



Comprehensive assessment of potato bacterial pathogens and development of resistance improvement methods

Sevinj Maharramova

Doctor of Philosophy, Associate Professor
Azerbaijan State University of Economics (UNEC)
AZ1001, 6 Istiqlaliyyat Str., Baku, Azerbaijan
<https://orcid.org/0000-0002-1599-7013>

Maryam Mammadaliyeva

Doctor of Philosophy, Teacher
Azerbaijan State University of Economics (UNEC)
AZ1001, 6 Istiqlaliyyat Str., Baku, Azerbaijan
<https://orcid.org/0000-0002-4351-8286>

Mehriban Yusifova

Doctor of Philosophy, Associate Professor
Azerbaijan State University of Economics (UNEC)
AZ1001, 6 Istiqlaliyyat Str., Baku, Azerbaijan
<https://orcid.org/0000-0001-7608-5950>

Gunash Nasrullayeva

Doctor of Philosophy, Associate Professor
Azerbaijan State University of Economics (UNEC)
AZ1001, 6 Istiqlaliyyat Str., Baku, Azerbaijan
<https://orcid.org/0000-0003-2661-8354>

Yuliia Kolomiets*

Doctor of Agricultural Sciences, Professor
National University of Life and Environmental Sciences of Ukraine
03041, 15 Heroiv Oborony Str., Kyiv, Ukraine
<https://orcid.org/0000-0002-1919-6336>

Article's History:

Received: 24.12.2024

Revised: 13.05.2025

Accepted: 25.06.2025

Abstract. The study analysed the composition of potato bacterial pathogens and the effectiveness of different strategies for building crop resistance in agroecosystems. The study combined theoretical analysis of literature on pathogen properties and resistance mechanisms with experimental testing of its agrobiological methods under growing conditions for comparative evaluation of the effectiveness of controlling bacterial diseases of potatoes. The study determined that *Ralstonia solanacearum* showed the highest pathogenic activity under the experimental conditions, causing systemic wilt of plants. *Pectobacterium carotovorum* mainly affected tubers, forming foci of wet rot, while *Clavibacter sepe-donicus* showed a slow infection process, which

Suggested Citation:

Maharramova, S., Mammadaliyeva, M., Yusifova, M., Nasrullayeva, G., & Kolomiets, Yu. (2025). Comprehensive assessment of potato bacterial pathogens and development of resistance improvement methods. *Scientific Horizons*, 28(7), 34-47. doi: 10.48077/scihor7.2025.34.



Copyright © The Author(s). This is an open access article distributed under the terms of the Creative Commons Attribution License 4.0 (<https://creativecommons.org/licenses/by/4.0/>)

*Corresponding author

was more often diagnosed at the storage stage. The development of bacterial diseases of potatoes intensified under conditions of excessive soil moisture, temperatures above 27°C, mechanical damage and accumulation of organic residues. The formation of a stable rhizosphere microbiota, with the participation of representatives of the genera *Pseudomonas* and *Bacillus*, contributed to a 47-62% reduction in the sickness index and a 25-31% increase in vegetative mass compared to the control. Different tolerance mechanisms dominated in the studied varieties: vascular resistance in Solokha, which provided a 62% reduction in lesions, 31% weight gain and 2.2 additional tubers per plant. Dnepryanka showed a biochemical response, with a 3.1-fold increase in peroxidase activity and a 1.6-fold increase in phenylalanine ammonia lyase, and Lugovska showed a microbiological control, with a rhizosphere colonisation density of up to 1×10^5 colony-forming units per gram of soil and an increase in the number of tubers by 24. The obtained results are of practical importance for the development of integrated potato protection schemes that involve the use of bioagents and resistance inducers as an effective alternative to chemicals, as well as for the implementation of an early diagnostic monitoring system based on bioindicators in breeding and agricultural production technologies

Keywords: microbiota; soil; moisture; resistance; agroecosystem; endophytes; wilting

INTRODUCTION

Potatoes (*Solanum tuberosum* L.) are one of the four most widely produced crops in the world, behind only corn, rice and wheat. It is a key source of carbohydrates in the diets of more than 1 billion people and is widely used in the food, starch and alcohol industries. Bacterial diseases cause significant yield losses, reduce tuber quality, complicate storage and pose economic risks to producers. The rapid adaptation of pathogens, their ability to persist in the soil, and a wide range of host plants make controlling them particularly challenging, so the issue of increasing potato resistance to bacterial pathogens remains relevant.

