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Genomic insights into '*Candidatus* Pseudomonas auctus' JDE115, a soybean endophyte with expanded nutrient acquisition and biocontrol-related gene repertoires

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Abstract Pseudomonas species are globally distributed bacteria that influence soil and plant health, functioning as both pathogens and plant growth-promoting rhizobacteria (PGPR). Genomic analyses have revealed the genetic basis for their ecological versatility, including the evolution of diverse nutrient acquisition and biocontrol traits. Here, we report the draft genome of 'Candidatus Pseudomonas auctus' JDE115, a novel soybean nodule–associated PGPR with biocontrol potential that may contribute to sustainable agriculture. The draft genome comprises 6.18 Mb with a GC content of 60.68%. Comparative genomic analyses with closely related Pseudomonas taxa revealed lineage-specific gene clusters associated with nutrient acquisition and biocontrol-related functions, including genes encoding extracellular serine proteases, siderophores, chitinases, hydrogen cyanide synthase, and non-ribosomal peptide synthetases. Functional annotation across KEGG, COG, Pfam, CAZy, and antiSMASH databases highlighted enriched pathways for phosphorus, sulfur, zinc, and potassium metabolism, as well as secondary metabolite biosynthesis. Several biosynthetic clusters, including arylpolyenes, cyclic lipopeptides, and β-lactones, appear to be expanded relative to other PGPR genomes, suggesting lineage-specific adaptations for rhizosphere persistence and pathogen suppression. Despite the agronomic importance of plant-associated Pseudomonas, the genomic basis of non-rhizobial soybean nodule endophytes with combined PGPR and biocontrol potential remains poorly understood.

Highlights

- Draft genome of novel soybean endophyte 'Candidatus Pseudomonas auctus' JDE115.
- Comparative genomics reveals lineage-specific biosynthetic gene cluster expansion.
- Enriched cyclic lipopeptide, arylpolyene, and β-lactone clusters suggest biocontrol roles.
- Genome encodes versatile nutrient acquisition and stress adaptation pathways.
- Findings broaden PGPR genomic diversity and support sustainable agriculture potential.

Keywords Pseudomonas, *'Candidatus* pseudomonas auctus', Plant growth-promoting rhizobacteria (PGPR), Comparative genomics, Biocontrol, Nutrient acquisition, Soybean endophyte, Sustainable agriculture

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Background

'Candidatus Pseudomonas auctus' JDE115 Ali et al., 2025 was recently described as a novel species [1]. While many Pseudomonas spp. have attracted attention for their beneficial role in plant health, others are important plant pathogens [2-4]. Several strains are recognized as plant growth-promoting rhizobacteria (PGPR) capable of suppressing numerous plant pathogens while enhancing crop resilience to both biotic and abiotic stresses [5–7]. Their efficacy is attributed to multiple mechanisms, including the biosynthesis of secondary metabolites (e.g., pyoverdines), the secretion of hydrolytic enzymes (e.g., chitinases, proteases), and the ability to solubilize essential nutrients such as phosphate and zinc [8, 9].

Among the diverse PGPR traits, the capacity of *Pseudomonas* strains to form robust biofilms in the rhizosphere is particularly important for long-term root colonization and effective competition with other soil microorganisms [10, 11]. Biofilm formation not only shields bacterial cells from environmental stressors but also supports the sustained delivery of growth-promoting metabolites and signaling compounds to plant roots [12]. In addition, many *Pseudomonas* spp. are known to elicit systemic resistance in plants, thereby enhancing defense against fungal, bacterial, and even pathogenic nematodes [2, 6]. Collectively, these multifaceted attributes highlight the agronomic potential of *Pseudomonas* populations in agricultural soils.

Despite the ecological importance and economic relevance of the genus, *Pseudomonas* remains highly diverse, and new species with distinct plant-associated traits continue to be isolated from varied environments. Advances in whole-genome sequencing have enabled more precise delineation of *Pseudomonas* taxa and provided deeper understanding of the genetic basis underlying their beneficial properties [13, 14]. In this context, we report the draft genome sequence of a recently characterized '*Candidatus* P. auctus' JDE115 isolated from soybean (*Glycine max* (L.) Merr.) root nodules [1], with evidence supporting its role as both a plant-growth promoter and a potential biocontrol agent. Our analysis emphasizes four key insights. First, JDE115 broadens the known genomic diversity of plant-associated *Pseudomonas*, displaying both core PGPR traits and unique gene clusters relative to its closest relatives. Second, its genome encodes lineage-specific adaptations, including expanded cyclic lipopeptide, arylpolyene, and β-lactone clusters, that may underpin its capacity for rhizosphere persistence, biofilm formation, and pathogen suppression. Third, comprehensive functional annotation across multiple databases (COG, KEGG, Pfam, GO, CAZy, CARD, and antiSMASH) anticipates a multidimensional perspective on plant-beneficial traits spanning nutrient cycling, secondary metabolism, and antimicrobial activity. Finally, these genomic insights establish a framework for the biotechnological application of JDE115 as both a biofertilizer and a biocontrol agent, while contributing to comparative studies of beneficial *Pseudomonas* lineages.

By situating the genome of JDE115 within a comparative and evolutionary context, this study advances our understanding of the genetic basis of plant–microbe interactions and underscores the agronomic potential of novel PGPR species. '*Candidatus* Pseudomonas auctus' JDE115 represents a recently described phylogenetically distinct soybean nodule endophyte. Unlike many previously characterized PGPR, JDE115 combines expanded secondary metabolite biosynthetic clusters with diverse nutrient acquisition systems, suggesting lineage-specific adaptations for persistence and pathogen suppression in the soybean rhizosphere.

Results

Description of the organism

'*Candidatus* P. auctus' JDE115 is a Gram-negative, facultatively aerobic, non-sporulating, motile, rod-shaped bacterium belonging to the order *Pseudomonadales* and the family *Pseudomonadaceae* [3]. Strain JDE115 exhibits morphological and physiological characteristics consistent with members of the genus *Pseudomonas* (Table S1). Phylogenetic analysis of the 16S rRNA gene places JDE115 in close relationship to *Pseudomonas glycinae* MS586 with 99% sequence similarity (Fig. 1).

Genome properties

The draft genome '*Candidatus* P. auctus' JDE115 has a total length of 6,183,199 bp with a GC content of 60.68% (Table 1). It encodes 5,648 genes, including 5,509 protein-coding genes (CDS) [13], and 70 RNA genes, comprising two complete rRNAs (5S, 16S, 23S), one partial rRNA (5S), and 62 tRNAs [15, 16] (Fig. 2). In addition, 69 pseudogenes were identified, of which nine are frameshifted, 61 are incomplete, and 6 contain internal stop codons. Coding regions represent 89.17% of the genome.

