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Article

Burkholderia gladioli Causing Brown Spot on Leaf Sheath of Sweet Corn (*Zea mays* L.) in Sinaloa, Mexico: An Emerging Disease

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Abstract

Brown spot on the leaf sheath is an emerging disease of sweet corn (*Zea mays* L.) in Sinaloa, Mexico, with an unknown etiology. This study aimed to identify the causal agent of the disease and assess its pathogenicity on commercial sweet corn hybrids. Bacterial strains were isolated from symptomatic leaf sheaths collected from commercial fields. Identification was performed through biochemical profiling (API 50CHB/E), pathogenicity tests on alternative hosts (potato, onion, celery), and molecular analysis (16S rRNA gene sequencing and phylogenetic reconstruction). Pathogenicity and virulence were confirmed by inoculating four sweet corn hybrids in a greenhouse. The strains were Gram-negative rods, identified as *Burkholderia gladioli* based on biochemical profiles and molecular data (99.8% 16S rRNA similarity; phylogenetic clustering within the *B. gladioli* clade). In greenhouse trials, the strains induced brown spot lesions on the leaf sheaths of all tested hybrids, replicating field symptoms fulfilling Koch's postulates. This is the first report of *B. gladioli* as the causal agent of brown spot on the leaf sheath of sweet corn in Mexico. The pathogen's broad host range highlights its potential as an emerging threat to horticultural crops in the region.

Keywords: *Burkholderia gladioli*; sweet corn; leaf sheath; brown spot; first report; Mexico; emerging disease; phytopathogen

1. Introduction

Sweet corn belongs to the Poaceae family and originated in the tropical environments of the American continent [1]. It is cultivated under diverse climatic conditions, and has a growth cycle of 75 to 90 days. Used exclusively for human consumption, whether fresh or processed, its genetic improvement has primarily focused on increasing sugar content. Sweet corn contains 5–6% sugar, 10–11% starch, 3% water-soluble polysaccharides, and moderate levels of protein, vitamins, and potassium [2]. It has been reported that cooking sweet corn ears at 115 °C for 25 minutes increases antioxidant levels by 44–54%, although vitamin C content is reduced by 25% [3]. Due to its nutritional value and health benefits [4], sweet corn is a crop of global importance, leading to a gradual expansion of its cultivation area in Sinaloa, Mexico. During the 2022–2023 growing season, 71,000 hectares were planted in this region [5]. However, the limited genetic diversity of sweet corn hybrids makes them susceptible to abiotic stresses, which in turn predisposes the crop to fungal diseases that

limit both yield and quality [6]. In dent corn, the most significant diseases are fungal. For example, stalk rot caused by *Fusarium temperatum* has been reported in Belgium [7]; the same species was associated with ear rot in sweet corn in the United States [8]. In Australia, Watson *et al.* [9] identified *F. verticillioides*, *F. proliferatum*, and *F. subglutinans* affecting stalks, peduncles, and kernels of sweet corn ears. Other fungi, such as *Rhizoctonia*, *Diplodia*, *Penicillium*, and *Aspergillus*, are implicated in seed rot and reduced germination. Additionally, *Colletotrichum graminicola* and *Diplodia* cause stalk and root rot in sweet corn, often leading to premature plant death, particularly toward the end of the growing cycle [6].

Although bacterial diseases are less frequently reported in sweet corn than in dent corn, notable cases do occur. These include leaf streak caused by *Xanthomonas vasicola* pv. *vasculorum* [10] and Stewart's wilt, caused by *Pantoea stewartii* subsp. *stewartii* (syn. *Erwinia stewartii*), which is considered one of the most significant bacterial diseases of sweet and dent corn in the United States [11]. *Pantoea ananatis* has been identified as the causal agent of leaf streak in maize in several countries, including Argentina [12], Ecuador [13], China [14], South Africa [15], Mexico [16], and Poland [17]. Furthermore, *Burkholderia gladioli* has been reported to cause stalk rot and leaf streak in dent corn in Mexico [18] and similar symptoms in Thailand [19]. This bacterium has also been associated with leaf streak in sweet corn in China [20] and causes panicle blight and grain rot in rice, symptoms similar to those induced by *B. glumae* [21].

Burkholderia was originally classified within the *Pseudomonas* genus; however, based on analyses of 16S rRNA sequences, DNA-DNA homology, fatty acid composition, and phenotypic characteristics, it was reclassified as a distinct genus [22]. *Burkholderia* is a bifunctional genus, as some species engage in mutualistic associations with plants, while others are pathogenic to economically important crops, animals, and humans.

Despite these reports, bacterial diseases in sweet corn have often been underestimated by farmers and field advisors in Sinaloa, Mexico. However, in recent growing seasons, a brown spot affecting the basal leaf sheath of sweet corn has been observed, and its etiology remains unknown. The symptoms appear after flowering. The initial symptoms consist of light brown spots with diffuse margins on the basal leaf sheath (Figure 1A). As the spots increased in size, they acquired an irregular, elongated shape, and turned dark brown with a slightly sunken appearance (Figure 1B). In more advanced stages, the lesions developed a straw-colored to whitish coloration with reddish margins (Figure 1C). In the field, no completely desiccated sheaths directly associated with the symptom, nor leaves affected as a consequence of sheath damage, were observed.