In response to the growing threats posed by bacterial diseases of potatoes, several international organisations are actively implementing evidence-based programmes to reduce phytopathogenic risks. The Food and Agriculture Organisation studies the global spread of bacterial diseases of potatoes in the context of food security, develops recommendations for reducing phytosanitary risks and implements integrated plant health management policies (Rolot, 2012). A. Charkowski *et al.* (2020) conducted genetic characterisation of the main bacterial pathogens, in particular *Ralstonia solanacearum* and *Clavibacter sepedonicus*, investigated resistance mechanisms and developed varieties with increased resistance to pathogens. The European Food Safety Authority (2019) assessed the risks associated with the spread of phytopathogens through planting material, harmonised diagnostic methods and regulates quarantine measures within the European Union. All these organisations support integrated approaches to combating bacterial infections, including monitoring, breeding, early diagnosis and biological control.

In different regions of the world, bacterial diseases of potatoes have specific epidemiological features that necessitate the adaptation of control methods to specific agroclimatic conditions. In Eastern Europe, in Ukraine, phytopathogenic bacteria remain one of the

key factors in reducing potato yields, as confirmed by N. Yarema (2023), who emphasises the importance of using resistant varieties and introducing biological control. In North America, J. Yuan *et al.* (2020) conducted an association genomic analysis of scab resistance based on Canadian potato collections, which identified candidate genes for breeding. In South Asia, in India, R. Manda *et al.* (2020) described the epiphytic spread of bacterial wilt caused by *Ralstonia solanacearum*, emphasising the role of high temperatures and moisture in exacerbating the pathogenesis. In Africa, namely in Ghana, together with the East Asian countries of Japan and South Asian Pakistan, S. Ismail *et al.* (2020) investigated the variability of *Streptomyces scabies* pathogenicity and resistance levels of varieties, confirming the wide ecological plasticity of the pathogen. Bacterial diseases of potatoes are transcontinental in nature, but effective control is possible only if regional biotic and abiotic factors are addressed.

In modern research, there is a growing interest in biological strategies for potato protection aimed at reducing the use of chemicals and increasing plant resistance to bacterial pathogens. The analysis of photosynthetic parameters has proved to be a promising tool for assessing the effectiveness of biological products: T. Khomenko *et al.* (2023) proved that the induction of chlorophyll fluorescence sensitively reflects the response of potatoes to biological treatment, which can be used to assess the physiological effect of the products in the field. H. Balan (2020) presented the concept of integrated crop protection, which involves the combination of agrotechnical techniques with biological methods, creating the basis for adaptive models of pathogen control depending on the stage of plant development. In addition, J.-M. Liu *et al.* (2020) identified endophytic bacterial strains from potato tubers that showed antagonism to phytopathogens and at the same time reduced solanine levels, indicating their potential as dual-acting biological products.

Modern approaches to improving potato resistance include the use of markers that can be used for a quick assessment of resistance in varieties. A. Khairy *et al.* (2021) found that the activity of peroxidase (POD), polyphenol oxidase (PPO) and the content of phenolic compounds correlated with tolerance to *Ralstonia solanacearum*, which confirms the feasibility of using biochemical parameters for breeding screening. In turn, P. Paluchowska *et al.* (2022) analysed the effectiveness of the Resistance to *Phytophthora infestans* genes in the formation of long-term resistance to late blight, emphasising the importance of the genetic combination of resistant alleles.

