

Article

Occurrence of *Streptomyces stelliscabiei* Causing Potato Common Scab in China and Resistance Evaluation of Potato Germplasm Resources

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Simple Summary

Potato scab is a soil-borne disease that seriously affects potato quality and market value. However, the diversity of pathogens and resistance resources for this disease in major potato-producing areas of China remains unclear. This study collected infected potato tubers from Heilongjiang Province, isolated and identified the pathogen, and discovered two pathogenic *Streptomyces* species, one of which was discovered for the first time in the country. Further, the study evaluated the disease resistance of 132 potato resources from both domestic and international sources, finding that the vast majority of materials were susceptible, with only a few showing high resistance. This study is the first to identify a new pathogen of potato scab in the country, reveal the diversity of pathogenic genes, and screen out valuable resistance resources, providing important evidence for understanding the epidemic patterns of this disease and breeding resistant varieties.

Abstract

Potato common scab is a widespread soil-borne disease that severely reduces tuber quality and market value. However, the diversity of common scab pathogens and the availability of resistance resources in major potato-producing regions of China remain poorly understood. In this study, potato common scab pathogens were isolated from diseased tubers collected in Heilongjiang Province, China, and identified based on morphological characteristics, 16S rRNA gene sequencing, and pathogenicity-related gene detection. Two pathogenic *Streptomyces* species, *Streptomyces scabiei* and *Streptomyces stelliscabiei*, were identified. Notably, *S. stelliscabiei* was identified in potato common scab samples collected in Heilongjiang Province for the first time, suggesting that it may represent an emerging causal agent of potato common scab in China. Molecular analysis revealed two pathogenicity-related gene profiles among the isolates—namely, *txtAB*⁺/*tomA*⁺/*nec1*⁺ and *txtAB*[−]/*tomA*⁺/*nec1*⁺—indicating diversity in virulence-associated gene composition. Resistance to potato common scab caused by *S. stelliscabiei* was further evaluated in 132 potato germplasm accessions, including domestic and introduced materials, local landraces, and widely cultivated cultivars. Significant variation in resistance levels was observed. Only two accessions were classified as highly resistant, six as resistant, and eighteen as moderately resistant, whereas the majority of accessions were susceptible or highly susceptible. Overall, this study provides the first evidence of *S. stelliscabiei* causing potato common scab in China, reveals pathogenicity-related gene diversity among common scab pathogens, and identifies valuable resistance resources



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for potato breeding. These findings contribute to a better understanding of potato common scab epidemiology and support the development of resistant cultivars.

Keywords: potato common scab; *Streptomyces stelliscabiei*; germplasm resistance; pathogenicity-related genes; pathogen diversity

1. Introduction

Potato (*Solanum tuberosum* L.) is one of the most important food crops worldwide and plays a crucial role in global food security. Potato common scab is a widespread soil-borne disease that primarily affects tubers, leading to superficial, raised, or pitted lesions that significantly reduce tuber quality and market value. Although common scab rarely causes substantial yield loss, its negative impact on tuber appearance severely restricts fresh-market and processing potato production, making it a persistent concern in potato-growing regions worldwide [1]. Potato common scab is caused by several pathogenic *Streptomyces* species, among which *Streptomyces scabiei* is the most frequently reported and widely distributed pathogen [2]. In recent years, additional pathogenic species, including *S. stelliscabiei*, *S. acidiscabies*, and *S. turgidiscabies*, have been increasingly identified in different geographic regions, highlighting the growing complexity of the pathogen population associated with this disease [3,4]. The emergence and spread of diverse pathogenic *Streptomyces* species pose challenges for disease diagnosis, epidemiological studies, and effective disease management strategies, particularly in regions where pathogen composition has not been systematically investigated.

The pathogenicity of common scab-causing *Streptomyces* species is closely associated with the production of thaxtomin phytotoxins, a group of nitrated dipeptides that inhibit cellulose synthesis and interfere with normal cell wall formation during tuber development, ultimately leading to the characteristic scab lesions on potato tubers [5,6]. Thaxtomin A, the major virulence determinant, disrupts the assembly of cellulose microfibrils in expanding plant cells, triggering abnormal cell division and tissue hypertrophy at infection sites [7]. Genes involved in thaxtomin biosynthesis are clustered within conserved pathogenicity islands on the *Streptomyces* chromosome [8]. These pathogenicity islands represent horizontally acquired genomic regions that integrate secondary metabolism, virulence regulation, and host interaction functions, playing a central role in the evolution of plant pathogenicity in *Streptomyces* species. It should be noted, however, that the pathogenicity island (PAI) can be genetically unstable and may undergo deletions, rearrangements, or gene loss events, resulting in variation in virulence gene composition among pathogenic isolates. Therefore, the absence of certain auxiliary genes (e.g., *tomA*) does not necessarily exclude pathogenic potential. Among these genes, the *txtAB* gene cluster encodes a nonribosomal peptide synthetase complex essential for thaxtomin biosynthesis and is widely regarded as a reliable molecular marker for pathogenic *Streptomyces* isolates [9]. In addition to *txtAB*, several auxiliary virulence-related genes located within or adjacent to the pathogenicity island contribute to disease development. The *nec1* gene has been shown to induce necrogenic responses in host tissues and is highly conserved among pathogenic *Streptomyces* species, whereas *tomA*, encoding a tomatinase, facilitates detoxification of host defense compounds and enhances host colonization efficiency [10–12]. Variations in the presence or absence of these virulence-associated genes among isolates reflect differences in pathogenic potential and may influence host specificity and disease severity. Therefore, molecular detection of pathogenicity-related genes such as *txtAB*, *nec1*, and *tomA* has become a widely accepted