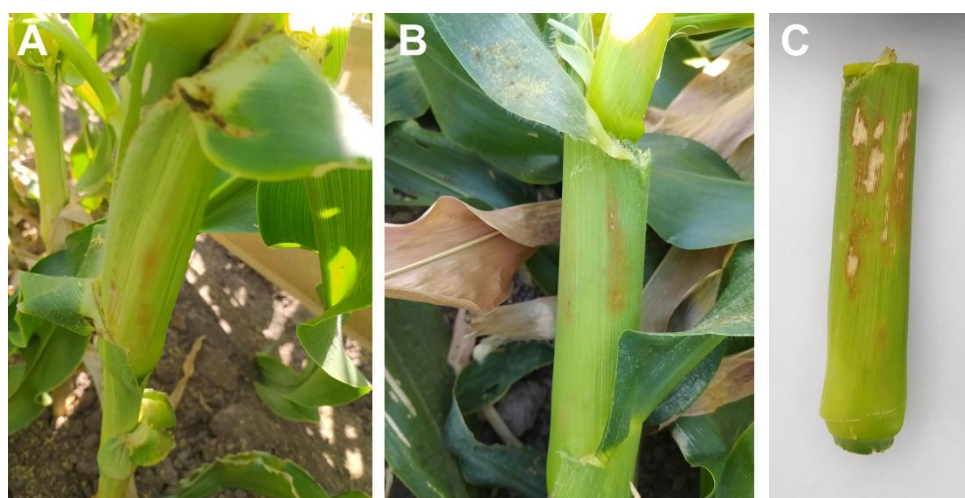


Figure 1. Symptoms of brown spot of leaf sheath in sweet corn observed during the 2022- 2023 growing season in commercial fields in Sinaloa, Mexico. **A)** Initial symptoms. **B)** Intermediate symptoms. **C)** Advanced symptoms depicting a lesion with a whitish center surrounded by a dark brown margin.

Preliminary studies indicate that an unidentified bacterium is consistently associated with these symptoms. Although the current damage does not appear to affect yield or quality, identifying the pathogen is fully justified, as it may represent an emerging disease linked to climate change and could become economically significant in the short or medium term. Given the interest from growers and field advisors in identifying the causal agent, and because this disease has not been previously reported in the region, the objectives of this study were to: a) identify the bacterial species associated with the disease using biochemical, physiological, and molecular techniques, and b) determine the pathogenicity of the bacteria in slices of potato, onion, and celery in the laboratory and in four sweet corn hybrids under greenhouse conditions.

2. Materials and Methods

2.1. Isolation of the Bacterium Associated with the Disease

Sweet corn plants exhibiting brown spot symptoms on the leaf sheath were sampled from commercial fields in the municipalities of Juan José Ríos and Ahome, Sinaloa, Mexico, during the 2023–2024 growing season. Disease incidence at harvest ranged from 30–35%, with 5–10% of the basal leaf sheath area affected per plant. No symptoms were observed on the stems beneath the symptomatic sheaths. Two composite samples, each consisting of three randomly selected symptomatic sheaths, were placed in an ice chest (10–12 °C), transported to the laboratory, and processed for bacterial isolation within 24 hours, following standard procedures [23].

2.2. Biochemical Identification

Bacterial strains were characterized biochemically and physiologically using Gram staining, the KOH string test, detection of diffusible pigments on Nutrient Agar (NA), oxidation/fermentation tests, catalase activity, growth in 5% NaCl, and growth at 40 °C, all performed as described by Schaad *et al.* [23]. Additionally, strains were tested using API 50 CHB/E medium strips (bioMérieux, Durham, NC, USA) according to the manufacturer's instructions. Briefly, a bacterial suspension was inoculated into each tube of the strip and incubated for 48 h at 30 °C. Fermentation of carbohydrates was indicated by a color change due to acid production and pH drop. The resulting biochemical profile was analyzed using the manufacturer's identification software, and the results were compared with previously published profiles for *B. gladioli* [24].

2.3. Hypersensitivity Reaction to Bacterial Strains on Tobacco

Colonies grown on NA for 48 h at 25 °C were suspended in sterile distilled water and adjusted to a concentration of 1×10^5 CFU mL⁻¹. Suspensions were infiltrated into the abaxial epidermis of tobacco leaves (*Nicotiana tabacum* cv. Xanthi) using a 3 mL syringe. Tissue necrosis observed 24–48 hours after infiltration was recorded as a positive hypersensitive reaction (HR) [23].

2.4. Molecular Characterization of the Bacterial Strains

2.4.1. DNA Extraction

Bacterial strains were incubated in nutrient broth at 25 °C for 24 hours on a Yamato orbital shaker (SOU-300, Monterrey, N.L, Mexico). The cultures were centrifuged at 13,000 rpm for 2 min, and the broth was decanted to collect the bacterial cells. Genomic DNA extraction was performed using the CTAB method, modified from Doyle [25]. A total of 600 µL of CTAB buffer solution (4% of 0.5 M EDTA, 10% Tris-HCl, 8% molecular-grade NaCl, 2% CTAB) and 6 µL of β-mercaptoethanol were added. The DNA was rehydrated with 30 µL of ultrapure water and stored at -20 °C. DNA quality and concentration were verified using a NanoDrop spectrophotometer.