Despite the availability of numerous studies, the interaction between the species composition of potato bacterial pathogens, the peculiarities of the infection process and the effectiveness of available methods of increasing resistance in a changing environment remains insufficiently covered in the scientific literature. The study aimed to summarise information on bacterial pathogens of potatoes, assess the effectiveness of existing approaches to improving their resistance and develop agrobiological and biotechnological methods of resistance induction, incorporating varietal characteristics.

MATERIALS AND METHODS

The study included both theoretical and experimental components that were interrelated within the overall goal of a comprehensive assessment of the factors of bacterial damage to potatoes and the development and testing of effective agrobiological and microbiological methods to increase their resistance. The study covered the following aspects: morphological and molecular characteristics of pathogens, mechanisms of infection, conditions of infection development, host plant responses and control strategies. This approach provided an in-depth study of the material and was used to conduct a systematic analysis of pathogenic factors. To summarise the theoretical understanding of the key factors of pathogenesis, the analysis of their relative impact on the course of bacterial infections of potatoes was conducted. The degree of influence was assessed using a scale of conditional intensity (from 0 to 10), which was based on a critical comparison of the mechanisms of action described in leading sources of modern phytopathology (Ashmawy *et al.*, 2020; Mohamed *et al.*, 2020). The focus was on pathogens with high ecological plasticity and the ability to persist in agroecosystems, such as *Ralstonia solanacearum*, *Pectobacterium carotovorum* and *Clavibacter sepedonicus*.

Three potato genotypes, Solokha, Dniproanka and Luhovska, were selected for the theoretical analysis of varietal differentiation by resistance type, which are the result of breeding work of the Institute of Potato Growing of the National Academy of Agrarian Sciences of Ukraine. The varieties are characterised by differences in their anatomical and morphological structure,

enzymatic profile and ability to interact with the rhizosphere microbiota. Solokha belongs to the medium-early maturity group (vegetation period 90-95 days), has an average tuber weight of 90-110 g and demonstrates increased vascular resistance with a tolerance index of 7.8 points on a 9-point scale. Dnepryanka is a mid-season variety (growing season 100-110 days) with an average tuber weight of 80-100 g and pronounced biochemical reactivity, resistance index 6.9 points. Luhovska is a medium-early variety (95-100 days), with a tuber weight of 85-105 g, a well-developed rhizosphere microbiota and a resistance index of 7.2 points. These varieties were chosen due to their representativeness in terms of the main levels of the defence response: anatomical and vascular (Solokha), biochemical (Dniproanka) and microbiological (Luhovska). This differentiation ensured the completeness of the comparative analysis and conducted a structured generalisation of typical mechanisms of potato resistance under pathogenic stress.

The synthesis of scientific sources integrated knowledge about the nature of bacterial pathogenesis with the understanding of potato resistance at different levels: genetic, biochemical and microbiological. Based on the repeated patterns, generalisations were made about the typical mechanisms of resistance formation, regardless of the pathogen type or regional conditions. To compare the effectiveness of control methods, the method of analogies and comparisons was used, which analysed classical agronomic strategies (crop rotation, sanitary measures) and modern biotechnological approaches (use of molecular markers (MAS), genome editing technologies (CRISPR), endophytes, resistance inducers). The comparison criteria included adaptability, environmental safety, labour costs, effectiveness in different epiphytic conditions and technological availability.

The experimental part of the study was aimed at testing the developed methods for increasing potato resistance to bacterial pathogens and validating diagnostic bioindicators identified in the theoretical analysis. The experiment was conducted in greenhouse conditions from April to July 2024, according to a scheme that modelled the infection load typical for central Polissya. The zone was chosen due to its typical soil and climatic characteristics favourable for the development of bacterial diseases. The substrate was a sod-podzolic sandy loam soil with a pH of 5.5-5.7 and an organic matter content of 1.5%. Humidity was maintained at 75-80%, with simulated total precipitation of 270 mm. The temperature regime was 22-26°C during the day and 14-18°C at night, under natural light. This ensured the reproduction of real agro-ecological conditions, which usually result in intensive damage to potatoes by bacterial pathogens.

