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Pectobacterium carotovorum subsp. *carotovorum* Causing Severe Soft Rot in Celeriac on a Family Farm in Slovakia

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ABSTRACT

In 2023 and 2024, soft rot caused significant losses (20-50 %) in celeriac (*Apium graveolens* var. *rapaceum*) on a family farm in southern Slovakia. Affected tubers exhibited watery rot, tissue collapse, and a foul odour, particularly evident 12-24 hours after washing. Four bacterial isolates were obtained from the margin of healthy and diseased tissue. All isolates were Gram-negative. Colony morphology and growth characteristics were recorded on potato dextrose agar. Pathogenicity was confirmed by Koch's postulates using detached celeriac tuber slices; three isolates induced rapid soft rot within 3 days, whereas one isolate produced no symptoms. A 1300 bp fragment of the 16S rRNA gene was amplified with universal primers 63F/1389R, bidirectionally sequenced, and compared with NCBI databases. Three pathogenic isolates were identified as *Pectobacterium carotovorum* subsp. *carotovorum* (99.45-99.92 % identity to strains from potato and Chinese cabbage, from China, Iraq and South-Korea). Phylogenetic analysis using the neighbour-joining method placed them within the *P. carotovorum* clade. The non-pathogenic isolate was identified as *Stenotrophomonas* sp. High infection rates in fields previously free of root crops suggest contamination originated in greenhouse seedling production. Replacement of greenhouse soil, disinfection of seedling trays, and strict hygiene during post-harvest washing are recommended to prevent recurrence.

Keywords: celeriac, Pectobacterium carotovorum subsp. carotovorum, bacterial disease, 16S rRNA

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1. INTRODUCTION

Large retail chains now enforce ever-stricter quality standards on producers. With only slight exaggeration, they scrutinize vegetables as if under a magnifying glass, demanding nearly flawless produce that stays fresh for days.
In 2023, a family farm in Csilizradvány (Čiližská Radvaň), Dunajská Streda District, Slovakia, suffered heavy losses in its celeriac crop: approximately 20% of the plants were attacked by an unknown pathogen, resulting in financial damage of tens of thousands of euros. In this highly competitive sector, even a single spoiled tuber in a shipment is unacceptable, as it risks contract termination and leaves tons of produce unsold. Regrettably, 2024 brought no improvement. That year, 50% of the planted crop was affected by the same pathogen, causing even greater financial losses and preventing the farm from fulfilling its orders.
The present study aimed to identify the causal agent. Based on the results, practical preventive measures were developed to protect future celeriac crops from this disease.

2. LITERATURE REVIEW

2.1 The importance of celery

Celery (*Apium graveolens*) is a vegetable and aromatic plant cultivated worldwide and valued for its medicinal properties. A. *graveolens* comprises three botanical varieties: var. *rapaceum*, known as celeriac, is grown for its edible hypocotyl and is particularly popular in Europe; var. *secalinum* is mainly cultivated in Asia as a leaf crop for fodder; and var. *dulce*, commonly called stalk celery, is widely grown in America and Western Europe for its crisp petioles (*Figure 1*).

Figure 1: Botanical varieties of Apium graveolens:
var. dulce (A), var. rapaceum (B), var. secalinum (C)

Source: Bruznican et al., 2020

Celery originates from the Mediterranean basin. Wild forms were used as medicine and flavouring in ancient times, but organised cultivation of improved vegetable varieties began in Italy during the 19th century, when types were classified into white, “Golden Self-blanching,” and green “Pascal” (Quiros, 1993)

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2.2 Morphological characteristics of celeriac

The celeriac plant is characterised by enlarged, tender, edible leaf stalks or petioles. These petioles are broad, attached to a swollen base, and composed mainly of parenchyma and collenchyma fibres. Vascular bundles are located beneath the epidermis on the markedly grooved abaxial surface, whereas the adaxial surface is smooth. The small flowers are arranged in large, compound umbels and are pentamerous, with free petals and stamens (Quiros, 1993).
Celeriac tubers are rich in iron, manganese, potassium, vitamin K, and phosphorus, and also provide reasonable amounts of vitamin C, folate, and magnesium (Shehata et al., 2011).
The edible portion of celeriac is a tuber formed from stem and root tissue. It consists of three parts: the stem above the cotyledon (epicotyl), the region below the cotyledon (hypocotyl), and the upper part of the primary root. Lateral root branches develop mainly on the sides and lower portion of the tuber. Fewer roots facilitate harvesting and cleaning. In contrast, stalk celery and blanched celery do not form tubers; their primary root remains unchanged throughout development.
Leaves – In the first year, celeriac forms a basal rosette. The leaves have long, thick petioles and shiny, lobed blades. In blanching types, petioles may reach 50-60 cm in length and 4-5 cm in thickness. The leaves are compound and odd-pinnate. Stem leaves are similar but smaller and, although resembling parsley, are easily distinguished from it.
Stem – The stem appears in the second year; it is ribbed and 80-120 cm tall. In exceptional cases (e.g., cold weather), it may emerge in the first year, but then the edible tuber fails to develop.
Inflorescence – Compound umbel bearing many flowers, each with two pistils.
Fruit – A twin schizocarp containing two seeds that lie flat against each other. The fruit is brown or greyish-brown with five ribs (three dorsal, two lateral). Seeds are small, with a thousand-seed weight of 0.4-0.5 g, and remain viable for 4-5 years (Takácsné, 2017).

2.3 Propagation and planting of celeriac

Celery is propagated by seed. It requires a growing period of approximately 120 days and can be established either by transplanting seedlings or by direct sowing.
In Hungary and Slovakia, celeriac is mainly grown from greenhouse-raised seedlings. This labour-intensive method is preferred because celeriac establishes poorly in open fields, particularly when soil moisture during early growth is below field capacity (pF 2.5). Medium-textured loamy soils with high water-holding capacity are therefore best suited for its cultivation (Cserni et al., 2015).

