity [17, 20].

The genus also occupies food-related niches, such as *G. arilaitensis* playing a role in ripening and pigmentation of European cheese rinds [20]. Conversely, polluted soils and industrial settings have selected for strains proficient in degrading xenobiotics [8]. The ecological range extends to insects, with isolates like *G. creatinolyticus* recovered from the gut of the tea looper moth (*Ectropis obliqua*), highlighting associations within insect microbiomes [21]. Reports from Asia, Europe, Antarctica, and marine systems confirm the global distribution of *Glutamicibacter* (Figure 3).

4. Morphology and cultural characterization

Glutamicibacter exhibits a characteristic rod–coccus growth cycle: cells appear as rods during exponential phase and transition to coccoid or short-rod forms in stationary phase [9, 22]. Unlike filamentous actinobacteria, they lack aerial mycelium and are non-motile. The cell wall is Gram-positive with peptidoglycan type A3α (Lys–Ala–Thr), and menaquinones are predominantly MK-9(H2)

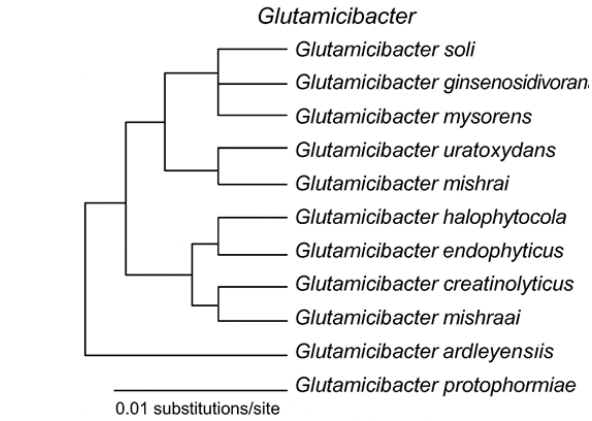


Fig. 2. Illustrative phylogenetic tree of the genus *Glutamicibacter*, reclassified from the genus Arthrobacter. The tree highlights representative species within the genus, showing their evolutionary distinction based on 16S rRNA phylogeny.

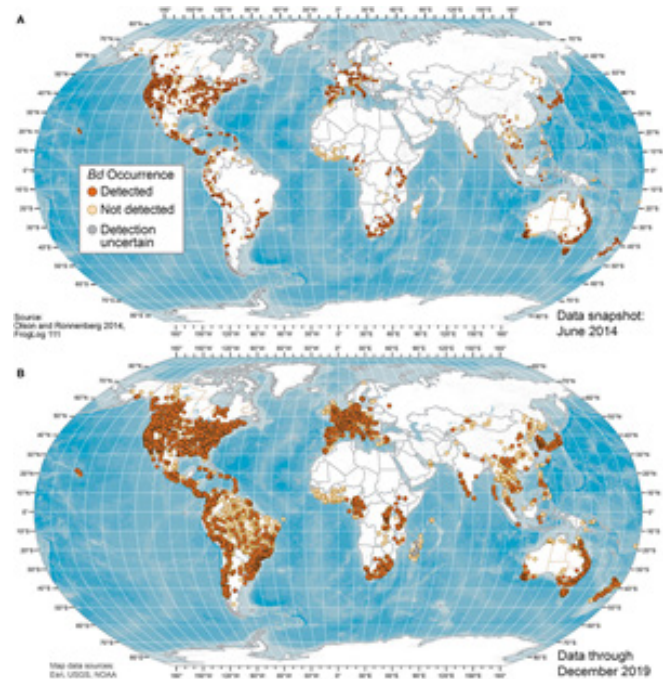


Fig. 3. Global distribution of Glutamicibacter species based on reported isolation sites and environmental/genome sequence data. Circles denote known locations where *Glutamicibacter* isolates have been characterized (soil, freshwater, marine, rhizosphere, food matrices, etc.). Presence inferred from environmental 16S rRNA / genome sequence submissions (9).

Table 1. Morphological diversity and cultural characteristics of *Glutamicibacter* spp (Representative morphology, colony appearance, and cultural characteristics of *Glutamicibacter* species, integrated with their phylogenetic relationships).

