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A *Cladosporium* strain 550W1 isolated from Lushan Russet Potato confers plant growth-promoting activity

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Abstract

Plant growth-promoting microorganisms (PGPMs) represent valuable biological resources for sustainable agriculture, and the discovery and functional characterization of new PGPM strains are therefore highly desirable. In this study, fungal strain 550W1 was isolated from tubers of Lushan Russet potato. Phenotypic assays confirmed that 550W1 promotes the growth of diverse plant hosts, including potato, *Arabidopsis thaliana*, soybean and the model legume *Medicago truncatula*. Our results suggested that 550W1 promoting plant growth may through biosynthesis and secretion of the phytohormones IAA, GA and CTK, and release of growth-regulating volatile organic compounds (VOCs). Strain 550W1 possesses remarkable halotolerance and broad pH adaptability ranging from pH 4.0 to 11.0. Morphological observation and ITS rDNA phylogenetic analysis preliminarily assigned it to *Cladosporium* sp., closely related to *C. halotolerans*. We performed hybrid whole-genome sequencing integrating Illumina short reads and Nanopore long reads. The estimated genome size of 550W1 is 31.27 Mb, while final assembly totals 28.49 Mb with 97.8% BUSCO completeness, indicative of high assembly quality. Genomic annotation identified biosynthetic gene clusters for phytohormone synthesis, NRPS clusters for siderophore production, and abundant stress-resistance genes. Multilocus sequence analyses (MLSA) of six markers produced result consistent with single-locus ITS phylogeny, by contrast, phylogenomic analysis and average nucleotide identity (ANI) calculations revealed that 550W1 clusters more

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closely with *C. endophyticum*. Given this incongruence, we designate this isolate *Cladosporium* sp. 550W1. Collectively, our findings demonstrate that *Cladosporium* sp. 550W1 functions as a novel PGPM strain to boost host plant performance.

Keywords:

Cladosporium sp. 550W1; PGPMs; Phytohormone; VOCs

1. Introduction

Plant–microbe interactions are ubiquitous in nature, plants employ sophisticated and precise mechanisms to distinguish beneficial symbionts from pathogenic invaders, and activate interconnected yet distinct signaling networks to trigger symbiotic or immune responses (Tan et al., 2025; Wang et al., 2025). Plant growth-promoting microorganisms (PGPMs) comprise a group of beneficial microbes that interact with plants to enhance growth and stress resilience via multifaceted mechanisms (Ge and Wang, 2025; Liu et al., 2025). PGPMs promote plant growth and enhance tolerance to abiotic stresses and biotic stresses by producing phytohormones and secondary metabolites, improving nutrient acquisition, and modulating the structure of host-associated microbial (Ge and Wang, 2025; Wang, 2026). Given the growing demand for eco-friendly and sustainable agricultural practices, the exploration, isolation, and functional characterization of novel PGPMs will provide effective biological tools to reduce chemical inputs, enhance crop productivity, and support the transition toward green, low-carbon, and sustainable agricultural systems, therefor are becoming more and more attractive.

Our previous work revealed correlation between endophytic communities and tuber quality in Lushan Russet Potato (Liao et al., 2025). In the present study, we isolated fungal strain 550W1 from Lushan Russet Potato, which showed prominent growth-promoting activity, and our data indicate that it is a novel PGPM strain.

2. Materials and Methods

2.1. Strain 550W1 isolation

Fresh and intact tubers of Lushan Russet Potato were harvested from an experimental field at the Lushan Botanical Garden on Lushan Mountain at an altitude of approximately 1100 m(Liao et al., 2025), and transported to the laboratory. Then

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were thoroughly surface sterilized, under aseptic conditions, potato tubers were cut into small tissue fragments and spread onto multiple types of solid culture media. All plates were incubated at 28 °C for 3–7 d to recover fungal isolates.

Strain 550W1 was primarily isolated from Murashige and Skoog (MS) medium. The pure strain 550W1 was deposited at the China General Microbiological Culture Collection Center with accession number CGMCC No. 41943 for long-term storage.