and effective approach for distinguishing pathogenic and non-pathogenic *Streptomyces* isolates and for assessing virulence diversity within common scab pathogen populations.

Currently, management of potato common scab relies on integrated strategies, including crop rotation, soil pH adjustment, irrigation management, and the use of disease-free seed tubers. However, these measures often provide inconsistent or limited control under field conditions [1,3,4]. Breeding and deployment of resistant cultivars remain the most effective and sustainable approach for long-term disease management [1,13]. The success of resistance breeding depends largely on the availability of reliable resistance sources and accurate evaluation systems based on locally prevalent pathogen populations. China is one of the world's leading potato-producing countries, and Heilongjiang Province represents a major potato production area in northeastern China [14]. Despite the economic importance of potato common scab in this region, comprehensive studies integrating pathogen isolation, molecular identification, pathogenicity-related gene characterization, and large-scale resistance evaluation of potato germplasm resources remain limited. In particular, information on the diversity of common scab pathogens and the resistance performance of domestic and introduced potato germplasm under inoculation with local pathogen populations is still lacking.

In this study, potato common scab pathogens were isolated from major potato-producing regions in Heilongjiang Province and identified using morphological characteristics and 16S rRNA gene sequence analysis. Two pathogenic *Streptomyces* species, *S. scabiei* and *S. stelliscabiei*, were identified, with *S. stelliscabiei* being reported for the first time in China. Furthermore, pathogenicity-related gene detection revealed two distinct gene profile combinations (*txtAB*⁺/*tomA*⁺/*nec1*⁺ and *txtAB*[−]/*tomA*⁺/*nec1*⁺) among the isolates. Based on inoculation with a local *S. stelliscabiei* strain, resistance to potato common scab was systematically evaluated in 132 potato germplasm accessions, including domestic and introduced materials, local landraces, and widely cultivated commercial cultivars. The results provide valuable insights into pathogen diversity, pathogenicity-related gene variation, and resistance distribution in potato germplasm, offering an important foundation for resistance breeding and sustainable management of potato common scab.

2. Materials and Methods

2.1. Collection of Potato Common Scab Samples

During the potato harvest period in 2023–2024, a total of 71 tubers with scab disease were collected from major potato-producing regions in Heilongjiang Province, China, including Harbin, Qiqihar, Mudanjiang, and Suihua. All the diseased tubers were of the main potato variety, Eugene. Field surveys were conducted to investigate the incidence and severity of potato common scab, and disease symptoms on naturally infected tubers were recorded under field conditions following standard plant disease survey procedures [1]. Tubers with representative scab lesions were selected and transported to the laboratory for subsequent pathogen isolation and identification, as commonly applied in studies of potato common scab caused by pathogenic *Streptomyces* spp. [3,15].

To ensure the accuracy and reliability of downstream pathogen isolation and identification, strict measures were implemented throughout sample collection, transportation, and temporary storage. Potato samples collected from different regions and sampling sites were handled independently, and direct or indirect contact between samples was strictly avoided to prevent cross-contamination among pathogens from different origins, as recommended for soil- and tuber-borne actinomycete pathogens [3]. All samples were stored under appropriate conditions prior to pathogen isolation.

2.2. Isolation and Purification of Pathogenic Bacteria

Potato tubers with common scab symptoms were thoroughly rinsed under slowly running tap water to remove adhering soil particles. The washed tubers were placed on sterile filter paper and air-dried naturally under dark conditions. Tissue blocks were excised from the margin between diseased lesions and adjacent healthy tissue, which is considered optimal for isolating pathogenic *Streptomyces* spp. [3,15]. The tuber surface was first disinfected with 75% (*v/v*) ethanol for 30 s. Using a sterile scalpel, uniform tissue blocks (approximately 1 cm² in area and 0.5 cm in thickness) were precisely excised. During the operation, all components except the tuber periderm should be removed as thoroughly as possible.