2.4.2. PCR Amplification

A 1200-base pair fragment of the 16S ribosomal RNA gene (16S rRNA) was amplified using primers F2C (5'-AGA GTT TGA TCA TGG CTC-3') and C (5'-ACG GGC GGT GTG TAC-3') [26]. The amplification was carried out under the following conditions: an initial denaturation at 95 °C for 4 minutes, followed by 34 cycles of denaturation at 95 °C for 1 minute, annealing at 60 °C for 1 minute, and extension at 72 °C for 1.5 minutes, with a final extension at 72 °C for 5 minutes. PCR was performed in a TC1000-G thermocycler (DLAB Scientific, Monterrey, N.L., México) with a total reaction volume of 25 µL. Each reaction contained 2 µL of DNA (50 ng/µL), 1X reaction buffer, 1.5 mM MgCl₂, 0.2 mM dNTPs, 0.5 µM of each primer, and 0.25 U of Taq DNA polymerase.

2.4.3. Phylogenetic Analysis

Sequences were edited using BioEdit v.7.7.1 software [27] and compared using the NCBI's BlastN algorithm. The bacterial sequences were aligned with 41 reference sequences from *Burkholderia* type specimens [28] and one *Paraburkholderia acidisoli* (DHF22) sequence as an outgroup. Sequence alignment was performed using the MUSCLE algorithm integrated in MEGA v.12.0.10 [29]. The best-fit nucleotide substitution model was selected based on the corrected Akaike information criterion in MEGA. The phylogenetic tree was constructed using the Maximum Likelihood (ML) and the Bayesian Inference (BI) methods. The ML analysis was performed in RAxML v 7.2.8 [30] using the GTRGAMMAI model and 1000 bootstrap replicates. Mr. Bayes 3.2.7 [31] was used to estimate the IB phylogeny with the GTR + I + G model, two independent Metropolis-Markov-chains Monte Carlo runs, 1 million generations, sampling every 1,000 trees, and a burn-in of 20%. Final tree editing was performed in iTOL v6 [32].

2.5. Rotting of Potato, Onion, and Celery Slices

Potato tubers, onion bulbs, and celery petioles were surface-disinfected by immersion in 0.5% sodium hypochlorite for 5 min, rinsed with sterile distilled water, and aseptically cut into 0.8 cm thick slices. Slices were placed in Petri dishes on sterile moist filter paper to maintain 100% relative humidity (RH) at 25 °C. Each slice was wounded with a sterile scalpel and inoculated with a loopful of bacteria taken from 48 h NA cultures. Control slices were treated similarly, but only with sterile water. After 72 h incubation at 25 °C, symptoms were recorded. Bacteria were re-isolated from symptomatic tissues and compared biochemically with the original strains. The experiment was conducted twice.

2.6. Pathogenicity Tests of Strains Obtained from Symptomatic Leaf Sheaths

Sweet corn seeds of hybrids Accentuate, 8909MRW, 1760MR and BSS1075 (Syngenta Agro, S.A. de C.V., Ciudad de Mexico, Mexico) were disinfected with 1.5% NaClO, sown in plastic pots containing 5 kg of pasteurized clay/loam/sand mix (at the ratio of 28.1:27.0:44.9, pH 7.0), and fertilized regularly with Miracle Gro fertilizer (The Scotts Company LLC; Marysville, OH) and irrigated as needed. One-month-old plants were inoculated by applying 25 µL of bacterial suspension (1×10^5 CFU mL⁻¹) between the stem and the first basal leaf sheath. Control plants received sterile water. Plants were arranged in a completely randomized design with six replicates (six plants; one per pot) per strain and covered with transparent polyethylene bags for 48 h to maintain high RH (94–96%), followed by a 12 h daily high-RH period for five days, after which they remained uncovered for 7 days (RH 50–75%). Disease severity was assessed 14 days post-inoculation (dpi) as leaf sheath diseased area (LSDA; cm²) [33]. The experiment was run twice. Bacteria were re-isolated from symptomatic tissues to fulfill Koch's postulates and their identity was confirmed using biochemical and molecular techniques.

2.7. Statistical Analysis of Data

All statistical analyses were conducted in R Studio version 1.4.1106. Data from LSDA were tested for homogeneity of variances and normality using Levene’s and Shapiro-Wilk tests, respectively, in the *car* package. A Kruskal-Wallis [34] test ($\alpha = 0.05$) was performed to assess differences between the two experimental replications; since no differences were detected, the data from both experiments were pooled for subsequent analysis. Pairwise comparisons between control and infected plants for each maize hybrid were performed in the Wilcoxon signed-rank test ($\alpha = 0.05$). The effects of bacterial strain and sweet corn hybrid on LSDA were evaluated using a Kruskal-Wallis [34] test ($\alpha = 0.05$), followed by a Bonferroni correction of Fisher’s least significant difference (LSD) test, using the *agricolae* package. The box plots were created using the *ggplot2* package in R Studio.