Species	Morphology	Colony / Cultural Features	Growth Conditions	References
G. arilaitensis	Gram-positive, rod–coccus cycle, non-motile, non-spore forming	Yellow, smooth, convex colonies (~2 mm, BHI agar)	10–30 °C (opt. 25–28 °C), up to 10% NaCl	Irlinger et al. 2005; Singh et al. 2018
G. ardleyensis	Gram-positive rods, rod–coccus cycle, motile	Yellow, circular, convex, smooth/rough (LB agar, 25 °C)	0–30 °C (opt. 25 °C), 0–10% NaCl, pH 7–8.5	Chen et al. 2005
G. creatinolyticus	Irregular rods (0.5–0.8 × 1.4–3.6 µm), coccoid in old culture, non-motile	Circular, smooth, yellow colonies (~1–1.5 mm, BHI agar, 24 h)	Optimum ~37 °C	Funke et al. 1995
G. protophormiae	Slightly club-shaped rods, coccoid in old culture, non-spore forming	Pale yellow to sulfur yellow colonies, no diffusible pigment	Optimum ~30 °C, tolerates 7% NaCl	Stackebrandt et al. 1983

and MK-9(H4) [9]. Genomic G+C content aligns with the *Micrococcaceae* range of 59–73 mol% [9, 22] (Table 1).

On solid media, colonies are smooth, circular to irregular, and pigmented cream, yellow, or orange, with an opaque to slightly mucoid texture, devoid of aerial mycelium. Optimal growth occurs on nutrient agar, tryptic soy agar, or actinomycete isolation agar at 20–30°C and pH 6.5–8.0. Some strains tolerate moderate salinity (5–7% NaCl) [23-25].

Physiologically, cultures are strictly aerobic, catalase-positive, and oxidase-negative. Strain-dependent biochemical activities include nitrate reduction, urease production, and hydrolysis of casein, starch, or gelatin. Carbohydrate utilization patterns vary, with some strains metabolizing glucose, arabinose, or xylose, while others show limited substrate specificity [26] (Figure 4).

5. Genomic insights and Biosynthetic Gene Clusters (BGCs)

Comparative genomics reveals significant intrageneric diversity and highlights BGCs of biotechnological interest (Figure 5). Whole-genome sequencing provides insights into the genetic basis of secondary metabolism and ecological adaptation in *Glutamicibacter* [27]. Genomes are relatively compact (3.4–3.7 Mb) yet encode a broad repertoire of genes for stress response, nutrient acquisition, and environmental persistence [27, 28].

A conserved core genome supports primary metabolism and housekeeping functions, while strain-specific genomic islands are enriched with genes for hydrolytic enzymes, siderophore biosynthesis, and plant growth-promoting traits, facilitating survival in soils and plant-associated niches [29, 30].

Genome mining using tools like antiSMASH has identified BGCs primarily for type-III polyketide synthases, siderophores, and terpenoids [31]. The general absence of large non-ribosomal peptide synthetase (NRPS) or polyketide synthase (PKS-I/II) clusters suggests a metabolic focus on smaller, adaptable metabolites rather than the complex antibiotics typical of *Streptomyces*. For instance, *G. arilaitensis* LJH19 carries predicted siderophore and terpene clusters, likely adaptations to iron-limited, cold, and cheese-associated environments, while *G. creatinolyticus* encodes siderophore-related operons for host-associated survival [27, 29].