The excised tissue blocks were further surface-sterilized in 1% (*v/v*) sodium hypochlorite (NaClO) solution for 30 s, rinsed three times with sterile distilled water, and then placed onto 1.8% water agar medium (agar 18 g, distilled water 1 L). Plates were incubated at 28 °C for 5–7 days to allow the emergence of actinomycete colonies, following standard procedures for isolating potato common scab pathogens. After incubation, individual colonies with morphological characteristics typical of *Streptomyces* spp. were selected and transferred onto oatmeal agar (OA) medium (oatmeal 40 g, agar 35 g, distilled water 2 L), which was sterilized at 121 °C for 30 min. Pure cultures were obtained by repeated streaking on OA medium for three successive rounds, as recommended for the purification of filamentous actinomycetes.

For long-term preservation, purified *Streptomyces* isolates were cultured on OA medium for 8–10 days. Spores were gently washed from the agar surface using sterile distilled water and transferred into centrifuge tubes. The spore suspensions were centrifuged at 8000× *g* for 15 min at 4 °C, and the supernatant was discarded. The spore pellets were resuspended in sterile 20% (*v/v*) glycerol solution to obtain spore suspensions, which were stored at −20 °C for subsequent analyses.

2.3. Molecular Identification of Potato Common Scab Pathogens

Genomic DNA of *Streptomyces* isolates was extracted using a bacterial genomic DNA extraction kit (Tiangen Biotech., Beijing, China) according to the manufacturer's instructions. Molecular identification was performed by amplification of the 16S rRNA gene using universal *Streptomyces* primers. The forward primer PA (5'-TTTGATCCTGGCTCAG-3') and reverse primer PH (5'-AAGGAGGTGATCCAGCCGCA-3') were used to amplify an approximately 1535 bp fragment of the 16S rRNA gene, as originally described by Edwards et al. (1989) [16]. PCR amplification was conducted in a total reaction volume of 50 µL, containing 25 µL of 2× Phanta Max Master Mix, 2.0 µL of forward primer (10 µM), 2.0 µL of reverse primer (10 µM), an appropriate volume of template DNA, and sterile double-distilled water added to a final volume of 50 µL. The PCR program consisted of an initial denaturation at 95 °C for 3 min, followed by 40 cycles of denaturation at 95 °C for 30 s, annealing at 55 °C for 30 s, and extension at 72 °C for 30 s, with a final extension at 72 °C for 5 min. PCR products were held at 4 °C until further analysis. Amplified products were separated by electrophoresis on a 1.2% (*w/v*) agarose gel and visualized using a gel documentation system. PCR products of the expected size were purified and submitted for Sanger sequencing by a commercial sequencing service provider. After sequence quality trimming and manual correction, the obtained 16S rRNA gene sequences were compared against reference sequences in the NCBI database (accessed on 20 December 2025) using the BLASTn algorithm. Sequences of *Streptomyces* species showing high similarity to the isolates were selected as reference sequences for further analyses.

Multiple sequence alignment was performed using CLUSTAL X software (version 1.86, accessed on 20 December 2025) [17]. Phylogenetic analysis was conducted using MEGA 11

based on the neighbor-joining (NJ) method, with evolutionary distances calculated using the Kimura two-parameter model (accessed on 20 December 2025). The robustness of the phylogenetic tree was evaluated by bootstrap analysis with 1000 replicates [18].

2.4. Detection of Pathogenicity-Related Genes

Genomic DNA was extracted from purified *Streptomyces* isolates as described above. The presence of three pathogenicity-related genes, *txtAB*, *nec1*, and *tomA*, was detected by PCR amplification using gene-specific primers. These genes are known to be closely associated with the pathogenicity of potato common scab-causing *Streptomyces* species, including thaxtomin biosynthesis and virulence regulation. The *txtAB* gene cluster serves as a molecular marker gene for this group of pathogenic bacteria, whereas the *nec1* and *tomA* genes have been identified as functional genes associated with pathogenicity. *TomA* can suppress the defense response within the host plant, weakening its ability to respond to pathogen infection. *Nec1* encodes a protein that can induce necrosis in plant tissues. *TomA* and *nec1* are widely present in the pathogen causing scab disease, and they work together to enhance the pathogen's virulence during the infection process. They are not essential for pathogenicity, but they play a significant role in the virulence of the strain. [4,19]. The primer sequences, expected amplicon sizes, and references are listed in Table 1.

Table 1. Primer sequences used for detection of pathogenicity-related genes in *Streptomyces* isolates.