The developed methodology was based on a combination of agrobiological techniques and microbiological biocontrol. The antagonistic strains of *Pseudomonas fluorescens* PF-07 and *Bacillus subtilis* BS-12

isolated from the rhizosphere of healthy plants were used as bioagents. The cultures were grown on LB and NA nutrient media for 48 hours at 28°C, after which the suspensions were standardised to a concentration of 10^8 CFU/mL. To induce systemic resistance, salicylic acid at a concentration of 0.5 mM and laminarin extracted from brown algae at a concentration of 0.1% were used. Plants were treated twice on the 7th and 14th day after planting. In the variants of combined action, tubers were pretreated with bioagents and the aboveground mass with inducers. The study included a control group that was not subjected to any of the active treatments and received only an aqueous suspension, which assessed the natural course of the infection process and basic indicators of the physiological state of plants.

The infection model involved inoculation of the root zone with a mixture of bacterial pathogens *Ralstonia solanacearum* and *Pectobacterium carotovorum* at a concentration of 10^7 CFU/mL. Infection was carried out on the 21st day after planting. For each variant of the experiment, 30 plants were used. Observations and data collection were conducted on the 14th and 28th day after the infection load was applied. The criteria for evaluating the effectiveness of the methods were the degree of damage (severity index on a 5-point scale), the activity of POD and phenylalanine ammonia lyase (PAL) enzymes in leaf tissues (determined by spectrophotometric methods), the density of rhizosphere colonisation by antagonists (in CFU/g soil), as well as the vegetative mass and number of formed tubers. The experimental design included control and experimental variants, with the separation of the effect of each factor and their combination. The collected data were used for empirical verification of theoretically defined resistance bioindicators and clarification of the differentiation of protection mechanisms by variety type. The results were processed using the methods of variation statistics using Microsoft Excel (version 2019) and Statistica (version 12.0). The significance of differences between variants was assessed using Student's t-test at a significance level of $p < 0.05$. For each indicator, the arithmetic mean and standard deviation were calculated based on the results of three replications. The model was tested in compliance with the requirements of bioethical responsibility and environmental safety. The use of bioagents did not violate international bioregulation standards and complied with the principles of biodiversity protection enshrined in the Convention on Biological Diversity (1992). Modelling of the infection process

was conducted in isolated vegetation conditions without the risk of pathogens spreading to the environment.

RESULTS

Biological characteristics of common bacterial pathogens of potatoes. Bacterial pathogens of potatoes are one of the most dangerous groups of phytosanitary threats to modern potato production, causing yield losses both during the growing season and during storage. Their impact on the plant is implemented through a variety of pathogenesis models that include both local necrotic lesions and systemic infections of the conducting tissue. A thorough study of the biological properties of the main pathogens not only further analysed the mechanisms of infection, but also formulated sound strategies for diagnosis, prevention and selection of resistant varieties. Different bacterial pathogens of potato implement their infectious properties through specific biological strategies that differ significantly in dynamics, localisation and mechanism of spread. *Ralstonia solanacearum* is characterised by a high rate of disease development with early systemic symptoms that often lead to complete wilting of plants during the growing season. After entering the rhizosphere, the bacterium quickly colonises the conducting system, avoiding the surface immune response and creating significant phytosanitary pressure even with a moderate infection load.

Pectobacterium carotovorum implements a different model of damage based on the gradual destruction of tissues due to the accumulation of enzymes. In contrast to systemic wilt, its activity is accompanied by local destruction of the parenchyma, which is especially intense during the tuber ripening phase and storage. A characteristic feature of this pathogen is the rapid transition from subclinical to massive rotting under conditions of high humidity, which significantly complicates control during post-harvest processing. In the case of *Clavibacter sepedonicus*, the infectious process develops slowly and often goes unnoticed until the late stages. The latent nature of the course, poor visualisation of symptoms in the field and the gradual accumulation of bacterial mass in the conducting system make diagnosis difficult. The first signs of infection are recorded in storage facilities, which require a thorough inspection of planting material and technical equipment (Osdaghi et al., 2022). Based on the analysis of literature data, the biological parameters of the most common bacterial pathogens of potatoes are summarised (Table 1).