2.4 Harvesting

The crop is harvested 80-100 days after transplanting. At harvest, tubers are measured and graded. Compared to lettuce, which must be harvested within a 1-2-day window, celeriac offers a more flexible harvest period of 7-10 days. After harvesting, celeriac is typically cooled by hydrocooling or hydro-vacuum cooling. Optimal storage and transport conditions are 0-1 °C with relative humidity above 95 %. Under these conditions, celeriac can be stored for more than 30 days (Raid, 2004).

2.5 Celeriac cultivation in Hungary and worldwide

According to the Hungarian Chamber of Agriculture (NAK) and the Hungarian Interprofessional Organization for Fruit and Vegetable (FruitVeB), domestic celeriac consumption is on the rise. Demand is steady and stable, making it an excellent option for farmers. In Hungary, areas registered for area-based support totalled 176 hectares in 2023, with the central growing regions in Pest

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County (88 ha) and Csongrád-Csanád County (66 ha). The country remains a net importer of celeriac: exports totaled 2,019 tons in 2022, while imports were approximately 2,502 tons. However, the trade balance has improved significantly in recent years (Agronapló, 2024).
In most countries, celery is consumed as stalk celery (the leaf stalks). In Hungary and Slovakia, however, the cultivation and consumption of celeriac is more widespread. In the European Union, celeriac is grown on several thousand hectares annually. The largest producers are Poland, Germany, the Netherlands, and Belgium; the largest consumers are France and Germany. The leading EU producers of stalk celery are Spain, Italy, and the United Kingdom (FruitVeb, 2020).

2.6 Diseases of celery

Celery mosaic virus is the most common viral disease of celery. Celery aphids transmit it and can also infect related crops such as carrot (*Daucus carota* L.), parsley (*Petroselinum crispum* Mill.), parsnip (*Pastinaca sativa* L.), coriander (*Coriandrum sativum* L.), and dill (*Anethum graveolens* L.). The virus is also known as apium virus 1, western celery mosaic virus, and celery ringspot virus (Hollings, 1964; Pemberton & Frost, 1986). Symptoms include yellowing foliage, mosaic or mottled patterns on leaves, vein clearing, and curled, wrinkled, or distorted leaflets. Infected plants may become stunted, and outer leaflets often grow horizontally, giving the plant a flattened appearance. Some strains cause more severe symptoms than others. The disease was first recorded on celery in California in 1922 (Poole, 1922).
Soft rot caused by *Pectobacterium carotovorum* (formerly *Erwinia carotovora*) affects many vegetable crops. Once established, the disease is difficult to control (Shi et al., 2020). P. *carotovorum* is regarded as one of the most destructive plant pathogens worldwide, with the broadest host range among soft-rot bacteria (Davidsson et al., 2013; Mansfield et al., 2012).
Pectobacterium (formerly *Erwinia*) *carotovorum* is a Gram-negative, plant-specific pathogen that infects a wide range of hosts, causing diseases such as blackleg in potatoes, by degrading plant cell walls. P. *carotovorum* colonises intercellular spaces and delivers effector molecules via a type III secretion system. It also secretes various exoenzymes through a type II secretion system that depolymerise pectin in the plant cell wall (Aizawa, 2014).
The disease can develop during storage, producing slimy, foul-smelling rot. Bacteria are carried from the field to storage on root surfaces. At higher temperatures, severe damage occurs readily, especially on wet roots. At low temperatures, infection typically requires wounds, whereas at warmer temperatures, the pathogen can enter intact tissue. To prevent losses, celeriac roots must be kept dry and undamaged before storage. Proper storage conditions are essential to minimise the problem (Kerek & Hartmann, 2018).
Pseudomonas syringae pv. *apii,* the cause of bacterial leaf spot, is a seed-borne pathogen. In greenhouses, it spreads rapidly through splashing water during sowing. Warm, humid conditions favour disease development. Infected seedlings then carry the bacterium to the field. Widespread or severe symptoms are uncommon in the field unless the crop is overhead-irrigated or exposed to light frost. The pathogen also survives in undecomposed celery residues.
Initial symptoms are small, water-soaked spots visible on both leaf surfaces. Because veins often bound lesions, they appear angular, square, or rectangular. These spots quickly turn brown and, as they age, may dry out, becoming papery and brownish. Lesions are usually small (less than 0.6 cm in diameter) and confined to the leaves. In greenhouse transplants, extensive foliar spotting can occur. In the field, however, the disease typically affects only older leaves sheltered by the canopy,

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unless irrigation is used. Under favourable conditions, individual spots may coalesce, producing significant mottling of the foliage.

Recommended control measures for bacterial leaf spot include the following (Koike et al., 2009):

- Use seeds certified free of *Pseudomonas syringae* pv. *apii*.
- Treat seeds with hot water (50 °C for 25 minutes); this significantly reduces inoculum but may lower germination.
- Use seeds that are at least 2 years old, as older seeds show reduced disease incidence.
- Disinfect transplanting trays, since bacteria can survive on contaminated trays.
- In greenhouses, reduce water pressure in overhead sprinklers to limit pathogen entry into leaves.
- Avoid overhead irrigation in the field.
- Avoid excessive nitrogen fertilisation, which appears to promote the disease.