Functional annotation showed that 4,485 genes (79.42%) were assigned to COG categories, while 3,169 genes (56.12%) were mapped to KEGG pathways [17]. Pfam domains were detected in 3,908 genes (69.17%), 586 genes (10.37%) were found to have signal peptides, and 500 genes (8.85%) were predicted to encode secretory proteins [18]. The whole-genome shotgun project has been deposited in GenBank under accession number PRJNA1196930 (Table S2).

Genome annotation results of '*Candidatus* P. auctus' JDE115

Comprehensive genome annotation of '*Candidatus* P. auctus' JDE115 was conducted using multiple functional databases, including NCBI nr [19], KEGG [17],

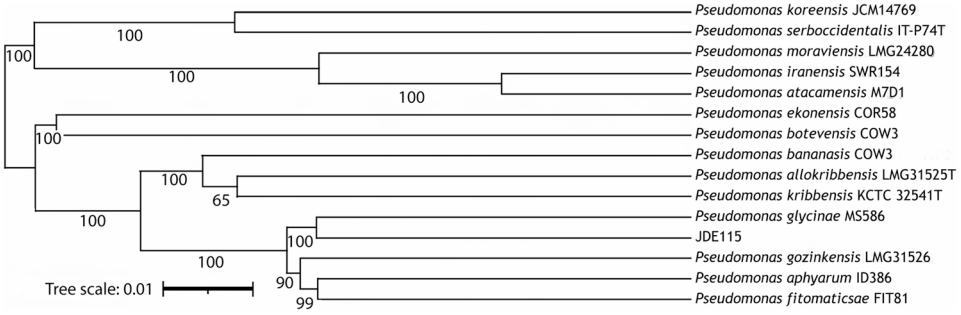

Fig. 1 Phylogenomic placement of '*Candidatus* Pseudomonas auctus' JDE115 Core-genome phylogeny based on whole-genome alignment showing the relationship of JDE115 to closely related *Pseudomonas* species. Bootstrap support values are indicated at branch nodes, and the scale bar represents substitutions per site (Adapted from Ali et al., 2025)

Table 1 Genome statistics of '*Candidatus* Pseudomonas auctus' JDE115 Ali et al., 2025

Attributes	Value	% of total
Genome size (bp)	6,183,199	100
DNA coding (bp)	5,513,388	89.17
GC base count (bp)	3,752,162	
GC content (%)	60.68	
Genes (total)	5,648	100
CDS (total)	5,578	98.76
Genes (coding)	5,509	97.54
CDSs (with protein)	5,509	97.54
Genes (RNA)	70	1.24
rRNAs	2, 1, 1 (5 S, 16 S, 23 S)	
complete rRNAs	1, 1, 1 (5 S, 16 S, 23 S)	
partial rRNAs	1 (5 S)	
tRNAs	62	
ncRNAs	4	
Pseudogenes (total)	69	
CDSs (without protein)	69	
Pseudogenes (ambiguous residues)	0 of 69	
Pseudogenes (frameshifted)	9 of 69	
Pseudogenes (incomplete)	61 of 69	
Pseudogenes (internal stop)	6 of 69	
Pseudogenes (multiple problems)	6 of 69	
Genes assigned to COGs	4,485	79.42
Genes with Pfam domains	3,908	69.17
Genes assigned to KEGG	3,169	56.12
Genes assigned to GOs	3,908	69.17
Genes with signal proteins	586	10.37
Genes assigned to secretory proteins	500	8.85

Swiss-Prot [20], GO [13], TCDB [21], Pfam, CAZy [22], and CARD [23]. Sequence similarity searches were performed with DIAMOND (E-value ≤ 1e − 5), and the best hits were retained on thresholds of ≥ 40% identity and ≥ 40% coverage. A statistical summary of annotated genes is presented in Figure S1.

Annotation revealed that 5,522 genes (97.77%) were assigned in NCBI nr, 2,604 genes (46.13%) in Swiss-Prot, 4,485 genes (79.42%) in COG, 3,908 genes (69.17%) in both Pfam and GO, and 3,169 genes (56.12%) in KEGG. The CAZy database identified 214 genes (3.79%), while 758 genes (13.43%) were mapped to TCDB. The lowest representation was observed in CARD, with 270 annotated genes (4.78%) (Figure S1 and Table S3).

COG functional annotation of '*Candidatus* P. auctus' JDE115 revealed genes distributed across multiple categories linked to plant-growth promotion and biocontrol (Table S4) [24]. The largest group was amino acid transport and metabolism (503 genes, COG E), which may support siderophore production, phytohormone biosynthesis, and nutrient cycling. Carbohydrate metabolism genes (268 genes, COG G) were also abundant, consistent with roles in exopolysaccharide (EPS) production important for biofilm formation and root colonization. Genes assigned to secondary metabolite biosynthesis (106 genes, COG Q) highlight the potential for antimicrobial compound production. A substantial number of genes associated with inorganic ion transport and metabolism (304 genes, COG P), suggest functions in phosphate solubilization, nitrogen metabolism, and metal ion uptake. Signal transduction genes (396 genes, COG T) indicate a strong regulatory capacity for quorum sensing and environmental adaptation, while genes involved in cell wall/membrane/envelope biogenesis (332 genes, COG M) may contribute to adhesion and biofilm stability. Additional categories included protein turnover, chaperones, and related functions (201 genes, COG O), supporting stress tolerance and survival under variable soil conditions. Defense mechanism genes (125 genes, COG V) point to antimicrobial potential and possible induction of plant systemic resistance. Finally, genes associated with cell motility (93 genes, COG N) emphasize the strain's ability to colonize roots and move effectively in the rhizosphere (Figure 3).

Metabolism-related pathways accounted for the largest proportion of annotated genes in '*Candidatus* P. auctus' JDE115, reflecting its ability to utilize diverse substrates and contribute to soil fertility (Figure S2) [25]. Amino acid metabolism was the most abundant category (309 genes), supporting roles in protein biosynthesis and