2.2. Molecular identification of 550W1

Fresh mycelia of strain 550W1 were harvested to extract genomic DNA using a fungal genomic DNA extraction kit (Bioer Technology, Hangzhou, China). The internal transcribed spacer (ITS) region of ribosomal DNA was amplified with primer pair ITS1 (5′-GGTCATTTAGAGGAAGTAA-3′) (Gardes and Bruns, 1993) and ITS4 (5′-TCCTCCGCTTATTGATATGC -3′)(White et al., 1990). Purified PCR amplicons were Sanger-sequenced by Sangon Biotech (Shanghai, China). The acquired ITS sequence of strain 550W1 was analyzed via the BLASTn tool hosted by the National Genomics Data Center(Members and Partners, 2026) (CNCB-NGDC, https://ngdc.cncb.ac.cn/blast/blastn). Genomic sequences of 18 publicly available *Cladosporium* strains were downloaded from NCBI (Supplementary Table1)(Zheng et al., 2025), and their ITS sequences were extracted for phylogenetic tree reconstruction with the ITS sequence of strain 550W1 using MEGA 7 software.

2.3. Colonial growth on different media

Five solid media were prepared: Potato Dextrose Agar (PDA), malt extract agar (MEA), Sabouraud dextrose agar (SDA), Czapek Dox agar (CDA) and MS medium. A uniform 5 mm mycelial plug punched from 7-d-old pure culture of strain 550W1 was placed at the center of each plate. All plates were incubated at 28 °C in darkness for 7 d, and colony growth status of strain 550W1 on different media was compared visually.

2.4. Morphological characterization of 550W1

Strain 550W1 was cultured on PDA at 28 °C under continuous darkness for 7 d. Colony traits including shape, color, texture, aerial mycelium, exudate and soluble pigment were documented. For microscopic observation, mycelial fragments from 7-d-old cultures were mounted on clean glass slides. Hyphae and conidia were visualized under an Olympus BX53 biological microscope (Olympus, Tokyo, Japan) equipped, conidial size and morphology were measured and imaged.

2.5. Physiological adaptability assays of 550W1

pH tolerance assay: PDA media were adjusted to pH gradients of 4.0, 5.0, 6.0,

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7.0, 8.0, 9.0, 10.0 and 11.0. Mycelial plugs (5 mm in diameter) were placed onto plates with different pH gradients and incubated at 28 °C in the dark for 7 d to assess pH adaptability.

NaCl salt tolerance assay: PDA media were supplemented with NaCl to establish concentration gradients of 0, 2.0, 2.5, 3.0, 3.5 and 4.0 mol L^{-1}. Identical mycelial plugs (5 mm in diameter) were inoculated and incubated at 28 °C in darkness for 7 d to observe growth under salt stress.

2.6. Liquid growth curve measurement

Five mm mycelial plugs were inoculated into 100 mL potato dextrose broth (PDB) in 250 mL Erlenmeyer flasks. Cultivation was performed at 28 °C with shaking at 200 rpm under dark conditions. Mycelial samples were harvested at 0, 1, 2, 4, 6 and 8 d post-inoculation. Collected mycelia were oven-dried at 60 °C to constant weight, the dry biomass was weighed to construct a growth curve.

2.7. Draft Genome Sequencing and annotation of 550W1

Draft genome sequencing of strain 550W1 was completed by Benagen Technology Co., Ltd. (Wuhan, China). A hybrid sequencing strategy combining the Illumina NovaSeq 6000 high-throughput sequencing platform and the Oxford Nanopore PromethION nanopore sequencing platform was applied. After quality filtering of raw sequencing reads, the Illumina library produced 5,795,056,430 bp from 38,766,484 reads (Supplementary Table2), and the Oxford Nanopore library generated 8,593,112,957 bp from 695,499 reads (Supplementary Table3). Jellyfish (version 2.2.10) was first used to calculate the k-mer frequency and depth distribution, GenomeScope (version 1.0) was employed to estimate the genome size of strain 550W1 based on the k-mer frequency–depth profile.

The initial genome assembly was performed using NECAT (available at https://github.com/xiaochuanle/NECAT) with Oxford Nanopore long reads. Next, two rounds of error correction on the primary assembly were carried out using ONT long reads via Racon (version 1.4.11). Finally, Pilon (version 1.23) with Illumina short reads was adopted to conduct two additional rounds of polishing to further correct the assembly after ONT-based error fixing.

To facilitate gene prediction, RNA extraction and RNA sequencing (RNA-seq) were carried out simultaneously on the Illumina NovaSeq 6000 platform, and the obtained transcriptomic data were integrated with genomic sequence data for

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subsequent gene prediction and annotation of the genome.