3. Results

3.1. Incidence and Isolation

The incidence of the disease at harvest ranged from 40 to 50%, while lesion size varied from 2 to 4.5 cm in length by 0.5 to 1.5 cm in width across the different sweet corn hybrids. In total, 33 bacterial isolates were obtained from symptomatic sweet corn tissue collected from nine commercial sweet corn lots during the sampling period.

Using Gram staining and the KOH string test, rod-shaped, Gram-negative isolates were selected. Based on colony phenotypic characteristics, 23 isolates were grouped into nine morphotypes. In a preliminary pathogenicity study on the sweet corn hybrid Accentuate, morphotypes A and D harbored 3 and 4 pathogenic isolates, respectively. Subsequently, one isolate from each morphotype was used for further study.

Biochemical and Physiological Characteristics

Two strains, designated A and D, obtained from symptomatic leaf sheaths for detailed biochemical and physiological characterization, were included in this study. Both strains were Gram-negative rods, positive in the KOH string test, formed circular, cream-colored colonies with smooth to corrugated surfaces and undulate edges (Figure 2). They did not grow in 5% NaCl nutrient broth, produced yellow diffusible pigments on NA, and induced a hypersensitive response in tobacco (var. Xanthi). Both strains were catalase- and oxidase-negative but capable of growth at 40 °C.

In API 50CHB/E tests, strain A was negative for glycerol, erythritol, D-arabinose, L-xylose, D-adonitol, methyl β -D-xylopyranoside, L-sorbose, L-rhamnose, methyl α -D-mannopyranoside, methyl α -D-glucopyranoside, N-acetylglucosamine, arbutin, salicin, D-maltose, D-lactose, D-saccharose, inulin, D-melezitose, D-raffinose, starch, glycogen, D-turanose, D-lyxose, L-arabitol, D-tagatose, potassium gluconate, potassium 2-ketogluconate, and potassium 5-ketogluconate; and positive for L-arabinose, D-ribose, D-xylose, D-galactose, D-glucose, D-fructose, D-mannose, dulcitol, inositol, D-mannitol, D-sorbitol, amygdalin, aesculin ferric citrate, D-cellobiose, D-melibiose, D-trehalose, xylitol, gentiobiose, D-fucose, L-fucose, and D-arabitol. Strain D showed a similar profile to strain A but differed by being positive for glycerol, D-arabinose, D-adonitol, D-lyxose, and D-tagatose. These results closely matched those previously reported by Palleroni [24] for *B. gladioli* (Table 1).

Table 1. Phenotypic characterization of strains A and D using API®50 CH carbohydrates as compared to *Burkholderia gladioli*.

	Strain A	Strain D	<i>Burkholderia gladioli</i> (Palleroni, 2015)
Colony Characteristics			
Shape	Smooth	Wrinkled	ND*
Edges	Undulate	Undulate	ND

Elevation	Flat	Flat	ND
Color	Cream	Cream	ND
Surface	Smooth and shiny	Rough and shiny	ND
Morphological characteristics			
Shape	Rod	Rod	ND
Gram staining	-	-	-
KOH string test	+	+	ND
Physiological characteristics			
Growth in nutrient broth with 5% NaCl	-	-	ND
Diffusible pigments	+	+	+
Hypersensitivity reaction	+	+	ND
Catalasa	-	-	ND
Oxidase	-	-	d ⁺
Oxidative metabolism	+	+	+
Growth at 40 °C	+	+	+
Potato rot	-	-	ND
Purple Onion, white onion and celery rot	+	+	ND
Carbon sources:			
Glycerol	-	+	+
Erythritol	-	-	-
D-Arabinose	-	+	+
L-Arabinose	+	+	+
D-Ribose	+	+	+
D-Xylose	+	+	+
L-Xylose	-	-	ND
D-Adonitol	-	+	d ⁺
Methyl-βD-Xylopyranoside	-	-	ND
D-Galactose	+	+	+
D-Glucose	+	+	d ⁺
D-Fructose	+	+	+
D-Mannose	+	+	+
L-Sorbose	-	-	ND
L-Rhamnose	-	-	-
Dulcitol	+	+	+
Inositol	+	+	+
D-Mannitol	+	+	+
D-Sorbitol	+	+	+
Methyl -αD-Mannopyranoside	-	-	ND
Methyl-αD-Glucopyranoside	-	-	ND
N-AcetylGlucosamine	-	-	+
Amygdalin	+	+	-
Arbutin	-	-	-
Esculin ferric citrate	+	+	ND
Salicin	-	-	d ⁺
D-Celiobiose	+	+	d ⁺
D-Maltose	-	-	-
D-Lactose	-	-	-
D-Melibiose	+	+	-
D-Saccharose	-	-	-
D-Trehalose	+	+	+
Inulin	-	-	-

D-Melezitose	-	-	-
D-Raffinose	-	-	-
Starch	-	-	-
Glycogen	-	-	-
Xylitol	+	+	d ⁺
Gentibiose	+	-	-
D-Turanose	-	-	-
D-Lyxose	-	+	+
D-Tagatose	-	+	+
D-Fucose	+	+	+
L-Fucose	+	+	+
D-Arabitol	+	+	+
L-Arabitol	-	+	-
Potassium Gluconate	-	-	ND
Potassium 2-Ketogluconate	-	-	+
Potassium 5-Ketogluconate	-	-	+

* ND=Not determined. +, more than 90% of the strains gave a positive reaction; -, fewer than 10% of the strains gave a positive reaction; d⁺, between 10 and 90% of the strains gave a positive reaction and the type strain was positive; d⁻, between 10 and 90% of the strains gave a negative reaction and the type strain was negative. + positive for the 2 strains tested; negative for the 2 strains tested.