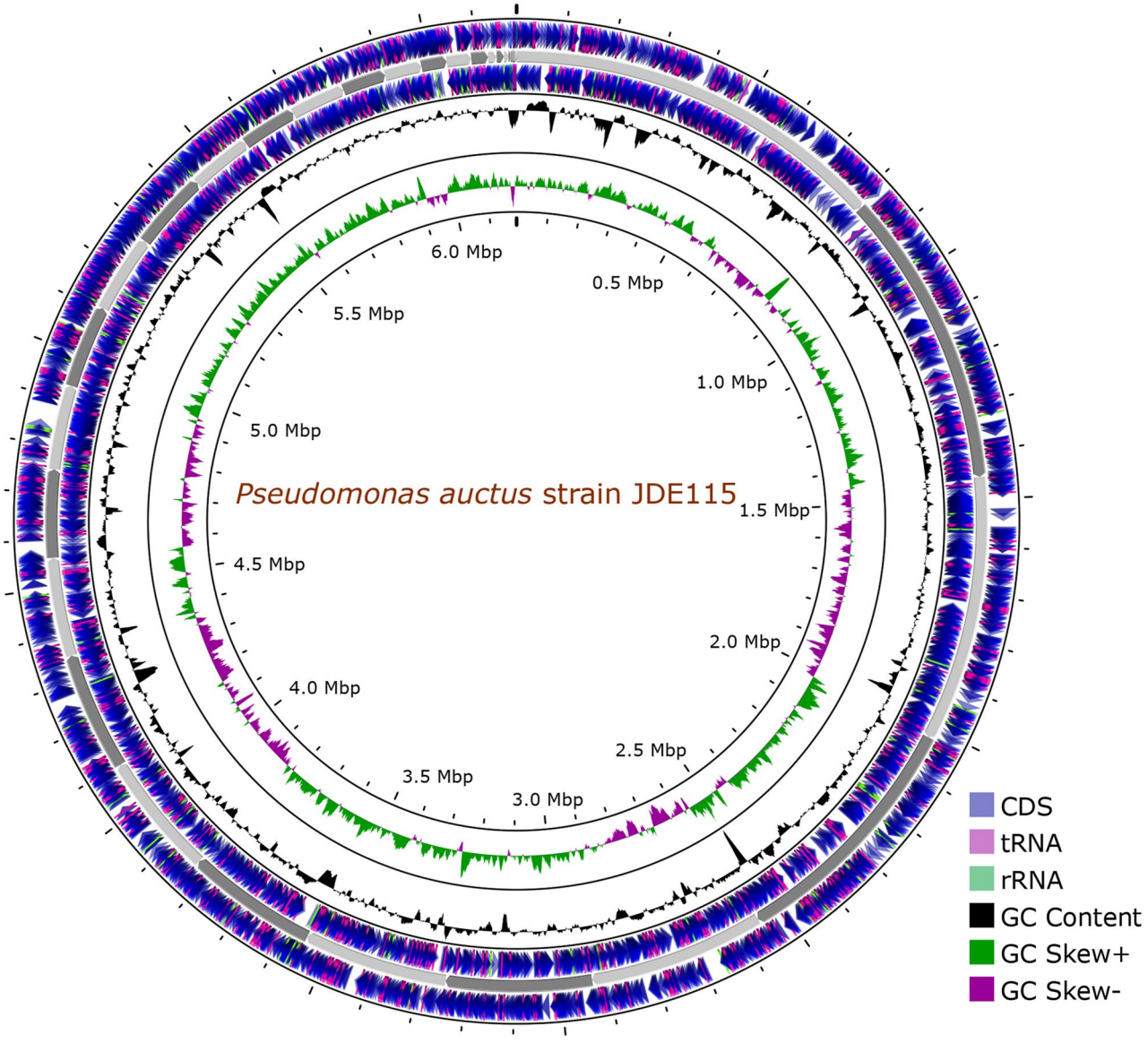

Fig. 2 Circular genome map of 'Candidatus Pseudomonas auctus' JDE115 Ali et al., 2025 generated with the Proksee server (https://proksee.ca/) Numbers indicate positions in megabase pairs (Mbp). From the innermost to the outermost rings: (i) genome scale; (ii) GC Skew; (iii) GC content; and (iv-v) coding sequences (CDS), tRNAs, and rRNAs

nitrogen cycling. Genes assigned to secondary metabolites biosynthesis (64) and carbohydrate metabolism (264) indicate strong capacities for organic matter degradation, potentially aiding phosphate solubilization and root colonization [26]. Additional genes involved in energy metabolism (193) and lipid metabolism (79) suggested flexibility in energy production, while xenobiotic biodegradation genes (83) point to potential functions in soil detoxification and bioremediation [27].

Transport and signaling functions were also prominent. Membrane transport (289 genes) and signal transduction (241 genes), highlight extensive capabilities for nutrient uptake, chemotaxis, and environmental sensing [10, 25]. Genetic information processing included genes for DNA replication and repair (55), transcription (5), and translation (79), underscoring genomic stability, while protein folding and degradation (60) support stress tolerance and survival under drought or nutrient limitation [28].

Traits linked to PGPR activity were evident. Motility (96 genes) and cellular community pathways (171) likely contribute to root colonization and biofilm formation [10]. Genes associated with cell growth and death (33) suggest regulatory mechanisms for population-level regulation, while those linked to immune system interactions (3), digestive functions (7), and endocrine regulation (16) may influence plant systemic resistance and hormonal balance. Additional genes related to