The raw sequence data reported in this paper, including both genomic sequencing reads and RNA-seq reads, have been deposited in the Genome Sequence Archive(Zhang et al., 2025) in CNCB-NGDC (Members and Partners, 2026) (GSA: CRA044266) that are publicly accessible at https://ngdc.cncb.ac.cn/gsa. Additionally, the draft genome sequence data reported in this paper have been deposited in the Genome Warehouse of CNCB-NGDC (Ma et al., 2025), under accession number GWHJYBU00000000.1 that will publicly accessible at https://ngdc.cncb.ac.cn/gwh.

2.8. Phylogenomic and multilocus sequence analyses (MLSA)

The 18 publicly available *Cladosporium* genome assemblies described above were used as closely-related references, and *Cercospora berteroae* CBS 538 was selected as the out-group taxon. MLSA was performed using the ITS sequence together with five protein-coding markers including *tef1*, *actin*, *tub2*, *gapdh* and *rpb2* from dataset comprising 20 taxa. Sequences of five protein-coding markers were extracted from corresponding genome assemblies by local BLAST searches against reference primer sequences (Supplementary Table8)(Berbee et al., 1999; Carbone and Kohn, 1999; Glass and Donaldson, 1995; Liu et al., 1999) , and introns were removed from these sequences. Sequences were concatenated in the order ITS-*tef1*-*actin*-*tub2*-*gapdh*-*rpb2*, yielding a final alignment matrix of 20 taxa × 2 909 bp. Pairwise sequence identity calculated from the concatenated matrix was used to generate the six-locus similarity heatmap.

The ML phylogenetic tree was inferred by IQ-TREE v3.1.3 with the -m MFP+MERGE mod Subsequently, phylogenomic comparative analyses were performed. fastANI v1.34 was used for all-against-all pairwise comparisons across the 19 genomes (excluding the outgroup) to generate a pairwise average nucleotide identity (ANI) matrix, which was used as the input for the genome-wide similarity heatmap. Mash v2.3 (k-mer size = 21, sketch size = 200 000) was employed for rapid pairwise distance calculation, and Mash distances were further calibrated against fastANI results to infer corresponding ANI values. A genome-wide ML phylogenomic tree was reconstructed using IQ-TREE v3.1.3 based on BUSCO-derived single-copy orthologous proteins (20 taxa, 405 944 amino-acid residues, 629 partitions).

2.9. Plant materials and cultivation conditions

Potato:

Lushan Russet Potato plantlets were cultured in 330 mL tissue culture bottles containing 50 mL of 1/2 MS medium under a 12 h light/12 h dark photoperiod, with a

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daytime temperature of 19 °C and a nighttime temperature of 13 °C. One week after subculture, each bottle was inoculated with approximately 100 fungal spores, while the control group was maintained without spore inoculation. Morphological changes of plantlets were photographed and observed after one month of culture.

***Arabidopsis thaliana*:**

Arabidopsis thaliana seeds were surface-sterilized. Briefly, seeds were treated with 75% (v/v) ethanol for 30 s, followed by immersion in 20% Kao bleach solution for 8 min with continuous shaking at room temperature. After disinfection, the seeds were rinsed five times with sterile distilled water to remove residual disinfectant. The sterilized seeds were germinated on solid MS medium, and uniform seedlings were transplanted into pots at 7 days after germination. All plants were cultivated in a growth room at 23 °C/19°C under a 16 h light/8 h dark photoperiod, watered with tap water twice each week. At 7 d post-transplanting, each pot was treated with 3 mL of 7-day PDB liquid culture of strain 550W1, control pots received an equal volume of sterile blank PDB. For phenotypic evaluation, the maximum rosette leaf length and leaf chlorophyll SPAD value were determined using a SPAD-502 PLUS chlorophyll meter (Konica Minolta, Japan).

For Volatile organic compounds (VOCs) split-plate assay. 7days Arabidopsis seedlings were transplanted onto one side of bipartite Petri dishes filled with MS medium, and a 5 mm 7-d-old mycelial plug of strain 550W1 was placed on the opposite side with PDA medium. Plates were sealed tightly with Parafilm and vertically incubated for 2 weeks under standard Arabidopsis growth conditions. Seedling morphology was observed and photographed to assess VOCs-mediated growth promotion.