Celery root rot. The genus *Phoma* is a dominant group of fungi widespread across many ecological habitats. More than 200 species have been described, making it one of the largest fungal genera. Many are serious phytopathogens of vegetable crops worldwide. Common examples include the following (Sultana & Hossain, 2021):

- *Phoma terrestris* (onion pink root, *Alliaceae*)
- *Phoma apiicola* (celery crown and root rot)
- *Calophoma complanata* (Syn. *Phoma complanata*) (parsnip Phoma rot, *Apiaceae*)
- *Phoma betae* (sugar beet blackleg, Amaranthaceae)
- *Plenodomus lingam* (Syn. *Phoma lingam*) (bean blackleg/Phoma leaf spot/stem spot, *Brassicaceae*)
- P. *cucurbitacearum* (rubbery stem spot and black rot of cucumbers, *Cucurbitaceae*)
- *Peyronellaea pinodella* (Syn. *Phoma pinodella*) (root and stem rot of peas, *Fabaceae*)
- *Boeremia exigua* (Syn. *Phoma exigua*) (Phoma basal rot of lettuce, *Asteraceae*)
- *Remotididymella destructiva* (Syn. *Phoma destructiva*) (tomato Phoma rot, *Solanaceae*)

Although primarily field diseases, some cause post-harvest spoilage, for example:

- *Boeremia exigua* var. *exigua* or var. *foveata* (potato scab)
- *Phoma cucurbitacearum* (black rot of cucumber)
- *Phoma apiicola* (crown and root rot of celery)
- *Calophoma complanata* (parsnip canker)
- *Phoma betae* (black leg of sugar beet)

Infections spread through soil, seeds, and plant debris on the soil surface (Sultana & Hossain, 2021).

Septoria leaf spot (*Septoria apiicola*). Septoria leaf spot is a severe disease caused primarily by *Septoria apiicola*. Large, round or slightly oval spots (3–10 mm diameter) with distinct brown margins appear on leaves. The pathogen overwinters on diseased plant parts, but the primary inoculum source is seed contaminated with small black pycnidia that remain infectious for 1-2 years. Seed dressing is an effective control method (Glits & Folk, 2000a). Resistance to leaf spot is polygenic (Ochoa & Quiros, 1989). Hybrids between Pascal celery and parsley showed immunity (Honma & Lacy, 1980). Screening of 144 celery varieties revealed no resistance, although two wild species, *Apium chilense* and *Apium nodiflorum*, exhibited high resistance to late leaf spot (Ochoa & Quiros, 1989). To date, no resistant varieties are available for large-scale cultivation (Zhu et al., 2011).

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Sclerotinia rot. *Sclerotinia sclerotiorum* (Lib.) de Bary is a necrotrophic fungal pathogen that infects a wide range of plants. It can colonise more than 400 plant species worldwide, mostly dicotyledons but also several agriculturally important monocotyledons. Infected leaves typically show watery lesions that spread rapidly down the petiole to the stem. In some hosts, dark lesions appear first on the stem; in others, watery stem lesions are the initial symptom. These lesions eventually become necrotic, and fluffy white mycelium – often with sclerotia – develops on the surface, providing the most distinctive sign of infection (Bolton et al., 2006).

Botrytis rot (*Botrytis cinerea*). The disease has been known in Hungary since 1964; the causal agent is the fungus *Botrytis cinerea*. It has an extensive host range, primarily dicotyledonous species and, less frequently, monocotyledons, including root vegetables of the *Apiaceae* family. Pale, watery, rotting spots appear on the taproot. The decayed tissue is odourless and flexible. At low storage temperatures, fine cobweb-like white mycelium develops, later becoming felt-like. Small greyish-brown and then black sclerotia subsequently form in the periderm and merge into a hard crust. As sclerotia mature, the white mycelial layer gradually thins. Eventually, the root shrinks and becomes woody. At higher temperatures, a dense grey layer of conidia covers the rotting areas; sclerotia form weakly or not at all. The pathogen survives as a saprophyte on plant debris in the soil. Soil fertilisers do not influence disease severity. Infection is introduced into storage on field-harvested taproots, with the fungus entering through wounds. The optimal temperature for fungal growth is 21–24 °C (Glits & Folk, 2000b).

3. MATERIALS AND METHODS

3.1 Location, technology, and time of testing

The celeriac plantation is located on a family farm in Csilizradvány (Čiližská Radvaň, Dunajská Streda District, Slovakia). The farm covers 5 hectares and includes 12 greenhouses for seedling production. Seedlings were transplanted to 8 hectares of open field using a Ferrari F-MAX 6-row planter mounted on a New Holland T5 110 tractor equipped with GPS guidance.
Celeriac tubers showing symptoms of infection were transported from the field to the HUN-REN-SZE PhatoPlant-Lab, Department of Plant Sciences, Albert Kázmér Faculty of Agricultural and Food Sciences of Széchenyi István University. All tests were conducted in the autumn of 2023 and 2024.

3.2 Plant material

Codex F1, Markiz F1, Dukiz F1, Princino F1, Dutch celeriac varieties.

3.3 Methods

3.3.1 Isolation of the pathogen

To isolate the bacteria, celeriac tubers were cut with a sterile knife, and a sample was taken from the margin between healthy and infected tissue using sterile distilled water. The suspension was placed in Eppendorf tubes. Aliquots were then plated onto potato dextrose agar (PDA) medium under a laminar flow hood. Petri dishes were incubated at room temperature for 1-2 days. Individual colonies were subcultured onto fresh sterile medium to obtain pure cultures, which were subsequently maintained.

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3.3.2 Gram characteristics

The Gram reaction of isolated bacteria was tested using the method of Suslow et al. (1981). A single colony from a 24-hour pure culture grown on PDA medium was mixed 1:1 with 3 % KOH on a glass slide and stirred. If the cell wall dissolved, the mixture became viscous and formed a thread when lifted with a pipette tip, indicating a Gram-negative reaction due to the release of DNA. In Gram-positive bacteria, the mixture remained watery because KOH does not dissolve the cell wall.