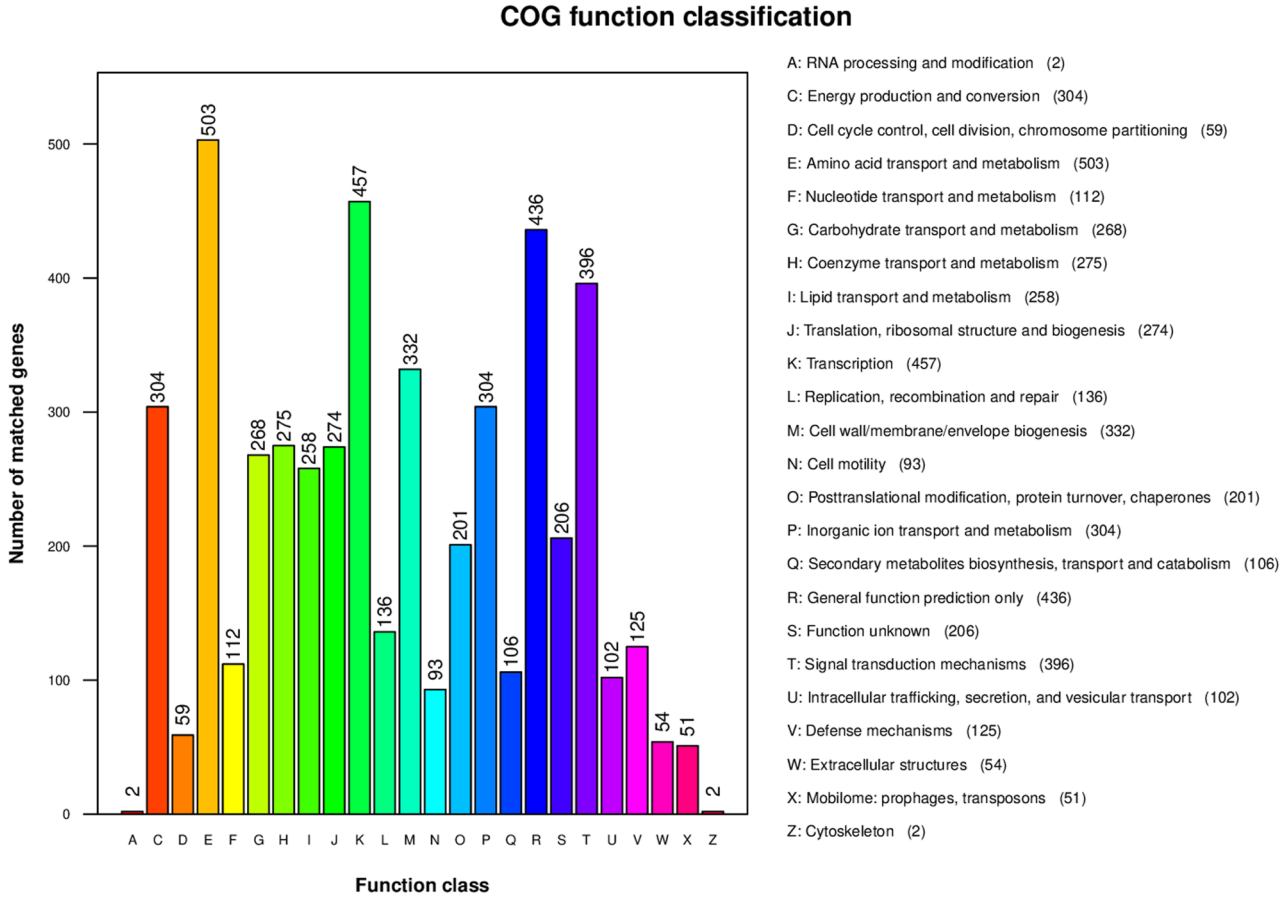

Fig. 3 Functional annotation results of the '*Candidatus* Pseudomonas auctus' JDE115 Ali et al., 2025 genome using the COG database (Supplementary Data 1) A total of 26 COG functional categories were identified. Categories are indicated on the X-axis by alphabetical codes, with their corresponding names listed to the right. The Y-axis represents the number of genes assigned to each category

environmental adaptation (15) and aging (20) indicate resilience and persistence in soil ecosystems (Tables S5 and S6).

In the gene ontology (GO) classification, the biological process category was dominated by genes associated with cellular (2,087) and metabolic processes (1,930), reflecting core roles in growth and survival (Figure S3). Additional processes, such as localization (808), biological regulation (745), and regulation of biological processes (741), indicate a coordinated genetic network for cellular organization and environmental adaptation. Genes linked to response to stimulus (409) and signaling (291) further underscore the strain's ability to sense and react to environmental changes.

Within the cellular component category, most genes were assigned to cellular anatomical entities (1,104), followed by protein-containing complexes (154) and virion components (27) (Figure S3). These assignments suggest a complex cellular architecture supported by extensive protein interaction networks, while the presence of virion-associated genes may represent evolutionary remnants or mechanisms for DNA exchange that enhance adaptability.

The molecular function category was enriched with genes encoding catalytic (2,056) and binding activity (1,713), emphasizing enzymatic efficiency and substrate interactions critical for biochemical transformations and nutrient cycling. Additional functions included transcription regulator (350), transporter (284), and ATP-dependent activity (221) highlighting regulatory and nutrient acquisition systems. The presence of molecular transducer activity (146), small molecule sensor activity (77), and structural molecule activity (54) further suggests advanced sensing capabilities and structural stability.

Antibiotic resistance (CARD) analysis

The genome of *'Candidatus* P. auctus' JDE115 was analyzed using the Comprehensive Antibiotic Resistance Database (CARD) [23]. A total of 270 antibiotic-resistance genes were identified, including those encoding efflux pump complexes and subunits that play key roles in multidrug resistance. Additional genes were associated with target protection proteins, antibiotic- inactivating

enzymes, and resistance to multiple antibiotic classes such as ß-lactams, fluoroquinolones, tetracyclines, and glycopeptides (Supplementary Data 1).

CAZyme gene families

A total of 214 carbohydrate-active enzyme (CAZyme) genes were identified and classified into six major enzyme families (Figure S4). Of these, 111 glycosyltransferases (GTs) are involved in the synthesis of polysaccharides and glycosylated compounds, whereas 67 glycoside hydrolases (GHs) contribute to the degradation of complex carbohydrates, underscoring their central role in carbohydrate metabolism.

In addition, 19 carbohydrate-binding modules (CBMs), were detected enhancing substrate recognition and enzymatic efficiency [56]. The genome further encoded 9 carbohydrate esterases (CEs) which remove ester-linked groups from polysaccharides, and four polysaccharide lyases (PLs), which contribute to the degradation of acidic polysaccharides [22]. Notably, four auxiliary activity (AA) genes were identified, representing redox active enzymes associated with lignocellulose degradation and oxidative reactions. Together these CAZyme repertoires highlight the strain's metabolic versatility, its potential role in root colonization, and its contributions to soil carbon turnover and nutrient availability (Figure S4). Among the predicted protein-coding sequences, several genes were annotated as extracellular serine proteases, including subtilisin-like enzymes with N-terminal signal peptides, indicative of secretion into the external environment (Table S7). The presence of these genes indicates that '*Candidatus* P. auctus' JDE115 possesses enzymatic functions that may contribute to pathogen suppression within its ecological niche [29–32].

Biosynthetic gene clusters in the genome of strain JDE115

The genome of '*Candidatus* P. auctus' JDE115 was screened using the antiSMASH database [33] which identified 12 secondary metabolite biosynthetic gene clusters (Table 2). These included clusters for siderophore, bacteriocin, NRPS-like, arylpolyene, NAGGN, NRPS, and β-lactone. Many of these biosynthetic pathways are associated with metabolites that enhance bacterial survival, promote plant growth, and contribute to biocontrol activity.

Table 2 Gene clusters with their cluster and gene number of secondary metabolites of '*Candidatus* Pseudomonas auctus' JDE115 Ali et al., 2025

Clusters	Clusters number	Gene number
Siderophore	1	8
Bacteriocin	2	20
NRPS-like	1	12
Arylpolyene	1	38
NAGGN	1	10
NRPS	5	144
ß-lactone	1	18

The arylpolyene (APE) biosynthetic cluster plays a protective role against oxidative stress in the rhizosphere, functioning analogously to carotenoids [34]. APEs are widespread in Proteobacteria and constitute one of the most common biosynthetic gene cluster families [35]. In '*Candidatus* P. auctus' JDE115 APEs may suggest its genomic capacity for oxidative stress resistance, supporting long-term persistence in plant roots. They are also implicated in biofilm formation, facilitating the transition from a planktonic state to a surface-attached lifestyle, thereby improving stress tolerance, root colonization, and persistence [12, 34]. Another biosynthetic cluster was linked to terpene and NRPS pathways. Terpenes are well recognized for their roles in modulating plant growth and triggering systemic resistance through the release of volatile organic compounds (VOCs) [36, 37]. Additional clusters for siderophores, bacteriocins, and NRPS products were also identified, representing important mechanisms for nutrient acquisition and pathogen suppression. Siderophores enhance iron availability while restricting pathogen access [38], bacteriocins function as narrow-spectrum antibiotics against competing microbes and NRPS-derived peptides may encode additional antimicrobial metabolites that further reinforce biocontrol activity [39].