Soybean:

Soybean (*Glycine max* L.) cultivar Huachun 6 seeds were sown on May 22, 2026, in the experimental field at the Poyang Lake Branch of Lushan Botanical Garden (Jiujiang, China). On June 5, 2026, inoculation with liquid-cultured 550W1 strain was carried out as described in the above section, plants grown under identical conditions without inoculation were set as blank controls. Plant sampling and phenotypic photography were conducted on July 11, 2026.

***Medicago truncatula*:**

M. truncatula A17 and *Sinorhizobium meliloti* ABS7 were used for inoculation assays according to previously study (Yang et al., 2023). Twelve hours after rhizobial

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inoculation, seedlings were supplemented with the spore suspension of strain 550W1. For spore preparation, strain 550W1 was cultured on solid PDA medium for six days, fungal spores were gently scraped from the medium surface using a sterile cell scraper and resuspended in sterile double-distilled water to a final concentration of 2×10^6 spores/mL, and 3 mL of the standardized suspension was applied to each pot. Seedlings inoculated solely with ABS7 were set as the control group. All plants were cultivated in an artificial climate chamber (Kesheng, Ningbo, China) with standardized conditions: 24 °C/20 °C day/night temperature, 15,000 lux light intensity, 12 h light/12 h dark photoperiod, and 60%–70% relative humidity. Plants were regularly irrigated with sterile water to maintain stable substrate moisture. Phenotypic and physiological evaluations were conducted at 21 days post-inoculation.

2.10. Nutrient mineralization assays

Commercial potassium-solubilizing and phosphorus-solubilizing agar media were purchased from Coolaber Technology (Beijing, China). Calcium-solubilizing medium was prepared by adding 2% calcium carbonate powder to PDA. A 5 mm 7-d-old mycelial plug was inoculated onto each medium and incubated at 28 °C for 7 d. Clear halo formation around colonies was recorded as positive mineralization activity.

2.11. Quantification of phytohormones

Strain 550W1 was cultured in PDB at 28 °C, 200 rpm under darkness. Culture supernatants were collected at 3 and 6 d post-inoculation. Concentrations of IAA, GA and CTK were quantified using commercial ELISA kits (Enzyme Exemption Industry, Jiangsu, China). Absorbance values were detected with a Bio-Rad microplate reader.

3. Results

3.1. Strain 550W1 belongs to the genus *Cladosporium* and exhibits prominent tolerance to a wide range of pH and high salinity

Strain 550W1 exhibited robust vegetative growth on a variety of culture media, including MS, PDA, MEA, SDA, and CDA. Among these tested media, PDA supported the most vigorous colony growth (Supplementary Fig. S1). This phenotypic observation demonstrated that strain 550W1 possesses high nutritional tolerance to variations in nitrogen and complex nutritional conditions. Accordingly, PDA medium was selected as the primary culture medium for subsequent cultivation and experimental manipulation in this study.

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On PDA medium, 550W1 forms nearly circular colonies with a dark green, velvety surface and dense aerial mycelium (Fig. 1A). To determine the taxonomic position of 550W1, its ITS rDNA sequence was amplified and sequenced. A BLASTn search was performed revealed that strain 550W1 was closely related to the genus *Cladosporium*. A phylogenetic tree based on the ITS sequences of strain 550W1 and the reference strains (Supplementary Table1)(Zheng et al., 2025) revealed that strain 550W1 formed a well-supported clade with reference strains of *C. halotolerans* and *C. endophyticum*, most closely with *C. halotolerans* (Fig. 1B). Further, light microscopy and scanning electron microscopy observations show septate hyphae, and spherical to subspherical conidia approximately 4μm wide and 4–8μm long, the conidial surface is verrucose, representing typical morphological traits of the genus *Cladosporium* (Fig. 1C-D, Supplementary Fig. S2)(Bensch et al., 2018).