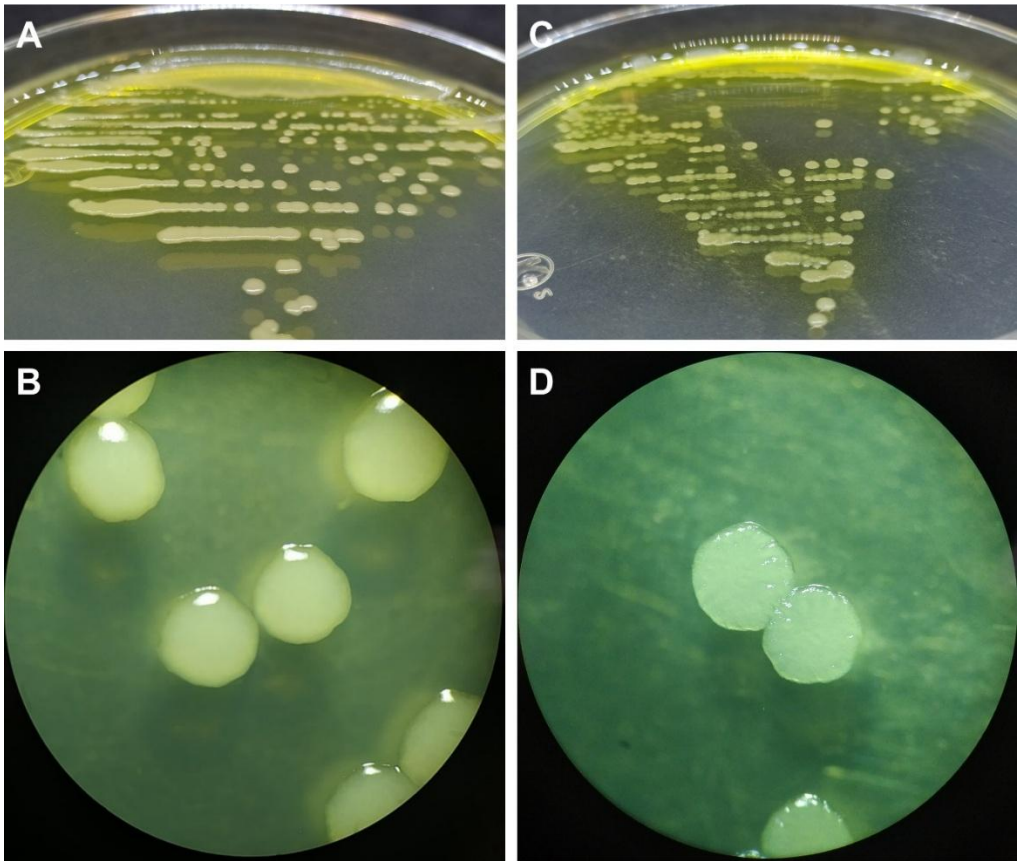


Figure 2. Colonies of *Burkholderia gladioli* of 72 h of age on NA. **A)** Strain A producing a yellow diffusing pigment in the medium. **B)** Shiny colonies, slightly corrugated and undulated margin of strain A under the stereomicroscope. **C)** Colonies of strain D producing yellow diffusing pigment in the medium. **D)** Colonies of strain D flat, corrugated with undulated margins under the stereomicroscope.

3.2. Pathogenicity Tests on Potato, Onion, And Celery

Both strains induced a slight soft rot in potato slices, characterized by darkening of the inoculated area. In contrast, more pronounced maceration was observed on slices of white onion, purple onion, and celery. Additionally, a diffusible yellow pigment was produced on all three host tissues following inoculation (Figure 3).