Five NRPS clusters were predicted to encode cyclic lipopeptides (CLPs), multifunctional metabolites involved in bacterial motility, root colonization, and antagonism against pathogens. Acting as biosurfactants, CLPs promote bacterial adhesion to plant roots [40, 41] and exhibit strong antifungal activity by disrupting pathogen membranes [42]. The NAGGN cluster was associated with stress adaptation and regulation of secondary metabolite production [43], while the β-lactone cluster was linked to antimicrobial activity through inhibition of cell wall synthesis and essential metabolic processes [42]. Collectively, these clusters underscore the broad metabolic potential of '*Candidatus* P. auctus' JDE115 to produce bioactive compounds that enhance its rhizosphere competitiveness, stimulate plant growth, and suppress plant pathogens.

Extracellular serine proteases

Genome annotation of *Candidatus* P. auctus JDE115 revealed genes encoding extracellular serine proteases, suggesting an additional mechanism underlying its biocontrol potential (Table S21). Secreted proteases are recognized virulence and defense factors in plant-associated microorganisms, particularly in their ability to degrade structural proteins of pathogens and pests [29]. In biocontrol bacteria, serine protease often target nematode

and fungal cuticle, eggshells, and intestinal proteins, leading to tissue degradation and mortality [29, 44, 45]. The presence of such genes in JDE115 implies a dual role: (i) nutrient acquisition in the rhizosphere by hydrolyzing proteinaceous substrates, and (ii) direct antagonist activity against plant-parasitic nematodes (PPNs) and fungal pathogens [29, 31, 44].

Evidence from other organisms supports this interpretation. In *Bacillus firmus* DS-1, the extracellular Sep1 protease, was shown to kill root-knot (*Meloidogyne* spp.) and soybean cyst nematodes (*Heterodera glycine* Ichinohe, 1952) by degrading multiple intestinal and cuticle-associated proteins. Likewise, nematicidal bacteria associated with the pinewood nematode *Bursaphelenchus xylophilus* (Steiner & Buhrer, 1934) Nickle, 1970 produces a ~ 70 kDa extracellular serine protease directly linked to nematode mortality. Comparable mechanisms are found in nematophagous fungi such as *Purpureocillium lilacinum* (Thom) Luangsa-ard, Houbraken, Hywel-Jones & Samson and *Pochonia chlamydosporia* (Goddard) Zare & W. Gams, where secreted serine proteases (e.g., PR1, VCP1) play critical roles in cuticle penetration and egg parasitism [30]. Beyond nematicidal activity, bacterial extracellular serine proteases have also been associated with antifungal effects, targeting cell wall proteins and compromising hyphal integrity [31, 32].

Taken together, these findings suggest that the proteases encoded by JDE115 may represent potential molecular mechanisms contributing to antagonism against nematode and fungal pathogens. While functional assays are required to confirm activity, the genomic evidence strongly supports their potential importance for rhizosphere survival and agricultural application.

Revealing insights from the genome

Phosphorus metabolism

The genome of '*Candidatus* P. auctus' JDE115 underscores its potential as a PGPR and biocontrol agent, particularly through genes involved in phosphorus (P) uptake, solubilization and regulation (Table S8). JDE115 encodes multiple genes involved in phosphate solubilization, transport, and regulation, consistent with PGPR-associated phosphorus mobilization in the rhizosphere [46]. Key determinants include glucose dehydrogenase (*gdh*) and pyrroloquinoline quinone (PQQ) biosynthesis genes (*pqqB*, *pqqC*, *pqqD*), which support gluconic acid-mediated phosphate solubilization [8]. Genes of the Pho regulon, such as *phoA*, *phoP*, and *phoQ*, facilitate sensing and regulation of phosphate availability [47, 48], while *pstS* and *phoA2* contribute to hydrolysis and transport of organic and inorganic phosphate [49]. Furthermore, genes such as *phnX* and *phnD1* suggest the capacity to metabolize phosphite and phosphonates, enhancing adaptability under P-limiting conditions and promoting sustainable nutrient cycling [48, 50].

Sulfur metabolism

The genome encodes ABC transporters, sulfate/thiosulfate-binding proteins, and the *cysTWA* operon enabling efficient uptake of sulfate and thiosulfate [51, 52]. Key genes such as *cysC*, *cysD*, and *cysH* support assimilatory sulfate reduction, producing cysteine for metabolism and growth [53]. The presence of *cysK* and *cysB* supports cysteine biosynthesis and regulation under sulfur limited conditions [52, 54] while *sufS* contributes to iron–sulfur cluster assembly (Table S9), which is essential for maintaining redox balance under oxidative stress [55]. In addition, *sbp* enhances sulfate uptake efficiency [56]. Together, these genetic systems may promote survival in sulfur-deficient soils and suggest genomic capacity for plant sulfur nutrition, with potential benefits for stress tolerance and crop productivity [57].

Zinc metabolism

JDE115 encodes high-affinity zinc uptake (*znuABC*) [58–60], regulatory (*zur*), and efflux (*zitB*, *zntA*) (Table S10) systems, indicating genomic capacity to maintain zinc homeostasis under fluctuating soil conditions [61–63].

Potassium metabolism

Genes encoding high-affinity (*kdpABCDE*), low-affinity (*trkAI*), and efflux (*kefBCFG*) potassium transport systems were identified (Table S11), suggesting genomic potential for potassium homeostasis and stress adaptation [64–66].

Biofilm formation and persistence

Biofilm formation is a critical trait of PGPR, providing protection against environmental stresses, antibiotics, and host immune responses thereby enabling survival in competitive soil ecosystems [67]. The presence of biofilm-associated genes in JDE115 support colonization potential (Table S12) [12, 67]. Curli fimbriae genes (*csgB*, *csgE*, *csgG*) support surface attachment and structural stability [68–70], while exopolysaccharide biosynthesis genes (*pgaA*, *pgaB*, *pgaC*) direct the production of poly-β-1,6-N-acetyl-D-glucosamine (PGA), essential for matrix formation and stress protection [71–73]. Multiple copies of *rkpK* further suggest genomic potential for EPS biosynthesis [74, 75].