Most remarkably, 550W1 showed active growth and sustained viability on PDA media supplemented with up to 2 M NaCl, growth was only completely inhibited when the NaCl concentration reached 4 M (Supplementary Fig. S3). This salt-tolerant phenotype is consistent with the known halotolerance of *C. halotolerans*, consistent with the close phylogenetic affinity shown by ITS analysis. Further 550W1 exhibited exceptionally wide pH adaptability, displaying robust and normal growth across a broad pH spectrum ranging from 4.0 to 11.0 (Supplementary Fig. S4). This broad tolerance indicates its strong capacity to thrive in both acidic and alkaline environmental conditions. The growth curve of 550W1 based on mycelial dry weight revealed that the strain entered the rapid logarithmic growth phase within the first 2 days, with biomass increasing steadily thereafter reached its maximum peak at approximately day 6 of incubation (Supplementary Fig. S5).

3.2 Strain 550W1 promotes growth of multiple plant species mainly through phytohormone secretion

Compared with uninoculated control (CK) plantlets, 550W1-inoculated potato plantlets showed significantly more vigorous growth, thicker stems, and darker green leaves, indicating a strong growth-stimulating capacity (Fig. 1E). Similarly, *Arabidopsis thaliana* plants inoculated with 550W1 exhibited significant growth

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promotion (Fig. 1F), with remarkable increases in maximum rosette leaf length and leaf SPAD values compared with the control group, reflecting enhanced vegetative growth and higher chlorophyll content (Supplementary Fig. S6). Growth-promoting effects of 550W1 were also observed in economically important crop species soybean (*Glycine max*), compared with uninoculated control plants, 550W1 inoculation plants notably improved plant biomass, and promoted overall growth performance (Supplementary Fig. S7). These results demonstrate that strain 550W1 exerts growth-promoting activity across diverse plant species.

To further evaluate the effect of 550W1 on growth-promoting and the symbiotic nitrogen fixation between legumes and rhizobia, we conducted co-inoculation experiments using the model legume plants *M. truncatula* A17. Plants were inoculated with *S. meliloti* strain ABS7 alone (CK) or co-inoculated with 550W1 at 12 hours post ABS7 inoculation (550W1). Phenotypic observation showed that 550W1 group plants exhibited vigorous growth than those in the CK group (Fig.1G). Stereomicroscopic observation revealed that 550W1 obviously increased the size of root nodules (Fig. 1H). Consistent with these morphological improvements, quantitative assays confirmed that 550W1 treatment substantially elevated key parameters including nodule size, plant fresh weight, and shoot fresh weight (Fig. 1I). Collectively, these results indicate that strain 550W1 may promote the symbiosis between *M. truncatula* and ABS7.

550W1 showed no detectible phosphate-solubilizing, potassium-solubilizing, or calcium-solubilizing activities (Fig. 1J), suggesting that its growth-promoting effect maybe not achieved by directly improving host nutrient availability. Instead, ELISA assays demonstrated that 550W1 synthesizes and secretes multiple plant hormones such as IAA, GA, and CTK in liquid culture (Fig. 1K). The concentrations of these phytohormones displayed dynamic changes over culture time (3 days and 6 days), IAA levels gradually decreased, whereas GA and CTK concentrations progressively increased (Fig. 1K). A divided-plate assay showed that VOCs emitted by strain 550W1 promoted *Arabidopsis thaliana* growth, with seedlings forming larger leaves and more adventitious roots (Supplementary Fig. S8). Taken together, 550W1 promotes plant growth may through phytohormone secretion, VOCs emission, and other potential

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growth-promoting metabolites.

3.3 Genomic sequencing and characterization of strain 550W1

To further explore the molecular basis underlying the plant growth-promoting effects of strain 550W1, the genome of strain 550W1 was sequenced using Illumina and Nanopore technologies. The estimated genome size was 31.27 Mb, and the final assembly was 28.49 Mb (Fig. 1L and Supplementary Table4). BUSCO analysis confirmed 97.8% completeness, indicating high assembly quality (Supplementary Table5). After integration and filtering, a total of 7,593 non-redundant protein-coding genes were predicted with an average CDS length of 1,503 bp and 2.39 exons per gene (Supplementary Table6). Furthermore, housekeeping genes (*tef1*, *actin*, *tub2*, *gapdh*, *rpb2*) were extracted from genomic sequences based on their corresponding primer-binding sites (Supplementary Table8), then multilocus sequence analysis (MLSA) was performed against publicly available genomes of *Cladosporium* species. Consistent with the results of the single-locus ITS phylogenetic analysis, strain 550W1 formed a well-supported monophyletic clade with reference strains of *C. halotolerans* and *C. endophyticum*, and was most closely related to *C. halotolerans* (Supplementary Fig. S9). However, the phylogenomic tree based on genome-wide information exhibited some topological discrepancies compared with the trees derived from house-keeping gene markers (Supplementary Fig. S10). Specifically, strain 550W1 clustered more closely with *C. endophyticum*, which was also supported by the average nucleotide identity (ANI) analysis results (Supplementary Fig. S11 and Supplementary Table9). Unfortunately, high-quality genome data from authentic ex-type strains were not accessible, preventing definitive species assignment. Accordingly, we designate this isolate as *Cladosporium* sp. 550W1 in the present study.