3.3.3 Pathogenicity test

Pathogenicity was confirmed on healthy celeriac slices, fulfilling Koch's postulates. Tubers were surface-sterilised with 96 % ethanol and rinsed with sterile water. They were then cut into 1 cm-thick slices and placed on filter paper moistened with sterile water in sterile 20 cm-diameter Petri dishes. The experiment was conducted in duplicate. Each slice was marked with the isolate number and inoculation site.

For inoculation, pure bacterial cultures grown for 3 days were used. One colony of each isolate was suspended in 100 µL of sterile distilled water, and 10 µL of the suspension was applied to the tissue surface using a pipette tip. Control slices received 10 µl of sterile distilled water. The slices were incubated at room temperature in glass Petri dishes on moist filter paper. Symptoms were evaluated after 3 days.

3.3.4 Polymerase Chain Reaction (PCR)

The polymerase chain reaction was performed on a PCRmax instrument (Cole-Parmer).

PCR mixture composition (50 µl):

- 37.5 µl sterile water
- 3 µl bacterial suspension
- 5 µl 10x Taq buffer + MgCl2
- 2 µl dNTPs (nucleotides: A, T, C, G; 5 mM)
- 1 µl primer 1389R (20 pmol/µl)
- 1 µl primer 63F (20 pmol/µl)
- 0.5 µl Taq polymerase enzyme (5 u/µl, Thermo Scientific)

The primer sequences used for PCR are universal bacterial primers specific for the 16S rRNA gene (Marchesi et al., 1998):

- 1389R (reverse) 5'-ACGGGCGGTGTGTACAAG-3'
- 63F (forward) 5'-CAGGCCTAACACATGCAAGTC-3'

(Invitrogen synthesized primers.)

The PCR cycling conditions were as follows: initial denaturation at 95 °C for 5 min, followed by 35 cycles of 94 °C for 15 s, annealing at 55 °C for 30 s, and elongation at 72 °C for 1 min. A final extension was performed at 72 °C for 5 min, after which the PCR products were held at 4 °C.

3.3.5 Gel electrophoresis

The PCR products were separated on a 1 % agarose gel stained with GelRed (Biotium). Electrophoresis was performed in a horizontal mini apparatus at 140 V using 1× TBE buffer (12.11 g Tris, 5.135 g boric acid, 0.372 g EDTA in 1000 ml sterile distilled water). Bands were visualised under transmitted ultraviolet light and photographed using the UVP BioDoc-It Imaging System.

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3.3.6 Purification of the PCR product

The PCR product was purified using the GeneJET PCR Purification Kit (Thermo Scientific) according to the manufacturer's instructions.

3.3.7 Determination of the nucleotide sequence of the PCR product

The purified PCR products were sent to Biomi Ltd. in Gödöllő, Hungary, for sequence determination.

3.3.8 Molecular analysis of the 16S rRNA gene

The nucleotide sequences of the 16S rRNA gene fragments for each isolate were determined. Sequences were checked using Chromas Version 2.6.6, assembled and analysed with CLC Sequence Viewer 8.0, and compared with selected NCBI database entries using the Kimura (1981) two-parameter method. A phylogenetic tree was constructed using the neighbour-joining method (Saitou & Nei, 1987).

4. RESULTS

4.1 Symptoms of the disease

In the field, diseased celeriac plants showed brownish discoloration and drooping stalks. Tubers exhibited slight wilting (*Figure 2* and *Figure 3*). However, the most severe symptoms appeared 12-24 hours after washing. Lesions that were not visible externally during washing spread rapidly and became clearly evident on the tuber surface. Buyers returned several consignments for this reason.

Figure 2: Diseased celeriac

Figure 3: Diseased celeriac cut up

4.2 Identification of culture marks

All isolates from celeriac grew readily on PDA medium and were easily maintained. Colonies of isolates Z-1a/1 and Z-1b/1 were white, opalescent, with intact edges, smooth surfaces, and slightly raised (*Figure 4*). Isolate Z-2/1 produced light ochre-yellow, opaque colonies with intact edges, smooth surfaces, and slight elevation (*Figure 4*). Isolate Z-3/1 formed slightly yellowish, faintly opalescent colonies with intact edges, smooth surfaces, and vigorous growth (*Figure 4*).

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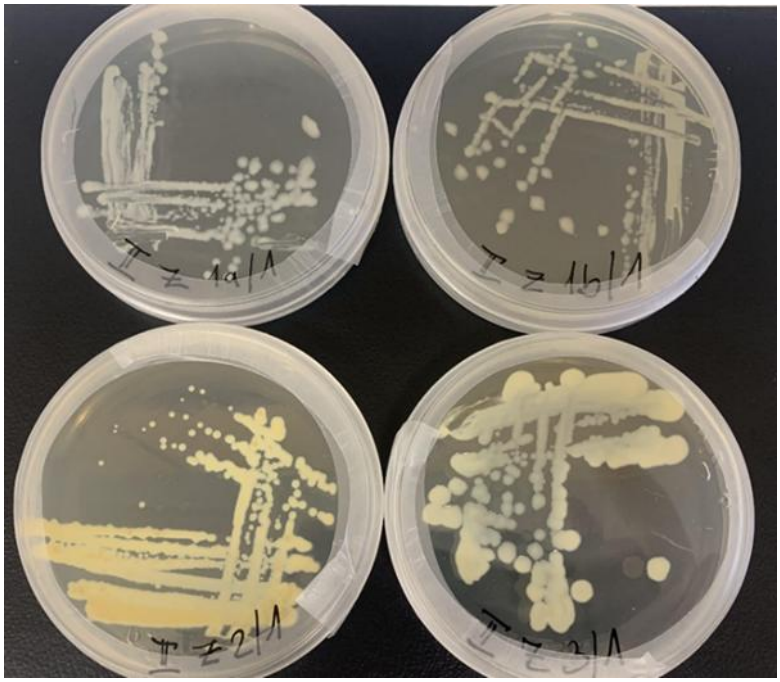

Figure 4: Pure cultures of isolates from celeriac

4.3 Gram characteristics

In all four isolates (Z-1a/1, Z-1b/1, Z-2/1, Z-3/1), the bacterial cell wall was dissolved by a 3 % potassium hydroxide solution *(Figure 5)*, indicating that the isolates are Gram-negative bacteria.