Target Gene	Primer Name	Primer Sequence (5'–3')	Fragment Size (bp)	Reference
<i>txtAB</i>	TxtAB1 TxtAB2	5'-CCACCAGGACCTGCTCTTC-3' 5'-TCGAGTGGACCTCACAGATG-3'	385	Wanner et al., 2006 [4]
<i>nec1</i>	Nf Nr	5'-ATGAGCGCGAACGGAAGCCCCGGA-3' 5'-GCAGGTCGTCACGAAGGATCG-3'	700	Bukhalid et al., 1998 [19]
<i>tomA</i>	Tom3 Tom4	5'-GAGGCGTTGGTGGAGTTCTA-3' 5'-TTGGGGTTGTACTCCTCGTC-3'	392	Wanner et al., 2006 [4]

PCR amplifications were carried out in a total reaction volume of 10 µL, containing 5 µL of 2× Taq PCR Mix, 3 µL of sterile double-distilled water, 0.5 µL each of forward and reverse primers, and 1 µL of genomic DNA template. The PCR amplification programs for *txtAB*, *nec1*, and *tomA* genes were performed according to previously published protocols with minor modifications [20]. The detailed thermal cycling conditions are summarized in Table 2. PCR products were separated by electrophoresis on 1.0% (*w/v*) agarose gels and visualized under ultraviolet light using a gel documentation system. The presence or absence of specific amplification bands corresponding to the expected fragment sizes was recorded photographically for subsequent analysis.

Table 2. PCR amplification conditions for pathogenicity-related genes.

Amplification Conditions	<i>txtAB</i>	<i>nec1</i>	<i>tomA</i>
Initial denaturation	94 °C 3 min	95 °C 3 min	95 °C 3 min
Denaturation	94 °C 30 s	95 °C 20 s	95 °C 20 s
Annealing	48 °C 30 s	60 °C 30 s	55 °C 30 s
Extension	72 °C 30 s	72 °C 2 min	72 °C 2 min
Final extension	72 °C 10 min	72 °C 10 min	72 °C 10 min
Number of cycles	30	40	40

2.5. Pathogenicity Identification

Representative test strains were selected and their pathogenicity was identified through pot re-inoculation method. The test strains were cultivated on oat medium for about 10 days, and the spores were washed off with sterile water and the concentration was adjusted to 1×10^7 CFU/mL. The susceptible variety Eugene was selected as the test material. When the seedlings were 15 to 20 days old, they were inoculated by root irrigation into flowerpots, with an inoculation volume of 150 mL per pot. A water control was set up, and each treatment was repeated three times. They were placed in a greenhouse for cultivation. After inoculation, a short-term dry period of 4 to 6 weeks was maintained. After maturity, the new tubers were harvested to detect the disease situation.

2.6. Evaluation of Resistance to Potato Common Scab

A total of 132 potato germplasm accessions provided by the National Potato Germplasm In Vitro Repository (Keshan, China) were subjected to resistance evaluation against potato common scab. Surface-sterilized potato tubers were planted in pots containing a sterilized substrate composed of perlite, vermiculite, peat, and sterile soil mixed at a ratio of 1:1:1:1 (*v/v/v/v*). Each germplasm accession was tested with 10 biological replicates. Following planting, uniform greenhouse pot management was implemented, with strict attention to indoor sanitation, as well as fluctuations in temperature and humidity.

The spores of *Streptomyces* grown on OMA medium for 7–10 days were washed with sterile water, centrifuged at $3000 \times g$ for 15 min, and the supernatant was discarded. A certain amount of the washed spores was taken for plate count to quantify the spore number of the pathogen. The spore suspension was then subjected to 10^1 , 10^2 ... 10^{10} -fold serial dilutions. Different dilutions of the spore suspension were spread on oat solid medium (20 μ L), and the total number of spores in the sample was calculated by plate count after 7 days based on the colony growth situation. When the seedlings were 15–20 days old, the spore suspension with a known total spore number was diluted to adjust the concentration to 1×10^7 CFU/mL. The spore suspension of *S. scabiei* with a concentration of 1×10^7 CFU/mL was inoculated into the roots of the tested resources by root drenching at 150 mL per pot. Disease symptoms were classified into five grades ranging from 0 to IV, as described in Table 3.

Table 3. Disease severity grading criteria for potato common scab.

Disease Grade	Symptom Description
0	Healthy tuber skin with no visible lesions
I	Tuber skin mostly healthy with 1–2 sporadic lesions
II	3–5 lesions present, covering approximately 1/4–1/3 of the tuber surface
III	5–10 lesions present, covering approximately 1/3–1/2 of the tuber surface
IV	Severely infected, with more than 10 lesions or lesion area exceeding 1/2 of the tuber surface

Based on the disease grades, a disease index (DI) was calculated using the following formula:

$$\text{Disease index (DI)} = \frac{\sum(n_i \times i)}{N \times i_{\max}} \times 100$$

where n_i represents the number of tubers in disease grade i , N is the total number of evaluated tubers, and $i_{\max}$ is the highest disease grade (IV).