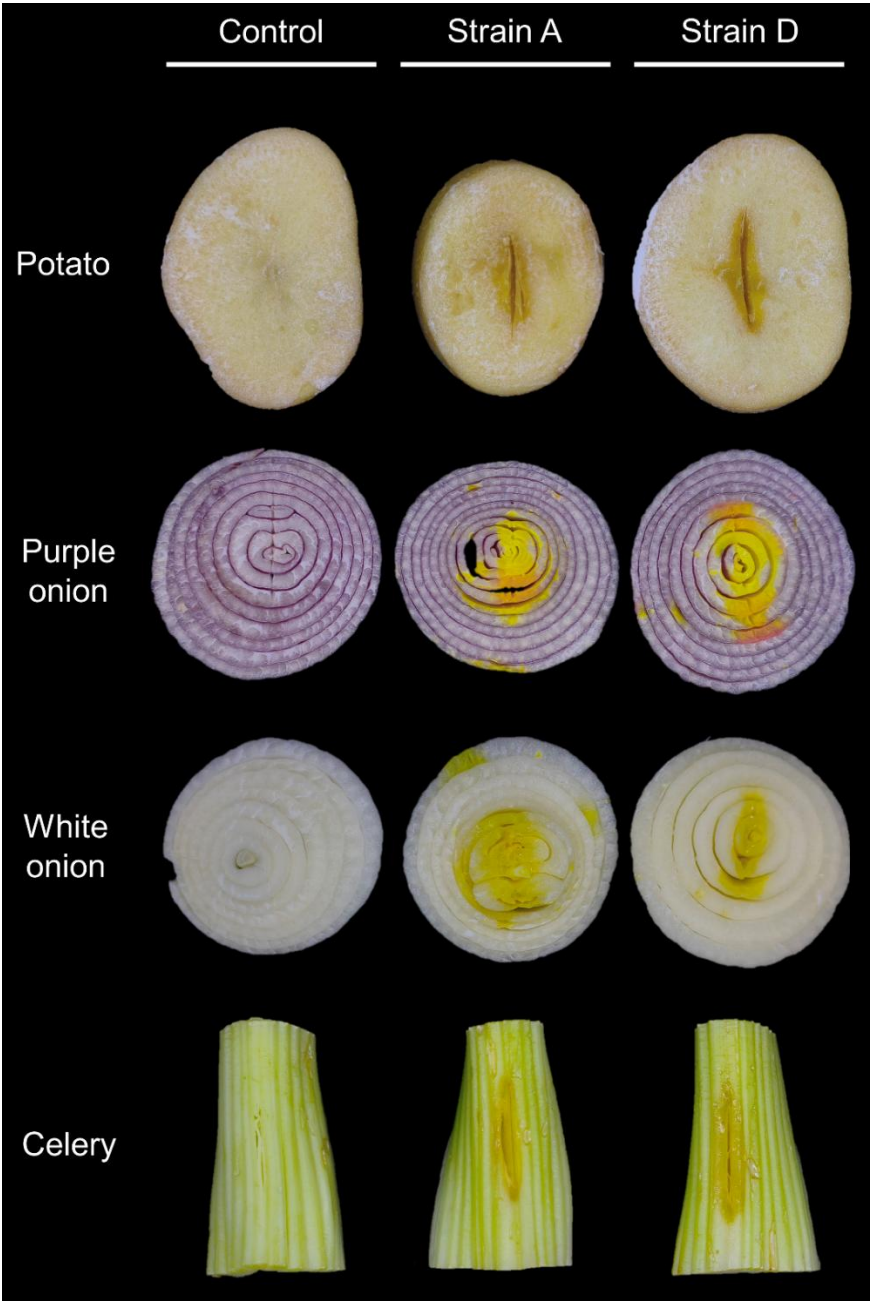


Figure 3. Soft rot in potato, purple onion, white onion, and celery slices 72 hr post-inoculation with strains A and D of *Burkholderia gladioli*.

3.2. Molecular Identification

Sequencing of the 16S rRNA gene revealed that both strains shared 99.8% similarity with reference sequences of *B. gladioli* (accessions CP002600 and KP306792). The sequences were deposited in GenBank under accession numbers PX794909 (strain A) and PX794908 (strain D). Phylogenetic analyses using maximum likelihood and Bayesian inference placed strains A and D within a well-supported clade containing several *B. gladioli* type strains, with a bootstrap value of 70% and a

posterior probability of 0.73 (Figure 4). This molecular confirmation aligns with the biochemical and physiological identification.