Gene annotation combined with GO and KEGG enrichment analyses identified a series of key candidate genes related to the biosynthesis of IAA, GA, and CTK (Supplementary Fig. S14 and Supplementary Table11). For IAA biosynthesis, genes encoding critical enzymes in the indole-3-pyruvate pathway and tryptamine pathway were annotated, including aromatic amino acid aminotransferase, YUC family flavin-dependent monooxygenase, and pyridoxal-dependent decarboxylase. For GA

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biosynthesis, multiple homologs of cytochrome P450 monooxygenases were detected. For CTK production, isopentenyl-transferase genes, which govern the rate-limiting step of CTK synthesis, were identified (Supplementary Fig. S14 and Supplementary Table11). These genomic features strongly support the ability of 550W1 to synthesize and secrete multiple plant growth-regulating hormones, which may form the core genetic basis of its growth-promoting activity. Furthermore, a variety of genes related to osmotic stress, oxidative stress tolerance, and secondary metabolism were identified, including non-ribosomal peptide synthetase (NRPS) genes involved in siderophore biosynthesis and key antioxidant genes such as superoxide dismutase (SOD) and catalase (CAT) (Supplementary Table11). The presence of these stress-related genes implies that 550W1 carries a complete genetic repertoire to enhance host fitness under adverse environments. Collectively, these genomic insights provide a solid foundation for understanding the multifunctional benefits of 550W1 to host plants, though further experimental validation is still required to fully characterize these stress-responsive pathways.

4. Discussion

In this study, a strain of *Cladosporium* sp. 550W1 was isolated from Lushan Russet Potato and was demonstrated have plant growth promotion for multiple plant species. The growth-promotion effects of 550W1 may involves multiple pathways, although this strain lacks traits that directly enhance nutrient availability, phytohormonal stimulation appears to be its primary mode of action, at early stages elevated level of IAA may promote root development and establishment, and later accumulation of GA and CTK may support shoot growth and tuberization(Qu et al., 2024). Strain 550W1 possesses considerable stress tolerance, genomic detection of NRPS, SOD, and CAT coding genes may imply its potential capacity to enhance plant tolerance against abiotic stresses. Siderophores could improve iron nutrition under limiting conditions and indirectly suppress pathogens by iron competition, while antioxidant enzymes could alleviate oxidative damage in stressed plants(Gu et al., 2020; Sun et al., 2017). Although direct in planta evidence for these stress-alleviating functions remains to be established experimentally, the genomic potential provides a valuable resource for further

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exploration of 550W1–plant interactions. Another notable feature of strain 550W1 is its likely broad host range, which is advantageous for developing widely applicable microbial inoculants. The robustness of 550W1 under extreme conditions (pH, salinity) further enhances its potential for field applications, particularly in saline or marginal soils where conventional agriculture faces challenges. Moreover, the isolation of this beneficial fungus from a local potato cultivar may highlights the value of exploring local crop varieties as reservoirs of beneficial microbes for modern agriculture.

CRediT authorship contribution statement

Libing Liao: Conceptualization, Data curation, Resources, Writing – original draft. **Yihong Hu:** Data curation, Formal analysis, Investigation, Visualization, Writing – original draft. **Yuhua Lu:** Data curation, Formal analysis, Investigation, Methodology, Validation, Visualization. **Nan Wu:** Investigation, Validation. **Shifeng Liu:** Funding acquisition, Project administration. **Min Zhong:** Project administration, Validation. **Deshui Yu:** Conceptualization, Funding acquisition, Project administration, Resources, Supervision, Writing – original draft, Writing – review & editing.

Declaration of competing interest

The authors declare that they have no conflict of interest.