According to the calculated disease index values, the resistance levels of different potato germplasm accessions were classified following the criteria shown in Table 4.

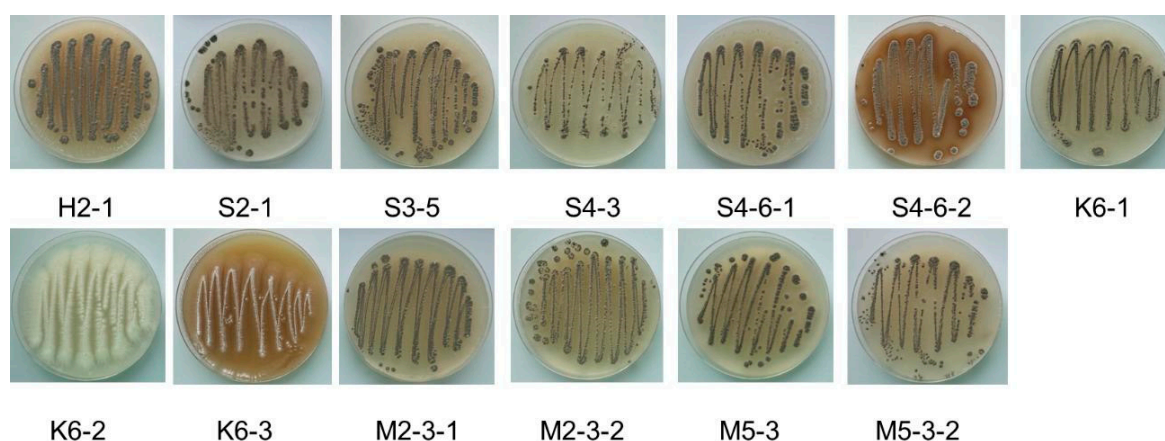
Table 4. Resistance evaluation criteria for potato common scab.

Resistance Level	Disease Index (DI)	Resistance Category
1	$DI < 10$	Highly resistant (HR)
2	$10 \leq DI < 30$	Resistant (R)
3	$30 \leq DI < 50$	Moderately resistant (MR)
4	$50 \leq DI < 70$	Susceptible (S)
5	$DI \geq 70$	Highly susceptible (HS)

3. Results

3.1. Isolation and Purification of Pathogenic Isolates

Actinomycete-like isolates were obtained from potato tuber lesions exhibiting common scab symptoms collected from Harbin, Qiqihar, Mudanjiang, and Suihua in Heilongjiang Province. A total of 13 actinomycete isolates were successfully isolated and purified. All 13 isolates developed radially growing mycelia on oatmeal agar (Figure 1). The isolates H2-1, S2-1, S3-5, S4-3, S4-6-1, S4-6-2, K6-1, M2-3-1, M2-3-2, M5-3, and M5-3-2 exhibited dark gray to blackish-gray aerial mycelia. Among them, isolate H2-1 produced a light brown diffusible pigment, whereas isolate S4-6-2 produced a rust-red pigment. In contrast, isolates K6-2 and K6-3 formed white aerial mycelia, with isolate K6-3 producing a brown pigment. These morphological characteristics are consistent with those commonly observed in *Streptomyces* species associated with potato common scab.

**Figure 1.** Colony morphology of actinomycete isolates obtained from potato common scab lesions on oatmeal agar.

3.2. Molecular Identification of Pathogenic Isolates

PCR amplification using primers PA and PH successfully amplified approximately 1500 bp 16S rRNA gene fragments from all 13 strains (Figure S1). The evolutionary history was inferred by using the Maximum Likelihood method based on the Tamura–Nei model. The tree with the highest log likelihood (−2704.55) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the Maximum Composite Likelihood (MCL) approach, and then selecting the topology with superior log likelihood value. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 0.0580)). The rate variation model allowed for some sites to be evolutionarily invariable ([+I], 60.73% sites). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 17 nucleotide sequences. All positions with less than 80% site coverage were eliminated.

That is, fewer than 20% alignment gaps, missing data, and ambiguous bases were allowed at any position. There were a total of 1382 positions in the final dataset. Evolutionary analyses were conducted in MEGA7 (Table S1). The corresponding sequences have been submitted to NCBI under accession number SUB15990706. Based on the alignment results, reference sequences with high similarity were selected to construct a phylogenetic tree (Figure 2). Phylogenetic analysis revealed that 10 of the 13 strains belonged to the genus *Streptomyces*, distributed across three species: 8 strains were *Streptomyces scabiei*, 1 was *Streptomyces ossamyceticus*, and 1 was *Streptomyces stelliscabiei*. Notably, this study represents the first detection of *S. stelliscabiei* in Chinese potato scab disease samples. Additionally, strain S3-5 showed the highest similarity to *Polaromonas jejuensis*, while K6-2 and K6-3 were most closely related to *Lentzea* sp. and *Amycolatopsis* sp., respectively. This indicates the presence of non-*Streptomyces* actinomycetes among the strains isolated from scab samples. The phylogenetic positions of these three non-*Streptomyces* strains are not depicted in Figure 2.