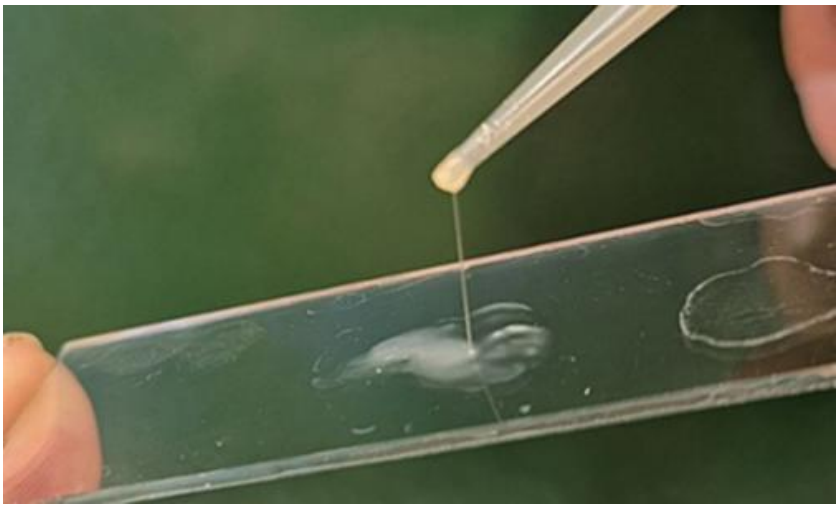

Figure 5: Under the influence of KOH, the cell walls of the bacterial isolates dissolved, exposing the DNA strands, thus revealing that the bacterial isolates were Gram-negative

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4.4 Pathogenicity test

Among the isolates, isolates Z-1/1a, Z-1/1b, and Z-3/1 caused rot on celeriac slices. No rot was observed in the case of isolate Z-2/1 (*Figure 6*).

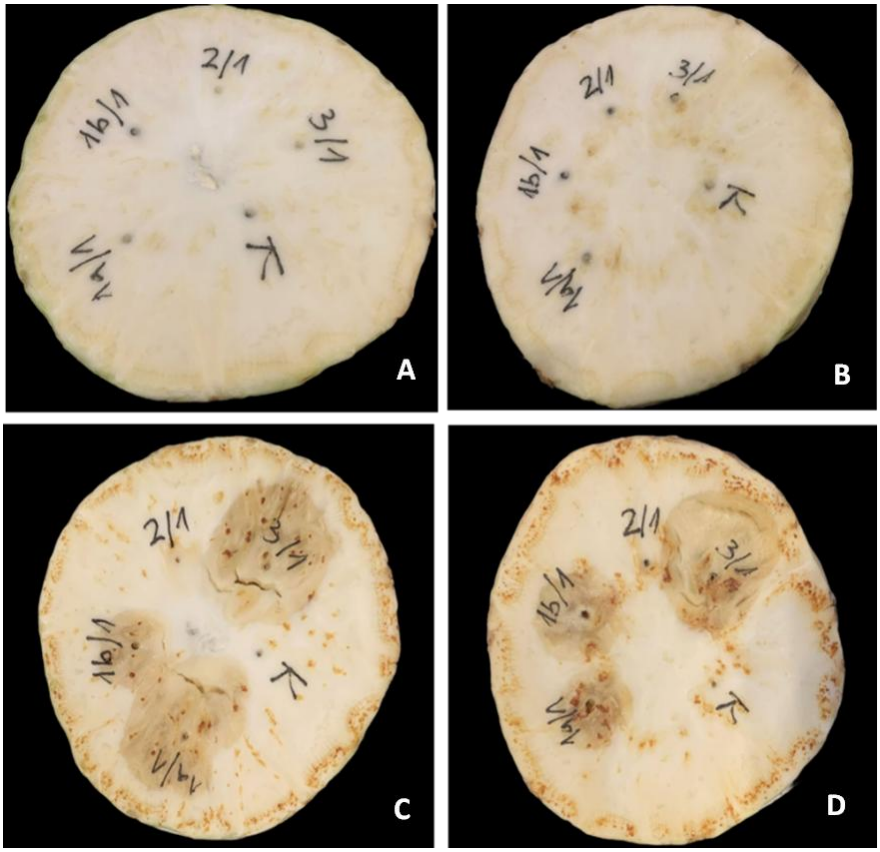

Figure 6: Experimental setup, isolates: Z-1a/1, Z-1b/1, Z-2/1, Z-3/1, K-control sterile distilled water. A and B at inoculation, C and D 3 days after inoculation. Rotting can be observed in isolates Z-1a/1, Z-1b/1, and Z-3/1.

Fulfilling Koch's postulates, the pathogens were re-isolated from symptomatic celeriac slices. Each isolate displayed the same cultural characteristics as in the original isolation. Isolate Z-2/1 did not cause rot, but it was successfully re-isolated from the inoculation site and showed identical cultural characteristics to the first isolation.

4.5 Molecular analysis of the 16S rRNA gene

When analysing the 16S rRNA gene, PCR reactions produced products of approximately 1300 bp in length for all four isolates (*Figure 7*).