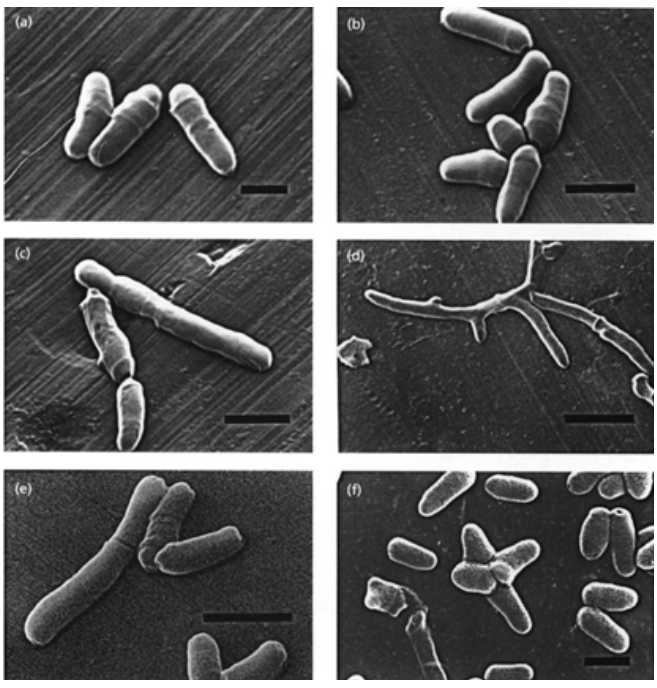


Fig. 4. Scanning and microscopy of Glu.spp adapted by Feng et al.,2017 Scanning electron microscopy (SEM) images of *Glutamicibacter* spp. showing characteristic morphology.This illustration highlights the rod–coccus growth cycle typical of the genus.

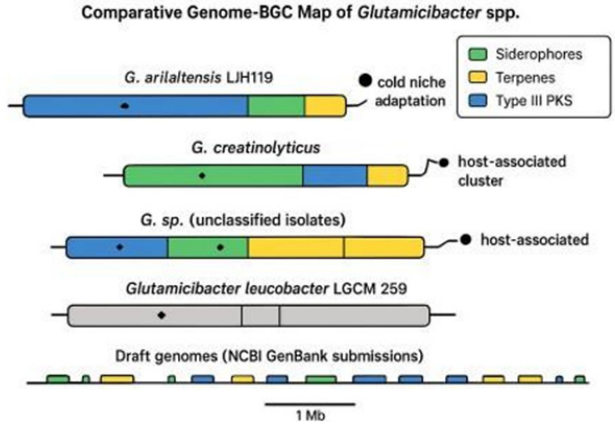


Fig. 5. Comparative analysis of biosynthetic gene clusters (BGCs) in identical *Glutamicibacter* genomes. Horizontal genome bars represent individual genomes, with colored blocks indicating different BGC types: NRPS (red), PKS (blue), terpenes (green), and siderophores (yellow). The alignment of blocks across genomes highlights the conservation of BGCs.

Adjacent regulatory genes can act as "genomic beacons" to activate silent clusters via approaches like CRISPR/dCas9 activation or heterologous expression [32]. Integrated pipelines combining genome annotation, BGC prediction (e.g., with PRISM, DeepBGC), networking (BiG-SCAPE), and validation through LC-MS/MS and molecular networking (GNPS) are standard for linking genetic potential to metabolite output [33].

Sequenced genomes available in public databases (e.g., *G. arilaitensis* LJH19, *G. creatinolyticus*, *Glutamicibacter* sp. FBE-19) underscore the genus's BGC diversity and ecological adaptations [34, 35]. Despite a smaller secondary metabolite repertoire compared to genera like *Streptomyces*, *Glutamicibacter* BGCs encode molecules of significant ecological and applied value, positioning the genus as an untapped resource [36, 37].

However, most BGCs lack functional validation. The regulatory mechanisms governing metabolite production are unclear, and the paucity of robust genetic tools hampers metabolic engineering and synthetic biology applications. Bridging this gap requires integrative multi-omics approaches, synthetic biology, and techniques like CRISPR-mediated activation and chromatin accessibility studies to elucidate BGC regulation (Table 2).

6. Metabolic and biotechnological potential

The metabolic diversity of *Glutamicibacter* underpins its adaptability across ecological niches such as soil, plants, dairy products, clinical settings, and saline environments [38, 29]. Catabolic pathways for carbohydrates, amino acids, lipids, and aromatics, supported by hydrolytic enzymes and stress-resistance proteins, facilitate nutrient cycling and competitiveness [17, 29].

In food biotechnology, strains like *G. arilaitensis* contribute to cheese ripening, flavor development, and proteolysis [39, 40]. Plant-associated isolates harbor genes for siderophore production, phosphate solubilization, and indole-3-acetic acid synthesis, conferring plant growth promotion and biocontrol benefits, especially in stressed soils [29]. Genome-mined BGCs for terpenes, siderophores, and type-III polyketides may contribute to antimicrobial activity or ecological fitness, with integrated metabolomics aiding in linking BGCs to bioactive compounds [41, 42].

The enzymatic repertoire holds industrial promise. Strains producing cold-active proteases, lipases, and esterases with broad substrate specificity are suitable for food, detergent, and pharmaceutical applications under mild conditions [41, 43]. Enzyme tolerance to salt and variable pH further enhances their bioprocess utility.