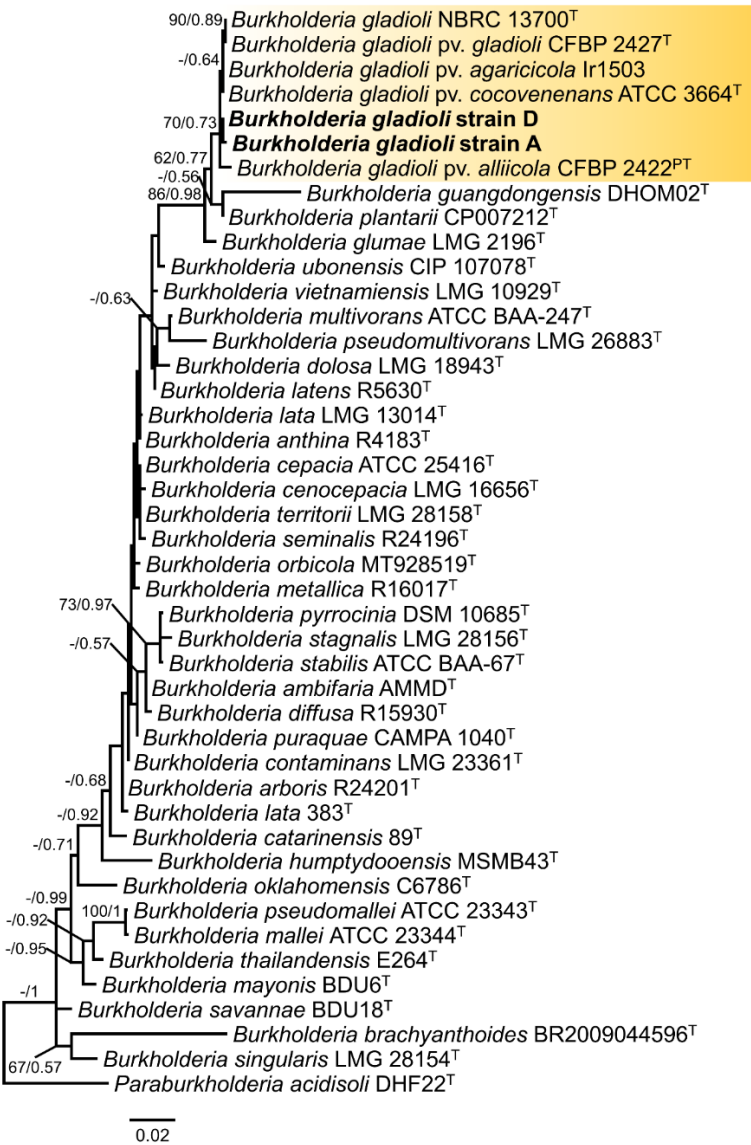


Figure 4. Maximum likelihood tree of the 16S rRNA gene of *Burkholderia*. The sequence of *Paraburkholderia acidisoli* type strain DHF22 was used as an outgroup. Strains from this study are shown in bold. Bootstrap values higher than 50% and posterior probabilities greater than 0.5 are shown above the branches. The scale bar indicates the number of nucleotide substitutions. ^T and ^{PT} indicate ex-type and ex-paratype strains, respectively.

3.2. Pathogenicity Tests on Sweet Corn Leaf Sheaths

Strains A and D of *B. gladioli* induced brown spot symptoms on the leaf sheaths of all four sweet corn hybrids tested, closely resembling field observations (Figures 5 B and C). Initial symptoms appeared 72 hours post-inoculation as small, clear brown lesions at the inoculation site. By day 14, symptoms were consistent with those observed in commercial fields. Non-inoculated plants remained asymptomatic throughout the experiment. Pairwise comparisons between control and infected plants were significant ($P \leq 0.001$) for all sweet maize hybrids (Figure 6).

The Kruskal-Wallis (34) test of LSDA revealed no significant differences between strains A and D ($X^2 = 0.68$, $P = 0.4087$; Figure 6). Damage caused by strain A across all sweet corn hybrids ranged from 1.40 to 3.73 cm², while strain D caused a LSDA ranging from 2.27 to 4.41 cm². The effect of the sweet corn hybrid was not significant ($X^2 = 3.43$, $P = 0.3286$; Figure 6), suggesting that all hybrids are

equally susceptible to bacterial infection, under greenhouse conditions. Koch’s postulates were fulfilled by re-isolating strains with identical cultural, biochemical, and molecular profiles from symptomatic tissues.



Figure 5. Non-inoculated plant and lesions caused after 14 days of inoculation, and inoculated in the leaf sheaths of sweet corn with *Burkholderia gladioli*. **A)** Non-inoculated plant. **B)** symptoms on the leaf sheath caused by strain A. **C)** symptoms on the leaf sheath caused by strain D.