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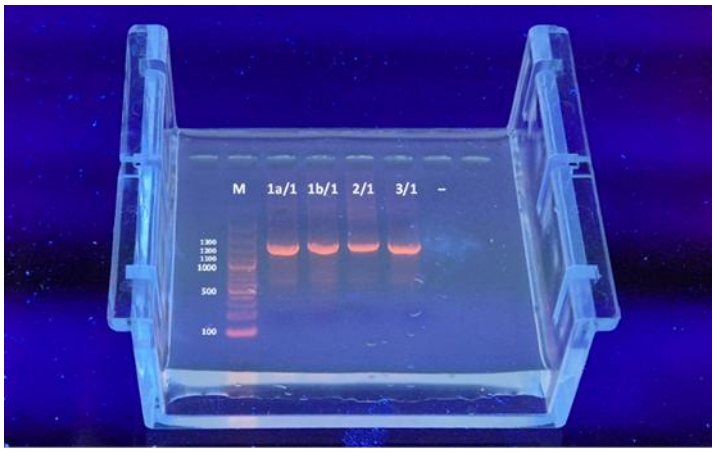

Figure 7: The PCR products were run alongside a 100 bp size marker (M). Z-1a/1, Z-1b/1, Z-2/1, Z-3/1 are the celeriac samples, – negative control. The PCR products obtained are 1300 bp long

The obtained nucleic acid sequences were compared with entries in the NCBI database, and a phylogenetic tree was constructed using a 1277-base alignment. The tree was built with 1000 bootstrap replications.

Molecular identification based on the 16S rRNA gene sequence showed that isolates Z-1a/1 and Z-1b/1 were identical. They shared 99.68 % identity with two potato and Chinese cabbage isolates from China and with a potato isolate from Iraq. Isolate Z-3/1 clustered on a separate branch, with 99.45 % identity to Z-1a/1 and Z-1b/1. It exhibited the highest similarity (99.92 %) to a South Korean isolate, a potato isolate, and a *Pinellia ternata* (Ban Xia, crow-dipper) isolate from China (Figure 8). Isolate Z-2/1 was identified as a *Stenotrophomonas* species.

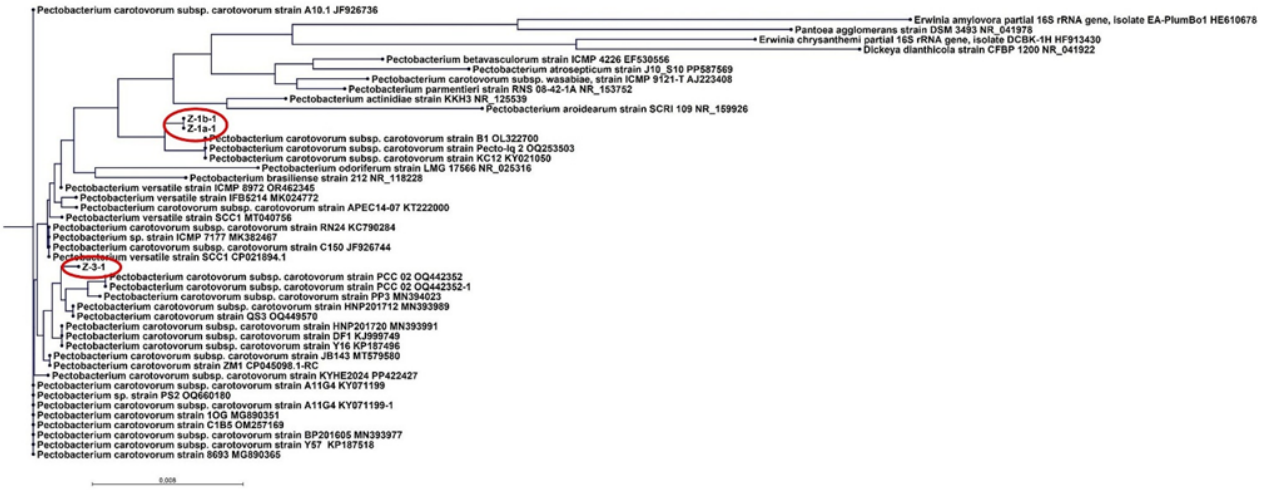

*Figure 8: Phylogenetic tree of Pectobacterium and various Erwinia, Pantoea, and Dickeya isolates (outgroup for rooting the phylogenetic tree)**

*The red ellipses indicate our own isolates. The numbers next to the branches in the figure show the bootstrap percentages, the vertical lines show the similarities, the horizontal lines show the differences, and the scale below the phylogenetic tree shows 8 base differences per 1000 bases.

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The pathogen isolated from celeriac was identified as *Pectobacterium carotovorum* subsp. *carotovorum* based on classical and molecular tests.
Isolate Z-2/1 was Gram-negative but did not cause rot on celeriac slices. Molecular identification placed it in the genus *Stenotrophomonas* sp. These bacteria are common in soil and on plants. The most widespread species, S. *maltophilia*, is highly versatile and can promote plant growth and health. It is used in agriculture, biocontrol, bioremediation, phytoremediation, and the production of economically important biomolecules (Ryan et al., 2009).