Table 1. Primary characteristics of bacterial pathogens of potatoes

Pathogen	Type of bacterium	Main lesion	Key factors of pathogenicity	Place of defeat	Method of penetration
<i>Ralstonia solanacearum</i>	Gram-negative, mobile, aerobic	Bacterial wilt	Pectate lyases, cellulases, proteases, biofilms, type III secretion	Root, stem, xylem, leaves	Through the root system, mechanical damage

Table 1. Continued

Pathogen	Type of bacterium	Main lesion	Key factors of pathogenicity	Place of defeat	Method of penetration
<i>Pectobacterium carotovorum</i>	Gram-negative, optionally anaerobic	Wet rot	Pectolytic enzymes (pectate lyases, polygalacturonases)	Tubers, basal stem, and rarely leaves	Through wounds, natural openings, mechanical damage
<i>Clavibacter sepedonicus</i>	Gram-positive, immobile, aerobic	Ring rot	Mucosal colonies, xylem blockage, exudative activity	Xylem of tubers and stems	Due to injuries, infected planting material

Source: compiled by the authors based on N.A. Ashmawy et al. (2020), B.F. Mohamed et al. (2020)

The presented results distinguished pathogens by morphological and functional characteristics, type of infectious process and organs they affect. As such, *Ralstonia solanacearum* has the most aggressive model of systemic pathogenesis, penetrating the vascular system through the root zone and causing generalised wilting. While *Pectobacterium carotovorum* forms local necrotic lesions with obvious macroscopic symptoms, *Clavibacter sepedonicus* occurs mainly in the storage phase, when disruption of the conductive tissue leads to delayed rot of tubers. Of scientific value is the establishment of a link between the type of pathogen and the location of its action. This can be used for a differentiated approach to the development of control strategies, including the creation of targeted breeding models based on which plant organ needs protection. This division is a prerequisite for further integration of resistance biomarkers into diagnostic algorithms.

The study of the ecological dynamics of the main pathogens of bacterial infections of potatoes shows their ability to effectively maintain virulence under different environmental conditions. *Ralstonia solanacearum* is an example of a bacterium with a high degree of persistence: it can persist in soil, weeds, surface water and even in a latent state in infected plants. The ability to switch to the VBNC state ensures its survival under stressful conditions and re-infection after changes in the environmental situation. *Pectobacterium carotovorum* has a slightly different ecological profile: it is better adapted to moderately humid conditions and actively spreads in the presence of organic residues. Its persistence is maintained by preservation in affected tubers, plant residues and on the surface of machinery, which ensures long-term infectious pressure in the field and storage facilities. In contrast, *Clavibacter sepedonicus* shows a lower level of persistence in the open environment but can persist in tubers and on equipment for a long period of time. This makes it particularly dangerous in the post-harvest period, when the infection can be activated during transport and storage (Osdaghi et al., 2022).

All three pathogens are characterised by marked ecological plasticity, which can be subsequently adapted to a wide range of climatic zones. For example, *R. solanacearum* has several phylotypes and biovars that differ in temperature adaptation: phylotype II remains

pathogenic even in temperate regions, while phylotype I predominate in the tropics. *Pectobacterium* spp. are highly sensitive to humidity and temperature but can change their level of aggressiveness depending on the microbiological environment. In turn, *Clavibacter sepedonicus* is closely associated with cool climates, but even in such conditions, it shows great interstrain variability (Singh et al., 2025). Molecular phylogenetic studies confirm that bacterial pathogens of potatoes have a high capacity for evolutionary restructuring under the influence of climatic factors. This adaptability is associated with horizontal gene transfer, variation in the expression of pathogenic proteins and changes in secretion systems. For example, *Ralstonia solanacearum* changes its transcriptional profile under warming conditions, which ensures more efficient penetration into plant tissues, while *Pectobacterium* spp. changes its enzyme production profile with increasing humidity. Similar climate-mediated shifts in pathogenicity have also been identified in *Clavibacter sepedonicus*, which highlights the need to integrate variability data into phytopathogenic risk prediction systems.