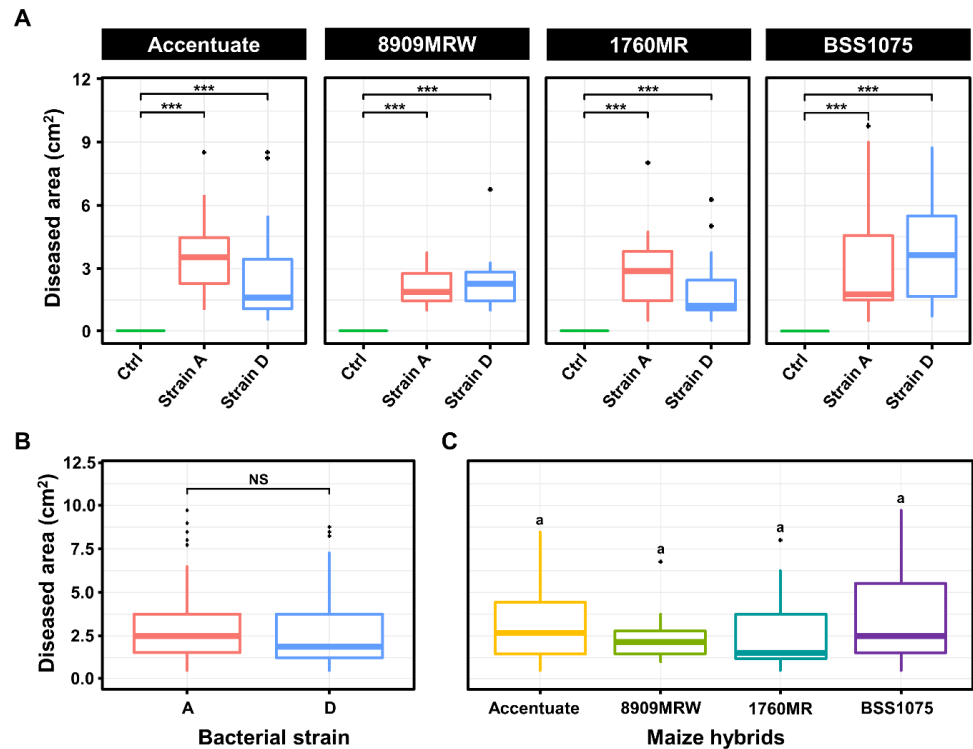


Figure 6. Pathogenicity test of *Burkholderia gladioli* strains A and D expressed as leaf sheath diseased area (LSDA; cm²). All data are shown as medians (25–75 percentiles). **A)** Significant pairwise comparisons of LSDA between non-inoculated (control) and inoculated plants of different sweet corn hybrids, based on the Wilcoxon signed-rank test (***, $P < 0.001$). **B)** Non-significant effect of bacterial strains, and **C)** sweet corn hybrids on LSDA after Kruskal-Wallis test ($P > 0.05$).

4. Discussion

The high percentage of biochemical test results from our strains, isolated from sweet corn leaf sheaths, aligned with those reported for *B. gladioli*. Notably, slight metabolic variations were observed between strains A and D; for instance, strain D was positive for glycerol, D-arabinose, D-adonitol, D-xylose, and D-tagatose utilization, whereas strain A was negative for these carbon sources. Furthermore, both strains failed to utilize N-acetyl-glucosamine, salicin, potassium 2-ketogluconate, and potassium 5-ketogluconate, in contrast to the typical *B. gladioli* profile described by Palleroni [24]. These findings confirm the metabolic versatility of *B. gladioli*, which is known to utilize a broad spectrum of carbon sources [24]. The observed intraspecific variation in substrate utilization is consistent with patterns reported in other bacterial genera, such as *Pectobacterium* within the Enterobacteriaceae [35,36].

The integrated biochemical, physiological, and pathogenicity data from this study fully support the molecular identification of the two *B. gladioli* strains obtained from symptomatic sweet corn plants in Sinaloa, Mexico. Both strains (A and D) successfully reproduced symptoms under greenhouse conditions identical to those observed in commercial fields (Figure 4). Notably, while the bacteria consistently induced brown spots on leaf sheaths, no stem symptoms were detected during this investigation.

The strains, originally isolated from naturally infected sweet corn, proved pathogenic on the commercial hybrids Accentuate, 8909MRW, 1760MR, and BSS1075. Interestingly, under field conditions, the damage appeared confined to the leaf sheath, without progressing to leaves or stems, a pattern that contrasts with reports of *B. gladioli* causing leaf stripe and stem rot in dent corn in other regions of Mexico [18]. First isolated from gladiolus bulbs, *B. gladioli* has since been identified in a wide range of hosts, including iris, saffron, maize, rice [37] and various orchids [38]. Its pathogenicity extends to multiple crops, where it has been associated with soft rot in purple onion bulbs, leek stalks, broccoli inflorescences, cactus cladodes, carrot roots, ginger rhizomes, and mushroom basidiocarps, and has been shown to colonize bean plants in greenhouse studies [39]. This is consistent with pathogenicity tests conducted on potato, onion, and celery using the isolated strains in this study.

Globally, *B. gladioli* has been implicated in garlic bulb decay and shown high pathogenicity on cactus, gladiolus, onion, and potato in Iran [40], as well as dry rot of saffron in the same country [41]. In Mexico, previous reports include onion bulb rot [42] and leaf stripe and stem rot in dent corn [18]. The bacterium has also been associated with ear soft rot of corn in the United States [43]. To our knowledge, this study is the first to report *B. gladioli* as the causal agent of brown spot on sweet corn leaf sheaths in Mexico. The broad and expanding host range of this bacterium highlights its potential as an emerging phytopathogen in the region, particularly for crops cultivated during the fall–winter season in Sinaloa. This work establishes a critical foundation for future studies on the host range, epidemiology, and management of this pathogen. Special attention should be given to dent corn, which occupies approximately 500,000 hectares in Sinaloa during the fall–winter cycle and in which *B. gladioli* has already been reported elsewhere in Mexico [18]. The potential economic impact on this major crop and on vegetable production in the state warrants careful monitoring and proactive research.

5. Conclusions

This study identified *B. gladioli* as the causal agent of the emerging brown spot disease on the leaf sheaths of sweet corn in Sinaloa, Mexico. The identification was confirmed through a polyphasic approach integrating biochemical profiles consistent with the species, pathogenicity tests on alternative potential hosts and sweet corn plants, and molecular analysis (16S rRNA gene sequencing and phylogenetic inference). The bacterium successfully reproduced field symptoms in the greenhouse, fulfilling Koch's postulates. This represents the first report of *B. gladioli* causing this specific symptomatology on sweet corn in Mexico, expanding its known host range and geographic distribution as a phytopathogen.

Given the bacterium's broad host range, which includes economically important crops like onion, garlic, and dent corn cultivated in the region, *B. gladioli* should be considered a potential emerging threat to horticultural production in Sinaloa. Future research should focus on determining the epidemiological conditions favorable for disease development.

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Data Availability Statement: The 16S gene sequences of the studied bacteria are available in National Center for Biotechnology Information (NCBI) database under the accessions PX794909 and PX794908. Further inquiries can be directed to the corresponding author.

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