Acknowledgments

We sincerely thank Professor Huairong Pan (Hunan University) for providing seeds of *Medicago truncatula* A17 and rhizobial strain ABS7, and Professor Rongxin Yang (Nanchang University) for supplying soybean cultivar Huachun 6. We appreciate Dr. Zhongke Sun (Henan University of Technology), Dr. Jianwei Guo (Kunming University), and Dr. Xinzhan Liu (Institute of Microbiology, Chinese Academy of Sciences) for their insightful advice and discussions regarding the taxonomy of strain 550W1. This work was supported by the National Natural Science Foundation of China (32160075 and 32560759) and National Key R&D Program of China (2024YFF1307405).

Figure legends

Fig. 1. Multifunctional plant growth-promoting characteristics of 550W1 isolated from Lushan Russet potato. (**A)** Colony morphology of strain 550W1 cultured on PDA

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medium for 7 days, showing dark green velvety aerial mycelium, bar=2 cm. (**B)** Maximum-likelihood phylogenetic tree constructed based on ITS rDNA sequences, illustrating the taxonomic placement of 550W1 within the genus *Cladosporium*. (**C)** and **(D)** Scanning electron micrographs of strain 550W1. H, Hyphae and spore at ×300 magnification, bar=100 μm; I, Morphology of individual spores at ×10 000 magnification, bar=2 μm. (**E)** Growth phenotype of potato plantlets cultured in vitro with or without 550W1 inoculation, bar=2 cm. (**F)** Pot-cultivated *A. thaliana* seedlings under control and 550W1 treatment to verify the growth-promoting activity of 550W1, bar=2 cm. (**G)** Root and shoot morphology of model legume *M. truncatula* A17 co-inoculated with rhizobium ABS7 (CK) versus ABS7+550W1, bar=3 cm. (**H)** Stereomicrograph of root nodules formed on *M. truncatula* A17 roots in CK and 550W1 co-inoculation groups, showing enlarged nodules upon 550W1 treatment, bar=500μm. (**I)** Quantifying symbiosis-related physiological indicators of *M. truncatula* A17, including nodule number, nodule length, nodule diameter, plant fresh weight and shoot fresh weight. Statistical significance was determined using Student's *t*-test (** $P < 0.01$, n=16). (**J)** Mineral-solubilizing capacity assay of strain 550W1 on three types of mineral media. From left to right: potassium-solubilizing medium, phosphate-solubilizing medium, and calcium-solubilizing medium. No obvious transparent dissolution halos were observed surrounding fungal colonies on all three culture plates, indicating that strain 550W1 lacks phosphate, potassium and calcium mineralization abilities. Bar=2 cm. (**K)** ELISA quantification of secreted IAA, GA and CTK from strain 550W1 cultured in PDB at 3 and 6 days. Blank PDB exhibited faint background signals, which were much lower than the those of the culture supernatants (data not shown). (**L)** Circular genome overview of 550W1. This circular plot visualizes the multi-dimensional genomic features of 550W1. The theoretical predicted genome size of this strain is 31.27 Mb, and the final assembled contig sequence length reaches 28.49 Mb. Tracks are arranged sequentially from the outermost ring to the innermost ring as follows: Outermost ring: Genomic coordinate scale in base pairs (bp); Second ring: Unique colored segments corresponding to each of the 20 assembled contigs with individual contig IDs labeled; Third ring: Gene density calculated within non-

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overlapping 50-kb sliding windows; Fourth ring: Genome-wide repeat sequence density based on 50-kb windows; Innermost ring: GC content distribution computed across 50-kbp sliding windows.