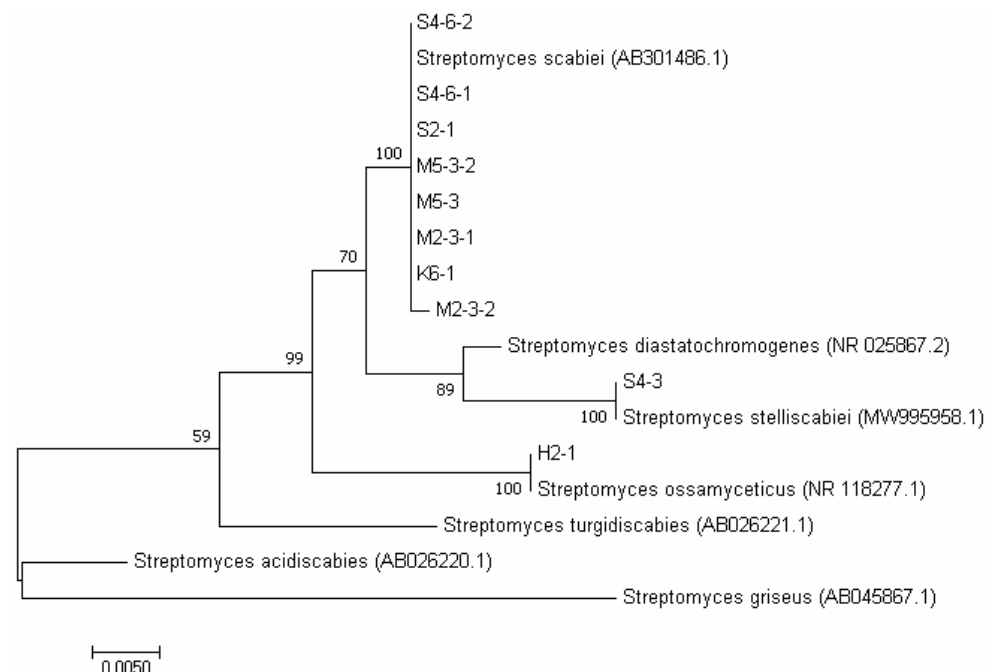


Figure 2. Phylogenetic relationships of actinomycete isolates from potato common scab lesions based on 16S rRNA gene sequences.

3.3. Detection of Pathogenicity-Related Genes

The thaxtomin biosynthetic gene cluster is located within two or three conserved pathogenicity islands on the chromosomes of common scab-causing *Streptomyces* species, in which *txtAB* serves as a molecular marker directly associated with pathogenicity, while *nec1* and *tomA* function as virulence-related regulatory genes. The isolated *Streptomyces* strains were subjected to PCR detection of three pathogenicity-related genes using specific primers. The results showed that isolate H2-1 did not harbor any of the three pathogenicity-related genes, indicating that *Streptomyces ossamyceticus* is likely a non-pathogenic *Streptomyces* species. Isolate M5-3-2 exhibited a pathogenicity gene profile of *txtAB*[−]/*tomA*⁺/*nec1*⁺, whereas isolates S2-1, S4-3, S4-6-1, S4-6-2, K6-1, M2-3-1, M2-3-2, and M5-3 all displayed a pathogenicity gene profile of *txtAB*⁺/*tomA*⁺/*nec1*⁺ (Figure 3).