Antibiotic resistance and cell wall integrity

Genome annotation also revealed multiple genes linked to antibiotic resistance and cell wall biosynthesis (Table S13). Genes encoding β-lactamase (*ampC*), penicillin-binding proteins (*pbpA*, *pbpB*, *mrcA*, *mrcB*), and a bacitracin export ATP-binding protein (*bceA*), suggest

resistance to β-lactam antibiotics and bacitracin. Additional defense mechanisms include thiol: disulfide interchange proteins (*dsbA*, *dsbB*), multidrug efflux pump subunits (*acrB*, *ebrA*), and peptidoglycan synthesis enzymes (*murG*, *mraY*) suggesting resistance against multiple antibiotics including penicillin, streptomycin, and vancomycin [59]. The presence of cell division genes (*ftsA*, *ftsZ*, *ftsK*) and DNA translocase (*bscA*) further indicates a well-regulated cell wall biosynthesis and repair system (Table S13). These features likely enhance bacterial survival under antibiotic stress, ensuring structural integrity and adaptability in competitive soil environments.

Iron acquisition and siderophore systems

The genome encodes multiple siderophore biosynthesis, transport, and uptake systems, including pyoverdine- and enterobactin-related genes (Table S14 and S15), suggesting strong genomic capacity for iron acquisition and competition in iron-limited environments [76–80].

Auxin biosynthesis

Analysis of '*Candidatus* P. auctus' JDE115 revealed key genes involved in the tryptophan-dependent auxin biosynthesis pathway, highlighting its potential as a PGPR (Table S16). Anthranilate synthase components (*trpE*, *trpG*, *trpD*), provide precursors for tryptophan biosynthesis, ensure a steady supply of substrate for IAA production [81, 82]. Tryptophan synthase subunits (*trpA*, *trpB*) catalyze a key step in tryptophan formation [83], while trpC (indole-3-glycerol phosphate synthase) and *aroC* (chorismate synthase) reflect an active shikimate pathway leading to aromatic amino acids biosynthesis [84]. The detection of *iaaM* (tryptophan-2-monooxygenase) indicates that '*Candidatus* P. auctus' JDE115 can convert tryptophan into indole-3-acetamide, an intermediate in the indole-3-acetamide (IAM) pathway of auxin biosynthesis [85]. Additional genes such as *trpF* (N-(5'-phosphoribosyl) anthranilate isomerase) and *aroE* (shikimate dehydrogenase) further support the strain's capacity to regulate auxin precursor synthesis (Table 3).

Motility and chemotaxis

The detection of multiple flagellar biosynthetic proteins (*fliA*, *fliY*, *flhB*, *motB*, and *flg* genes) indicates an active and well-regulated flagellar assembly system, essential for bacterial mobility in soil environments [86]. Flagellar motor switch proteins (*fliG*, *fliM*, *fliN*) and flagellar hook-associated proteins (*flgE*, *flgK*, *flgL*) ensure proper flagellar rotation and directional movement toward plant roots [87]. Additionally, basal body components (*flgB*, *flgC*, *flgD*, *flgG*) reinforces the structural integrity of the flagellum (Table S17), supporting efficient motility in diverse soil conditions (Table 3).

Chemotaxis is a critical mechanism guiding bacterial movement toward root exudates and other favorable niches [88]. JDE115 encodes several chemotaxis-related genes (*cheA*, *cheW*, *cheR2*) to regulate signal transduction and flagellar movement in response to environmental cues [88]. The chemotaxis response regulator protein (*cheA*) and chemotaxis methyltransferase (*cheR2*) facilitate bacterial adaptation to fluctuating nutrient gradients, promoting efficient root colonization [89] (Table S18). Furthermore, the presence of swarming motility protein (*swgA*) suggests that JDE115 is capable of forming cooperative bacterial communities, enhancing its persistence and competitiveness in the rhizosphere [90] (Table 3).

Hydrogen cyanide production and chitinase activity

The genome of *'Candidatus* P. auctus' JDE115 encodes the *hcnABC* gene cluster responsible for hydrogen cyanide production, a potent antimicrobial compound, that suppresses fungal pathogens and plant-parasitic nematodes [91]. In addition, the presence of chitinase D (Table S19) equips the bacterium to degrade chitin, a key structural component of fungal cell walls and nematode eggshells, thereby reinforcing its biocontrol potential [92] (Table 3).

Nitrogen metabolism and ethylene regulation

In the genome of *'Candidatus* P. auctus' JDE115, nitrogen metabolism is supported by genes such as *ureA* (urease subunit gamma) and *ureC* (urease subunit alpha), which facilitate the bacterium's ability to utilize urea as a nitrogen source [93]. Another important feature is the presence of *accA_2* (Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha) and *acdA_2* (Acyl-CoA dehydrogenase), which are involved in ethylene regulation (Table S20). These genes contribute to modulating ethylene levels, a key plant hormone, thereby reducing ethylene-induced stress, promoting root elongation, and enhancing overall plant growth under diverse environmental conditions [94] (Table 3).

Additional metabolic and stress-response traits

In addition, motility related genes such as *fliA*, *fliM* supports effective root colonization [95], strengthening rhizosphere interactions (Table S11). The genes *gdhI* (Glucose 1-dehydrogenase) and *zwf_1* (Glucose-6-phosphate 1-dehydrogenase) contribute to phosphate solubilization and NADPH production. The presence of *rkpK* (UDP-glucose 6-dehydrogenase) facilitates extracellular polysaccharide synthesis and biofilm formation, while *gdhA*/*gdhB* (Glutamate dehydrogenases) are involved in nitrogen metabolism (Table S21). Together, these genomic capacities suggest the strain's plant growth promoting capacity and biocontrol potential (Table 3).

Table 3 Key plant-beneficial traits summarize genes for phosphate solubilization, siderophores, chitinases, Serine proteases, auxin biosynthesis, etc. The genome of *'Candidatus* P. auctus' JDE115 harbors an integrated suite of genes enabling: 1) biocontrol and antimicrobial traits (HCN, chitinase, proteases, siderophores, CLPs, β-lactones), 2) nutrient acquisition and mobilization (P, N, S, Zn, Fe) and hormone regulation (ethylene modulation), 3) colonization and plant interaction (motility, chemotaxis, biofilm), and 4) stress adaptation (oxidative, nutrient-limited conditions). Together, these traits equip JDE115 to colonize soybean roots, promote plant growth, and suppress pathogens, supporting its potential as a biofertilizer and biocontrol agent