5. DISCUSSION AND CONCLUSION

Based on the research results, we concluded that isolates Z-1a/1 and Z-1b/1 are identical, whereas isolates Z-2/1 and Z-3/1 differ in their 16S rRNA gene sequences. The isolates also showed distinct growth characteristics, including differences in colony colour and growth rate; isolates Z-1a/1 and Z-1b/1 were indistinguishable in these respects. The results confirmed that Z-1a/1, Z-1b/1, and Z-3/1 are pathogenic, while Z-2/1 is a non-pathogenic, beneficial bacterium belonging to the genus *Stenotrophomonas*. Further species-level identification of this isolate is warranted, as *Stenotrophomona***s** spp. play important ecological roles in nitrogen and sulphur cycles, and several species promote plant growth or protect plants from pathogens (Ryan et al., 2009).
After reinfecting healthy celeriac slices, symptoms were monitored at room temperature. Over several days, the pathogen spread most rapidly and aggressively in slices inoculated with isolate Z-3/1, consistent with its vigorous growth on culture medium. In contrast, maceration was markedly slower in slices inoculated with Z-1a/1 or Z-1b/1. These observations further support the conclusion that Z-1a/1 and Z-1b/1 are identical, whereas Z-3/1 represents a distinct strain within *Pectobacterium carotovorum* subsp. *carotovorum*.
After analysing the isolates, it was confirmed that the pathogens are common soil-dwelling bacteria. Infection could have occurred in either the greenhouses or the field. Although the 2023 crop suffered 20 % losses, in 2024 celeriac was planted in fields previously used only for barley, winter wheat, and maize. Despite this rotation, losses reached 50 %, indicating that the plants were already infected at the seedling stage in the greenhouse. Although seed transmission cannot be completely ruled out, it is unlikely with high-quality seeds. The increasing infection rate year after year strongly suggests that the primary source is the greenhouse environment.
Based on these findings, the following measures are essential:

- Replace the greenhouse soil completely.
- In the future, keep seedling trays off the ground by placing them on plastic sheets.
- Exercise greater care when separating rotten tubers during washing and polishing; even minor wounds can lead to rapid contamination of healthy plants—a problem that typically becomes evident only after delivery to retail-chain warehouses.

Further experiments are needed to pinpoint exactly where the pathogen enters the plant. Soil tests in the greenhouses would be particularly valuable, and the results could help other local growers facing similar challenges and prevent future problems with other sown or planted vegetables.

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A gumós zeller pektobaktériumos betegsége egy felvidéki családi gazdaságban

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ÖSSZEFOGLALÁS

2023-ban és 2024-ben a Felvidéki családi gazdaságban termelt zellerállományt veszteség érte, a kiültetett növények 20-50 %-át megtámadta egy ismeretlen kórokozó. A zellergumók kellemetlen szagú, baktériumok jelenlétére utaló lágyrothadás tüneteit mutatták. A gumókat felvágva barnuló elfolyósodott növényi szöveteket figyeltünk meg. A fertőzött szövetekből mintát vettünk az egészséges és a beteg rész határáról. A táptalajon növekvő baktérium izolátumokból tiszta kultúrákat hoztunk létre. Az izolátumok a Gram teszt után minden esetben Gram negatív baktériumok jelenlétére utaltak. Jellemeztük az egyes izolátumok tenyészbélyegeit is. Elvégeztük a patogenitási tesztet a Koch Posztulátumokat teljesítve. A molekuláris azonosítás a 16s rRNS gén 1300 bp nukleinsav szekvenciája alapján az izolátumok közül hármat *Pectobacterium carotovorum* subsp. *carotovorum* kórokozónak határozott meg (99,45-99,92 %-os azonossággal burgonyából és kínai kelből, Kínából, Irakból és Dél-Koreából származó izolátumokkal), míg a negyedik nem patogén *Stenotrophomonas* fajnak bizonyult, amelyek jótékony hatással lehetnek a növények növekedésére és egészségére, felhasználhatók a mezőgazdaságban, a biokontrollban, a bioremediációban és a fitoremediációs stratégiákban, valamint gazdasági jelentőségű biomolekulák előállításában. A korábban gyökérzöldségekkel nem fertőzött területeken tapasztalt magas fertőzési arányok arra utalnak, hogy a fertőzés az üvegházi palántanevelésből származik. A megelőzése érdekében ajánlott az üvegházi talaj cseréje, a palántanevelő tálcák fertőtlenítése és a betakarítás utáni mosás során szigorú higiéniai előírások betartása.

Kulcsszavak: gumós zeller, Pectobacterium carotovorum subsp. carotovorum, baktériumos betegség, 16s rRNS

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REFERENCES

Agronapló. (2024, January 3). *Megéri zellert termeszteni* [It is worth growing celeriac]. https://www.agronaplo.hu/agrarhirek/20240103/megeri-zellert-termeszteni-30403

Aizawa, S.-I. (2014). The flagellar world: Electron microscopic images of bacterial flagella and related surface structures from more than 30 species. In *Pectobacterium carotovorum – Subpolar hyper-flagellation* (pp. 58-59). Academic Press.

Bolton, M. D., Thomma, B. P. H. J., & Nelson, B. D. (2006). Sclerotinia sclerotiorum (Lib..) de Bary: Biology and molecular traits of a cosmopolitan pathogen. *Molecular Plant Pathology*, *7*(1), 1-16. https://doi.org/10.1111/j.1364-3703.2005.00316.x

Bruznican, S., De Clercq, H., Eeckhaut, T., Van Huylenbroeck, J., & Geelen, D. (2020). Celery and celeriac: A critical view on present and future breeding. *Frontiers in Plant Science*, *10*, 1699. https://doi.org/10.3389/fpls.2019.01699

Cserni, I., Pető, J., & Hüvely, A. (2015). A zeller növekedésének és egyes értékmérő paramétereinek vizsgálata [Examination of celery growth and certain quality parameters]. *Gradus*, *2*(2), 236-241. https://gradus.kefo.hu/archive/2015-2/2015_2_AGR_003_Cserni.pdf

Davidsson, P. R., Kariola, T., Niemi, O., & Palva, E. T. (2013). Pathogenicity of and plant immunity to soft rot pectobacteria. *Frontiers in Plant Science*, *4*, 191. https://doi.org/10.3389/fpls.2013.00191

FruitVeb. (2020, May 29). *Zöldségtermesztés II. rész* [Vegetable production II]. FruitVeB Bulletin. https://fruitveb.hu/fruitveb-bulletin-2019-zoldsegtermesztes-ii-resz

Glits, M., & Folk, Gy. (2000a). A zeller szeptóriás levélfoltossága [Septoria leaf spot of celery]. In *Kertészeti növénykórtan* [Horticultural plant pathology] (pp. 443-444). Mezőgazda Kiadó.