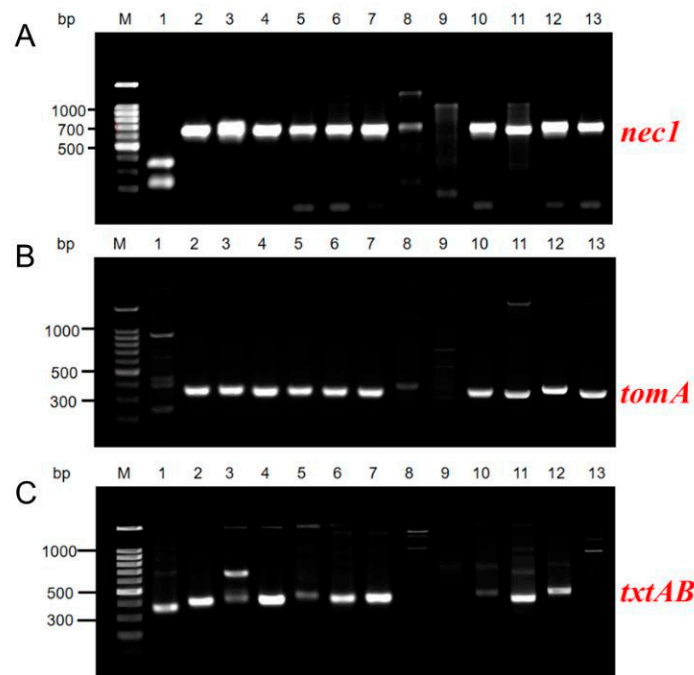


Figure 3. Detection of pathogenicity-related genes (*txtAB*, *nec1*, and *tomA*) in *Streptomyces* isolates associated with potato common scab. Agarose gel electrophoresis of PCR products for pathogenicity-related genes. M, DNA marker; lanes 1–13, H2-1, S2-1, S3-5, S4-3, S4-6-1, S4-6-2, K6-1, K6-2, K6-3, M2-3-1, M2-3-2, M5-3, and M5-3-2. (A) *nec1*; (B) *tomA*; (C) *txtAB*.

3.4. Pathogenicity Identification

The pathogenicity of the isolated *Streptomyces scabiei* and *Streptomyces stelliscabiei* was verified by pot re-inoculation. The results showed that both pathogens could cause brown scab-like lesions on potatoes, and the pathogenicity of *S. scabiei* was stronger than that of *S. stelliscabiei*. The control group had no abnormal symptoms. The pathogen was isolated, purified and identified from the diseased tubers after treatment. The sequencing results indicated that the isolated strains were consistent with the inoculated strains. The results were consistent in three repeated experiments, confirming that both were the pathogenic bacteria of potato scab disease, but there were interspecific differences in pathogenicity (Figure 4).

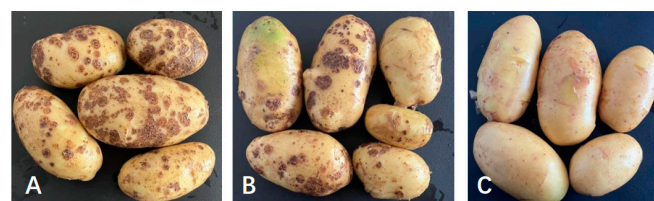


Figure 4. The occurrence of disease in potted plants after inoculation. (A) *Streptomyces scabiei*; (B) *Streptomyces stelliscabiei*; (C) Clean water control.

3.5. Evaluation of Resistance to Potato Common Scab Among Potato Germplasm Resources

The resistance of 132 potato germplasm accessions—including domestic and introduced materials, local landraces, and widely cultivated commercial cultivars—to potato common scab caused by *Streptomyces stelliscabiei* was evaluated based on disease incidence and disease index values (Table S2). According to the resistance classification criteria established in this study, the tested germplasm exhibited a wide range of responses to infection, indicating substantial variation in resistance levels among accessions of diverse genetic backgrounds.

Among the evaluated germplasm, two accessions, Ica Guantiva and 395046.66, were classified as highly resistant (HR), with disease index values of 8.33 and 8.82, respectively. Six accessions, including 395019.82, 395025.13, LBr-12, Multa, 395049.27, and 395049.90, were identified as resistant (R), with disease index values ranging from 15.91 to 25.00. In addition, eighteen accessions, such as 395023.63 and Norkota, were categorized as moderately resistant (MR), all exhibiting disease index values below 50. In contrast, eleven accessions were classified as susceptible (S), with disease index values between 50.00 and 69.23, whereas the majority of the germplasm (95 accessions) showed high susceptibility (HS), with disease index values equal to or greater than 70.00 (Figure 5).



Figure 5. Disease symptoms of potato common scab in representative potato germplasm accessions with different resistance levels. (A) Ica Guantiva (HR); (B) 395046.66 (HR); (C) LBr-12 (R); (D) Multa (R); (E) 395049.22 (MR); (F) CIP391930.1 (MR); (G) T9613-14 (S); (H) Shanghai local potato (HS).

4. Discussion

Potato common scab is a complex soil-borne disease caused by multiple pathogenic *Streptomyces* species, and its occurrence and severity are strongly influenced by pathogen composition, virulence characteristics, and host resistance. In this study, an integrated approach combining pathogen isolation, molecular identification, pathogenicity-related gene detection, and resistance evaluation of potato germplasm was employed to elucidate the pathogen diversity and resistance landscape of potato common scab in Heilongjiang Province, one of the major potato-producing regions in China.