Furthermore, the ability to degrade casein, gelatin, starch, complex polysaccharides, and xenobiotics highlights potential in bioconversion, bioremediation, and generating value-added products. Combining these adap-

Table 2. Genome insights and biosynthetic gene clusters (BGCs) identified in *Glutamicibacter* spp.

Species / Strain	Genome Size (Mb)	Key Genomic Features	Identified BGCs / Tools Used	Ecological / Biotechnological Significance	Reference
G. arilaitensis LJH19	~3.4-3.6	Psychrotrophic, conserved core genome; genomic islands with hydrolytic enzymes, siderophores, PGP traits	Siderophors, terpenes (antiSMASH, DeepBGC, PRISM)	Adaptation to iron-limited cold niches; cheese associated flavor and ripening functions	Singh et al., 2021; Bechtel et al., 2025
G. Creatinolytcus	~3.5–3.7	Host associated; stress response operons; siderophore related,clusters	Siderophores,stress-resistance clusters	Survival in host environments; potential clinical relevance, antimicrobial activity	Romero et al., 2020; Singh et al., 2021
G. sp. (unclassified isolates,NCBI submissions)	~3.4–3.7	Core genome conserved; genomic islands with nutrient assimilation & PGP genes	Type-III PKS,terpenes, siderophores (antiSMASH, PRISM, DeepBGC)	Potential roles in rhizosphere, biocontrol, and bioremediation	Das et al., 2020
Glutamicibacter leucobacter LGCM 259 (host related)	~3.6	Host interaction genes; stress and nutrient adaptation	Putative siderophore and terpene BGCs	Host adaptation; useful model for exploring pathogenicity–commensal balance	O' Brien M et al., 2020
Draft genomes (NCBI GenBank submissions)	3.4–3.7	Strain-specific genomic islands; hydrolytic enzyme genes, siderophore biosynthesis	Multiple small clusters for terpenes, siderophores; absence of large NRPS/PKS clusters	Expanding the pangenome; highlights potential for novel secondary metabolites and niche-specific adaptations	NCBI Genome database, 2025

Table 3. Diverse applications of *Glutamicibacter.*

Category	Features / Traits	Applications / Relevance	References
Metabolic Diversity	Catabolism of carbohydrates, amino acids, lipids, aromatic compounds; hydrolytic enzymes; stress resistance proteins	Nutrient cycling, ecological competitiveness, adaptation to harsh environments	Das et al., 2020; Oliverira et al., 2020; Singh et al., 2021
Food Industry	Cheese ripening, flavor compound synthesis, proteolysis	Dairy microbiology; improved food quality	Iqbal S et al., 2023; Morales et al., 2021
Plant Interaction	Siderophore production, phosphate solubilization, indole-3-acetic acid (IAA) synthesis, hydrolytic enzymes	Plant growth promotion, biocontrol, stress-prone soil adaptation	Singh et al., 2021
Secondary Metabolites / BGCs	Terpenes, siderophores, type III polyketide synthases	Antimicrobial activity, ecological fitness, natural product discovery	Becker et al., 2021; Nguyen et al., 2021
Industrial Enzymes	Cold-active proteases, lipases, esterases; salt and pH-tolerant enzymes	Food processing, detergents, pharmaceuticals; bioconversion of substrates	Javed et al., 2024; Raina & Rood, 2019
Bioremediation / Bioconversion	Degradation of casein, gelatin, starch, complex polysaccharides, xenobiotics	Environmental bioremediation, value-added product generation	Singh et al., 2021; Oliveira et al., 2020
Integrated Biotechnological Potential	Combination of metabolic pathways, BGC-derived secondary metabolites, and versatile enzymes	Applications in sustainable agriculture, food biotechnology, environmental bioremediation, natural product discovery	Ahmed et al., 2022. Singh et al., 2021.

tive pathways, BGC-encoded metabolites, and diverse enzymes makes *Glutamicibacter* a versatile candidate for applications in sustainable agriculture, environmental cleanup, and natural product discovery [29] (Table 3).