Activity	Gene	Product	Function
Biocontrol and Antimicrobial			
	hcnABC cluster	Hydrogen cyanide production	Suppressing fungal pathogens and plant-parasitic nematodes.
	Chitinase D	Chitinase production	Degrades chitin in fungal cell walls and nematode eggshells
	Extracellular serine proteases	Serine proteases	Degrades nematode cuticle and fungal cell wall proteins,
	Biosynthetic gene clusters (BGCs)	Siderophores	Enhance iron uptake while limiting pathogen access
		NRPS/CLPs (cyclic lipopeptides)	Promote motility, root adhesion, and strong antifungal activity
		Arylpolyenes (APE)	Protect against oxidative stress and support biofilm formation
		β-lactones and bacteriocins	Antimicrobial activity against competitors
Nutrient Acquisition and Metabolism			
Phosphorus metabolism	*gdh*	glucose dehydrogenase	Gluconic acid–mediated phosphate solubilization
	pqqB	PQQ biosynthesis protein	Oxidoreductase-like
	pqqC	PQQ synthase	Final ring cyclization
	pqqD	Small peptide chaperone that binds and delivers the precursor peptide (PqqA) to PqqE	A radical SAM enzyme, initiating PQQ biosynthesis
	Pho regulon (*phoA*, *phoP*, *phoQ*)		Sensing and regulating phosphate availability
	pstS, *phoA2*		Phosphate transport
	phnX, *phnD1*		Utilization of phosphite and phosphonates
Sulfur metabolism	*cys* operon	Multiple enzymes (ATP sulfurylase, APS kinase, PAPS reductase, sulfite reductase)	Assimilation of sulfate → sulfide
	cysK	O-acetylserine sulfhydrylase A (OASS-A)	Catalyzes the final step in cysteine biosynthesis
	cysB	LysR-type regulator (CysB)	Transcriptional activator of cys regulon
	sufS	Cysteine desulfurase (SufS)	Sulfur transfer from cysteine → Fe–S clusters
	sbp	Sulfate-binding protein	Periplasmic uptake of sulfate into cell
Nitrogen metabolism	*ureA*	Urease γ subunit	Small structural subunit of urease
	ureC	Urease α subunit (catalytic)	Hydrolyzes urea → $CO_2 + NH_3$
	gdhA	$NADP^+$-dependent glutamate dehydrogenase	Assimilation of ammonium → glutamate
	gdhB	NAD^+-dependent glutamate dehydrogenase	Catabolism of glutamate → α-ketoglutarate + NH_4^+
Ethylene regulation	*accA_2*	Acetyl-CoA carboxylase subunit α (biotin carboxylase, AccA2)	Reduces stress and promotes root elongation
	acdA_2	Acyl-CoA dehydrogenase	Reduces stress and promotes root elongation
Colonization and Plant Interaction			
Motility genes	*flg* family		Flagellar assembly and movement toward roots
	fliA	Sigma factor 28 (σ^28)	Transcription of late flagellar/chemotaxis genes
	fliM	Motor switch protein (C-ring)	Controls flagellar rotation direction (CW/CCW)
Chemotaxis genes			Response to root exudates
	cheA,	Histidine kinase CheA	Autophosphorylates, transfers phosphate to CheY/CheB
	cheW	Coupling protein CheW	Connects MCP receptors to CheA in signaling complex
	cheR2	Methyltransferase CheR2	Methylates MCPs, tuning receptor sensitivity (adaptation)

Table 3 (continued)

Activity	Gene	Product	Function
Biofilm formation	*rkpK*	UDP-glucose 6-dehydrogenase	Extracellular polysaccharide synthesis- capsule (K-antigen) biosynthesis
Swarming motility protein	*swgA*	Membrane-associated MATE family transporter	Community behavior enhancing rhizosphere competitiveness
Stress Response and Adaptation			
Arylpolyene cluster (APE)	*ApeA*, *ApeB*, *ApeC/D*, etc.	Encodes a polyketide-like synthase system that produces arylpolyene pigments	Protection from oxidative stress, persistence in roots
NADPH production genes	*gdhI*	Glutamate dehydrogenase (GDH1)	Links nitrogen metabolism and TCA cycle; produces/consumes glutamate
	zwf_1	Glucose-6-phosphate dehydrogenase	First enzyme of oxidative PPP; generates NADPH and ribose precursors
sufS gene	*sufS*	Cysteine desulfurase (SufS)	Catalyzes removal of sulfur from L-cysteine

These genomic features suggest that '*Candidatus* P. auctus' JDE115 harbors a diverse repertoire of genes associated with nutrient acquisition, stress adaptation, and potential biocontrol-related functions. By competing for nutrients, suppressing pathogens, and promoting plant growth, JDE115 is predicted to contribute to both metabolic versatility and environmental adaptability, making it a strong candidate for applications in sustainable agriculture.

The strain '*Candidatus* P. auctus' JDE115 was selected for genome sequencing because of its remarkable plant growth-promoting and biocontrol properties. The draft genome sequence revealed genes associated with biocontrol activity, plant-microbe communication, rhizosphere colonization, and the biosynthesis of key metabolites such as siderophores, chitinase, extracellular serine protease, and hydrogen cyanide. In addition, annotation uncovered pathways related to nutrient assimilation, stress tolerance, and hormone regulation, highlighting its potential as a robust PGPR and biocontrol agent. These genomic insights deepen our understanding of plant-microbe interactions and supports the development of sustainable agricultural strategies through comparative studies with other beneficial microbes.

Discussion

The genome sequence of '*Candidatus* P. auctus' JDE115 predicts new insights into the evolutionary and functional diversity within the genus *Pseudomonas* and highlights mechanisms that may underlie its dual role as a plant growth promoter and biocontrol agent. Comparative analysis revealed both conserved PGPR traits and lineage-specific innovations that likely contribute to its ecological success in the soybean rhizosphere.

A central feature of the JDE115 genome is the expansion of secondary metabolite biosynthetic clusters, including cyclic lipopeptides [40–42], arylpolyenes [34, 35], and β-lactones. While siderophores [38, 76–79] and bacteriocins [39] are common across PGPR, these expanded clusters suggest evolutionary specialization for oxidative stress tolerance, root colonization, and suppression of fungal and nematode pathogens [12, 34, 42, 43, 80]. Such enrichment relative to close *Pseudomonas* relatives underscores the adaptive potential of JDE115 and highlights the value of comparative genomics in distinguishing lineage-specific strategies for rhizosphere competitiveness.

The presence of multiple nutrient acquisition and regulation systems further supports its functional versatility. Genes for phosphorus solubilization [46–50], sulfur assimilation [51–56], and zinc [58–61] and potassium transport [64, 65] illustrate broad metabolic adaptability. Together with siderophore-mediated iron uptake, these pathways position JDE115 as an efficient nutrient mobilizer, capable of enhancing host nutrition while simultaneously outcompeting soilborne pathogens.

Annotation of extracellular serine proteases [29–32, 44, 45], chitinases [92], and hydrogen cyanide [91] synthase strengthens the case for direct antagonism against plant pathogens and plant-parasitic nematodes. While functional validation will be necessary, the convergence of these traits across PGPR and nematicidal microbes points to shared ecological strategies that have been reinforced in JDE115.