Glits, M., & Folk, Gy. (2000b). A sárgarépa botrítiszes rothadása [Botrytis rot of carrot]. In *Kertészeti növénykórtan* [Horticultural plant pathology] (pp. 431-432). Mezőgazda Kiadó.

Hollings, M. (1964). Some properties of five viruses of celery (*Apium graveolens* L.) in Britain. *Journal of Horticultural Science*, *39*(2), 130-141. https://doi.org/10.1080/00221589.1964.11514100

Honma, S., & Lacy, M. L. (1980). Hybridization between pascal celery and parsley. *Euphytica*, *29*, 801-805. https://doi.org/10.1007/BF00023227

Kerek, M., & Hartmann, K. (2018). A sárgarépa és a petrezselyem növényvédelmi technológiája [Plant protection technology of carrot and parsley]. *Növényvédelem*, *54*(3), 118-130.

Kimura, M. (1981). Estimation of evolutionary distances between homologous nucleotide sequences. *Proceedings of the National Academy of Sciences of the United States of America*, *78*(1), 454-458. https://doi.org/10.1073/pnas.78.1.454

Koike, S. T., Davis, R. M., & Turini, T. A. (2009). *UC IPM pest management guidelines: Celery* (pp. 1-52). University of California Agriculture and Natural Resources.

Mansfield, J., Genin, S., Magori, S., Citovsky, V., Sriariyanum, M., Ronald, P., Dow, M., Verdier, V., Beer, S. V., Machado, M. A., Toth, I., Salmond, G., & Foster, G. D. (2012). Top 10 plant pathogenic bacteria in molecular plant pathology. *Molecular Plant Pathology*, *13*(6), 614-629. https://doi.org/10.1111/j.1364-3703.2012.00804.x

Marchesi, J. R., Sato, T., Weightman, A. J., Martin, T. A., Fry, J. C., Hiom, S. J., Dymock, D., & Wade, W. G. (1998). Design and evaluation of useful bacterium-specific PCR primers that amplify genes coding for bacterial 16S rRNA. *Applied and Environmental Microbiology*, *64*(2), 795-799. https://doi.org/10.1128/AEM.64.2.795-799.1998

Ochoa, O., & Quiros, C. F. (1989). Apium wild species: Novel sources for resistance to late blight in celery. *Plant Breeding*, *102*(4), 317-321. https://doi.org/10.1111/j.1439-0523.1989.tb01262.x

 DOI: 10.17108/ActAgrOvar.2025.66.2.32

Pemberton, A. W., & Frost, R. R. (1986). Virus diseases of celery in England. *Annals of Applied Biology*, *108*(2), 319-331. https://doi.org/10.1111/j.1744-7348.1986.tb07653.x

Poole, R. F. (1922). Celery mosaic. *Phytopathology*, *12*, 151-154.

Quiros, C. F. (1993). Celery – *Apium graveolens* L. In G. Kalloo & B. O. Bergh (Eds.), *Genetic improvement of vegetable crops* (pp. 523-534). Pergamon Press.

Raid, R. N. (2004). Celery diseases and their management. In *Diseases of fruits and vegetables: Volume I* (pp. 441-453). Kluwer Academic Publishers.

Ryan, R. P., Monchy, S., Cardinale, M., Taghavi, S., Crossman, L., Avison, M. B., Berg, G., van der Lelie, D., & Dow, J. M. (2009). The versatility and adaptation of bacteria from the genus Stenotrophomonas. *Nature Reviews Microbiology*, *7*, 514-525. https://doi.org/10.1038/nrmicro2163

Saitou, N., & Nei, M. (1987). The neighbor-joining method: A new method for reconstructing phylogenetic trees. *Molecular Biology and Evolution*, *4*(4), 406-425. https://doi.org/10.1093/oxfordjournals.molbev.a040454

Shehata, S. M., Abdel-Azem, H.-S., El-Yazied, A. A., & El-Gizawy, A. M. (2011). Effect of foliar spraying with amino acids and seaweed extract on growth, chemical constituents, yield and its quality of celeriac plant. *European Journal of Scientific Research*, *58*(2), 257-265.

Shi, Y., Jin, Z., Meng, X., Wang, L., Xie, X., Chai, A., & Li, B. (2020). Development and evaluation of a loop-mediated isothermal amplification assay for the rapid detection and identification of *Pectobacterium carotovorum* on celery in the field. *Horticultural Plant Journal*, *6*(5), 313-320. https://doi.org/10.1016/j.hpj.2020.07.004

Sultana, F., & Hossain, M. M. (2021). Diseases of vegetables caused by Phoma spp. In M. Rai, B. Zimowska, & G. J. Kövics (Eds.), *Phoma: Diversity, taxonomy, bioactivities, and nanotechnology* (pp. 91-119). Springer. https://doi.org/10.1007/978-3-030-81218-8_6

Suslow, T. V., Schroth, M. N., & Isaka, M. (1981). Application of a rapid method for Gram differentiation of plant pathogenic and saprophytic bacteria without staining. *Phytopathology*, *72*(7), 917-918. https://doi.org/10.1094/Phyto-72-917

Takácsné Hájos, M. (2015). A termesztési mód és a bioaktív anyagok vizsgálatának eredményei különböző gyökérzöldség fajoknál [Results of cultivation methods and bioactive compounds in various root vegetables]. *Debreceni Szemle*, *1*, 20-29. https://epa.oszk.hu/04600/04620/00029/pdf/EPA04620_debreceni_szemle_2015_01_020-029.pdf

Zhu, X., Gao, G.-X., & Wang, X. (2011). Overview of studies on celery late blight disease. *China Vegetables*, *1*(14), 1-8.