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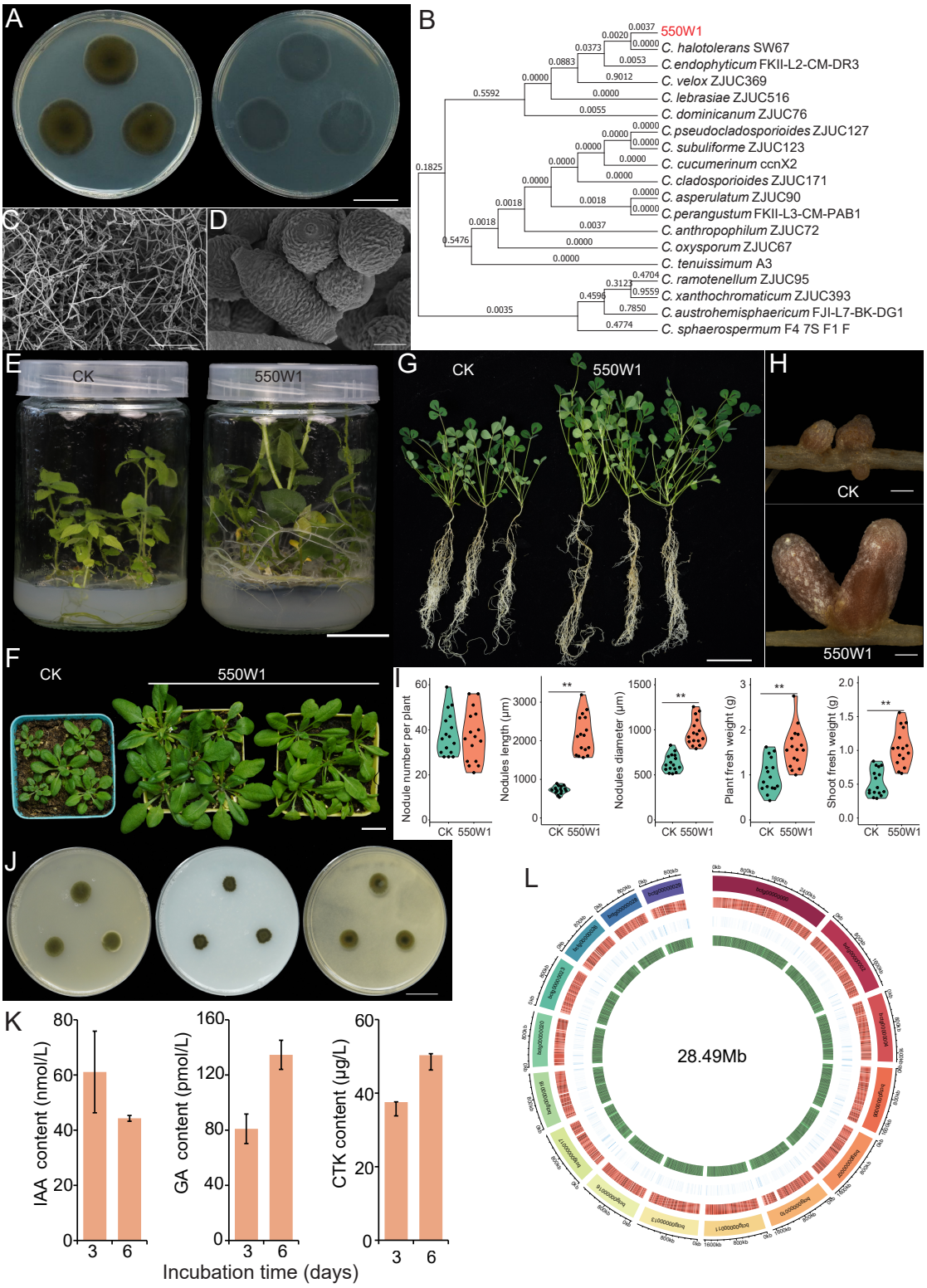
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A
B
550W1
C. halotolerans SW67
C. endophyticum FKII-L2-CM-DR3
C. velox ZJUC369
C. lebrasiae ZJUC516
C. dominicanum ZJUC76
C. pseudocladosporioides ZJUC127
C. subuliforme ZJUC123
C. cucumerinum ccnX2
C. cladosporioides ZJUC171
C. asperulatum ZJUC90
C. perangustum FKII-L3-CM-PAB1
C. anthropophilum ZJUC72
C. oxysporum ZJUC67
C. tenuissimum A3
C. ramotenellum ZJUC95
C. xanthochromaticum ZJUC393
C. austrohemisphaericum FJI-L7-BK-DG1
C. sphaerospermum F4 7S F1 F
C
D
E
CK
550W1
G
CK
550W1
H
CK
550W1
F
CK
550W1
I
Nodule number per plant
Nodules length (μm)
Nodules diameter (μm)
Plant fresh weight (g)
Shoot fresh weight (g)
CK 550W1
J
K
IAA content (nmol/L)
GA content (pmol/L)
CTK content (μg/L)
Incubation time (days)
L
28.49Mb