Two pathogenic *Streptomyces* species, *Streptomyces scabiei* and *Streptomyces stelliscabiei*, were identified from potato common scab lesions collected across multiple regions in Heilongjiang Province. *S. scabiei* is widely recognized as the dominant causal agent of potato common scab worldwide and has been frequently reported in Europe, North America, and Asia [3,21]. In contrast, Ma Yue et al. reported in 2025 that 16 species of pathogenic bacteria causing potato scab have been discovered in China, including *Streptomyces scabies* and *Streptomyces turgidiscabies*, but *Streptomyces stelliscabiei* has not yet been detected [22]. *Streptomyces stelliscabiei* has been reported only sporadically in a limited number of countries and regions, including Japan and parts of Europe. Notably, *S. stelliscabiei* was detected for the first time in China in this study [14]. This finding expands the known geographic distribution of this pathogen and suggests that the pathogen population associated with potato common scab in China may be more diverse than previously recognized. The occurrence of *S. stelliscabiei* in Heilongjiang Province may be associated with long-term seed potato exchange, introduction of foreign germplasm, or adaptation of local *Streptomyces* populations under regional ecological conditions. The emergence of this pathogen underscores the necessity of continuous monitoring of common scab pathogen composition, particularly in major seed potato production areas [23].

The pathogenicity of common scab-causing *Streptomyces* species is primarily associated with the production of thaxtomin phytotoxins, which are encoded by genes located within conserved pathogenicity islands [24]. Consistent with previous studies, the *txtAB* gene was detected in all pathogenic isolates, confirming its role as a core molecular marker for pathogenic *Streptomyces* [9,12]. In contrast, variation was observed in the presence of the virulence-related genes *tomA* and *nec1*, resulting in two distinct pathogenicity gene combinations (*txtAB*⁺/*tomA*⁺/*nec1*⁺ and *txtAB*[−]/*tomA*⁺/*nec1*⁺). The coexistence of different pathogenicity gene profiles among isolates suggests heterogeneity in virulence regulation and potential differences in host–pathogen interactions. Previous studies have shown that *nec1* is involved in necrogenic activity, while *tomA* contributes to host colonization and virulence modulation [4,12]. The *txtAB* gene cluster serves as the primary molecular marker gene for this group of pathogenic bacteria, with additional pathogenic genes including *txtC*, *txtA*, and *txtR*. Notably, strains deficient in *txtAB* identified in this study were verified to harbor *txtC* and *txtA*. These findings highlight the importance of considering pathogenicity gene composition when evaluating pathogen aggressiveness and resistance responses.

Resistance evaluation of 132 potato germplasm accessions revealed substantial variation in response to potato common scab caused by *S. stelliscabiei*. The germplasm collection included domestic and introduced accessions, landraces, and widely cultivated commercial cultivars, providing a comprehensive representation of genetic diversity. However, only a small proportion of the evaluated germplasm exhibited high or moderate resistance, with two highly resistant, six resistant, and eighteen moderately resistant accessions identified. The predominance of susceptible and highly susceptible accessions indicates that effective resistance to potato common scab remains scarce in current potato germplasm, consistent with previous reports highlighting the limited availability of strong resistance source [13,25]. Moreover, the high susceptibility observed in several widely cultivated cultivars suggests that resistance to common scab has not been a primary selection target in many breeding programs, particularly in regions where the disease was previously considered secondary. Importantly, resistance evaluation in this study was conducted using inoculation with a local *S. stelliscabiei* isolate, providing a realistic assessment of resistance performance under regional pathogen pressure. This approach enhances the relevance of the identified resistant germplasm for local breeding and disease management and avoids potential mismatches between resistance sources and prevalent pathogen populations [26].

5. Conclusions

Breeding resistant cultivars is widely regarded as the most effective and environmentally sustainable strategy for controlling potato common scab [1]. The identification of resistant germplasm resources in this study provides valuable materials for resistance breeding and genetic studies. The highly resistant accessions, in particular, represent promising parental lines for resistance introgression and further investigation of resistance mechanisms. In addition, the combined analysis of pathogen diversity and resistance performance underscores the necessity of integrating pathogen surveillance into resistance breeding programs. The presence of multiple pathogenic *Streptomyces* species and variable pathogenicity gene profiles suggests that durable resistance may require broad-spectrum mechanisms effective against diverse pathogen populations. This study conducted resistance evaluation of resources against *Streptomyces scabiei*, a globally prevalent and highly pathogenic dominant strain. The resistance of the screened resistant resources to other scab-causing pathogens and to complex pathogen communities will be further validated in subsequent experiments, so as to further assess the broad-spectrum resistance of these resistant resources. Future studies integrating quantitative resistance analysis, multi-pathogen

inoculation, and genomic approaches will be critical for advancing potato common scab resistance breeding.

Supplementary Materials: The following supporting information can be downloaded at: <https://www.mdpi.com/article/10.3390/biology15040344/s1>, Table S1: Taxonomic identification of isolates based on 16S rRNA gene sequence analysis; Table S2: Evaluation of resistance to potato common scab in 132 potato germplasm accessions. Figure S1: PCR amplification of the 16S rRNA gene from actinomycete isolates associated with potato common scab.

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