7. Biomedical and industrial applications

7.1. Biomedical applications

Glutamicibacter is gaining biomedical relevance. Clinical isolates, such as *G. creatinolyticus*, have been associated with opportunistic infections and abscesses in humans and animals, indicating host colonization potential [27]. Although pathogenicity is rare, genomic studies of clinical strains provide insights into host-adaptation strategies, antimicrobial resistance genes, and virulence factors, informing biosafety assessments [44]. BGC-encoded siderophores, terpenes, and type-III polyketides may yield compounds with antimicrobial, antioxidant, or anticancer properties [29]. Cold-active enzymes (lipases, proteases, esterases) offer opportunities for pharmaceutical biocatalysis and drug processing under mild, compound-preserving conditions [32].

7.2. Industrial applications

The metabolic versatility and environmental resilience of *Glutamicibacter* suit various industrial uses. In dairy biotechnology, *G. arilaitensis* aids cheese ripening through proteolysis, amino acid catabolism, and flavor compound production [39]. Plant-associated strains enhance crop productivity, stress tolerance, and pathogen resistance via phytohormone and siderophore production, offering eco-friendly alternatives to chemical inputs [45]. In environmental biotechnology, *Glutamicibacter* species are employed for wastewater treatment and soil detoxification due to their xenobiotic degradation capabilities [46, 47]. Their tolerance to salinity, osmotic stress, and pH variation facilitates their use in enzyme production pipelines and bioconversion processes [48, 49].

8. Emerging trends and research needs

Despite growing interest, critical research gaps limit the full exploitation of *Glutamicibacter*. Taxonomic resolution requires refinement through high-quality, closed genomes from diverse isolates to clarify species boundaries and address pan-genome-based misassignments.

Accurate genome reconstruction using hybrid sequencing and annotation pipelines (PGAP, Prokka) is essential for defining BGC boundaries and inferring horizontal gene transfer. While genome mining predicts BGCs, their functional validation remains scarce. Integrating LC-MS/MS, GNPS molecular networking, heterologous expression, and regulatory activation is crucial to link clusters to chemical structures and biological activities [30]. The expression dynamics and regulation of BGCs are poorly understood; transcriptomics, chromatin accessibility profiling, and CRISPR activation under varied conditions can help unlock cryptic metabolites.

The ecological roles of *Glutamicibacter* metabolites in consortia (e.g., cheese, rhizosphere) are largely unknown. Co-culture experiments, stable isotope probing, and community metabolomics are needed to understand these context-dependent functions [20].

Translational and safety studies are incomplete. Prior to field or food applications, strains must be screened for virulence factors, antimicrobial resistance genes, and mobile genetic elements. For industrial enzyme use, detailed biochemical and structural studies, including kinetics, thermostability, cold adaptation mechanisms, and protein engineering, are required [29].

Although genomic pathways suggest bioremediation potential for xenobiotics, aromatics, and steroids, validation through bench-scale and mesocosm trials is necessary to assess degradation rates and ecological impacts. Synthetic biology applications are currently constrained; developing genetic tools (vectors, promoters, CRISPR/Cas systems) for heterologous BGC expression is a prio-

rity.

Realizing *Glutamicibacter* as a model for natural product discovery and industrial deployment will require coordinated efforts in field bioprospecting, high-quality sequencing, chemical analytics, and safety assessments [29].

Conclusion

Glutamicibacter possesses exceptional metabolic versatility and adaptive genomic traits, promising applications in bioremediation, food bioprocessing, enzyme technology, sustainable agriculture, and industry. Genome-wide analyses have identified genes for siderophores, terpenes, type-III polyketides, hydrolytic enzymes, stress-response proteins, and plant growth-promoting factors. The occurrence of opportunistic clinical isolates underscores the need for biosafety evaluations in translational applications. However, *Glutamicibacter* remains less studied compared to model actinobacteria.

Current research is incomplete, with BGCs largely undefined, functional validation minimal, ecological interactions poorly evidenced, high-quality reference genomes scarce, and genetic engineering tools underdeveloped. Future exploration of *Glutamicibacter*'s biotechnological potential must leverage integrated genomics, transcriptomics, metabolomics, synthetic biology, and ecological experimentation.

Strategic pursuit of these avenues will enhance our understanding of microbial adaptation and actinobacterial diversity while facilitating the discovery of novel metabolites, enzymes, and bioactive compounds for medicine, agriculture, food science, and environmental biotechnology. In conclusion, *Glutamicibacter* represents a critical link between fundamental microbiology and applied biotechnology, serving as a prototype for studying microbial adaptation and a reservoir of unexploited functional resources.

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