From a comparative perspective, JDE115 represents a novel branch of plant-associated *Pseudomonas* with a unique combination of nutrient cycling, stress response, and antimicrobial gene clusters. Its genome provides a valuable reference for disentangling the evolutionary processes that shape beneficial versus pathogenic lifestyles in this genus. While this study is based on genome analysis, all functional interpretations are derived from predicted gene content. Experimental validation of metabolite production and enzymatic activity will be addressed in future studies. Nevertheless, comparative genomics provides a robust framework for identifying lineage-specific traits associated with plant-beneficial lifestyles.

Conclusions

This study extends the genomic landscape of PGPR by characterizing the soybean-associated bacterium *'Candidatus* P. auctus' JDE115. Through comparative analysis, we identify lineage-specific biosynthetic clusters and nutrient acquisition systems that likely support its persistence and biocontrol potential in the rhizosphere. These genomic traits position JDE115 as a promising candidate for future functional studies and comparative analyses aimed at sustainable agricultural applications. By integrating genomics with ecological and functional perspectives, our work contributes to a broader understanding of plant–microbe interactions and supports the development of genomically informed strategies for sustainable crop production.

Methods

Isolate

'*Candidatus* P. auctus' JDE115 was isolated from surface-sterilized soybean (*Glycine max*) root nodules collected at the Virginia Tech Kentland Farm (Blacksburg, VA, USA). The strain was cultured in LB lite broth and preserved in 20% glycerol at -80°C as described previously [1].

History of the genome project

This isolate was evaluated for its biological properties as a PGPR and biocontrol agent. It enhanced soybean growth and protected plants from soil-borne fungal pathogens, particularly *Agroathelia rolfsii* (Sacc.) Redhead & Mullineux. In addition, it suppressed soybean cyst nematode (*Heterodera glycine* Ichinohe, 1952) and indicated potential root colonization, competitive ability, and effective nutrient utilization [107, 108]. Based on these attributes, the strain was selected for whole-genome sequencing, and a high-quality draft genome has been deposited in GenBank. A summary of the organism's characteristics is presented in Table 2. The selection of strain JDE115 for genome sequencing was based on its demonstrated plant growth-promoting and biocontrol activity, which has been experimentally characterized and is reported in separate studies [107, 108].

Growth conditions and DNA preparation

Strain JDE115 was grown in LB lite broth at 28 °C with shaking at 200 rpm until mid-log phase (OD ≈ 0.6). Genomic DNA was extracted using the DNeasy® UltraClean® Microbial Kit (Qiagen®, USA), quantified with NanoDrop® spectrophotometer and Qubit® fluorometer, and assessed for purity by agarose gel electrophoresis, following previously described protocols [1].

PCR run, purification, and Sanger sequencing

PCR amplification of *'Candidatus* P. auctus' JDE115 genomic DNA was performed using primers 27F/1492R. Amplicons were purified and sequenced by the Sanger method following previously described protocols [1].

De novo sequence assembly and annotation

Genomic DNA of '*Candidatus* P. auctus' JDE115 was sequenced on the Illumina® NovaSeq PE150 platform (paired-end, 150 bp), generating 312.6× coverage. The 312.6× value reflects raw sequencing depth calculated from the total bases generated, whereas the 45× coverage reported in Table S2 corresponds to effective assembly coverage derived from the final curated contigs after read trimming and quality filtering. De novo assembly was performed with Flye v2.9 using a genome size estimate of 6.2 Mbp [96–98]. Assembly completeness was evaluated with Gepard dot plots, and genome visualization was carried out with CGView [99]. Genome annotation was performed with Prokka v1.14 [100], which applied Prodigal for gene prediction [101]. A supplemental assembly generated with SPAdes v.3.15.5 [102] confirmed dataset completeness, as described previously [1].

Sequence data

The sequence data is available from GenBank accession number PRJNA1196930.

Bioinformatic tools

De novo assembly of *'Candidatus* P. auctus' JDE115 was performed using Flye v2.9 and validated with SPAdes v3.15.5. Assembly quality was assessed with Gepard and CGView. Genome annotation was performed using Prokka v1.14, which employed Prodigal v2.6.3 for gene prediction. Functional assignments were obtained from multiple databases, including KEGG, COG, Pfam, Swiss-Prot, GO, CAZy, TCDB, and CARD, using DIAMOND [103]. Functional assignments were obtained from multiple databases, including KEGG, COG, Pfam, Swiss-Prot, GO, CAZy, TCDB, and CARD, using DIAMOND [103]. For metabolic pathway reconstruction, we primarily relied on COG annotations, as this database predicts functional categories and EC numbers directly linked to metabolic processes. Other databases were used to complement gene functional characterization, but COG served as the reference framework for presenting pathway-specific gene sets (e.g., phosphate, sulfate, zinc, siderophore, auxin, and urea metabolism) (Table S8-S21). Secondary metabolite gene clusters were identified with antiSMASH [104].

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s12864-026-12632-y.

Supplementary Material 1.
Supplementary Material 2.
Supplementary Material 3.
Supplementary Material 4.
Supplementary Material 5.
Supplementary Material 6.
Supplementary Material 7.
Supplementary Material 8.
Supplementary Material 9.
Supplementary Material 10.
Supplementary Material 11.
Supplementary Material 12.
Supplementary Material 13.
Supplementary Material 14.
Supplementary Material 15.
Supplementary Material 16.
Supplementary Material 17.
Supplementary Material 18.
Supplementary Material 19.
Supplementary Material 20.
Supplementary Material 21.
Supplementary Material 22.
Supplementary Material 23.
Supplementary Material 24.
Supplementary Material 25.
Supplementary Material 26.
Supplementary Material 27.
Supplementary Material 28.
Supplementary Material 29.
Supplementary Material 30.
Supplementary Material 31.

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Authors' contributions
MSA and JDE conceptualization; MSA, SLR, and DCH methodology; MSA, FTZM and JDE investigation, data curation, formal analysis, visualization, and writing original draft preparing, reviewing & editing; JDE, SLR, MRE, and DCH supervision. All authors contributed to editing, reading, and approving the final manuscript.

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Data availability
The draft genome sequence of *'Candidatus* Pseudomonas auctus' JDE115 has been deposited in GenBank. Raw sequencing reads are available in the NCBI Sequence Read Archive (SRA) under accession numbers PRJNA1196930. Genome annotation files and supplementary datasets generated and analyzed during this study are available in the supplementary materials provided with this article. Additional data supporting the findings of this study are available from the corresponding author upon reasonable request.

Declarations

Ethics approval and consent to participate
Not applicable.

Consent for publication
Not applicable.

Competing interests
The authors declare no competing interests.

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