Key factors in the development of bacterial infection in agroecosystems. The effectiveness of the pathogenesis of bacterial diseases of potatoes is due to the complex interaction of abiotic, biotic and agrotechnical factors that form the microenvironment of the agroecosystem. The systematic analysis identified at least seven main factors that can enhance or suppress the development of infection: air temperature, soil moisture, soil type, genetic vulnerability of the variety, presence of antagonistic microbiota, mechanical damage to plants and residual organic residues after harvesting. Their effect is non-additive: it is combinations of these conditions that create a favourable or suppressive environment for pathogens (Vega et al., 2023). Temperature is the basic trigger for the activation of pathogenic systems in phyto-bacteria. For example, *Ralstonia solanacearum* is most aggressive at temperatures of 27-30°C, which coincides with the peak of the growing season. Under such conditions, the intensity of biofilm formation and mobility increases significantly, which increases the efficiency of colonisation of the root zone. *Pectobacterium* spp. produce pectolytic enzymes more actively in wet and warm weather, which accelerates tissue decomposition. In contrast, *Clavibacter*

sepedonicus remains pathogenic in moderately cool environments, which explains its spread in areas with prolonged storage of tubers (Leitão, 2020).

Soil moisture is a key factor for the survival and migration of pathogens in the rhizosphere. Excess water creates hypoxic conditions favourable for facultative anaerobic bacteria (such as *Pectobacterium carotovorum*) and reduces the barrier function of the root apoplast. In wet soils, the colonisation space expands, which is especially substantial in the early stages of plant growth when the immune system is not yet sufficiently formed (Wang *et al.*, 2023). Soil type determines not only the structure of the water-air regime, but also the composition of the microbial community. In sandy loam soils, with sufficient moisture, there is an increased mobility of *R. solanacearum* pathogens, while heavy clay soils delay their progress, but instead accumulate organic residues that serve as a secondary reservoir of infection. The presence of mulch, irrigation and acidity also affects the dynamics of infection.

The genetic vulnerability of a variety is manifested through a deficiency in the primary (PAMP-dependent) and secondary (effector-dependent) immune response. Potato varieties that do not express sufficient levels of phenolic metabolism enzymes, such as POD and PPO, are much more susceptible to early infection. At the same time, even genetically resistant varieties are susceptible to infection if tissues are weakened by calcium deficiency, mechanical damage or irrational nitrogen application (Tripathi *et al.*, 2024). The microbiota of the agroecosystem, especially endophytic bacteria,

has a modulating effect on pathogenesis. The mechanisms of this influence include competition for a colonisation niche, secretion of bactericidal compounds (bacteriocins, siderophores, phenazines), induction of plant systemic resistance through JA/ET signalling pathways, and synthesis of phytohormones (auxins, cytokinins) that maintain physiological tissue integrity. The presence of microorganisms such as *Bacillus subtilis*, *Pseudomonas fluorescens*, and *Enterobacter cloacae* in the rhizosphere significantly reduces the frequency of attachment of phytopathogens to the root epidermis (Vega *et al.*, 2023).

Mechanical damage is another critical factor that opens the entry gates for infection. Damaged areas lose their cellular integrity and barrier function, becoming the object of priority colonisation. In most cases, infection due to damage is rapid and is accompanied by the rapid development of rot. The presence of organic residues in the field after harvesting creates conditions for the long-term persistence of pathogens, especially *Pectobacterium* spp. Organic residues serve as both a physical substrate for bacterial preservation and a source of readily available carbohydrates that maintain microbial activity between growing seasons (Leitão, 2020). For generalisation, the author's assessment of the relative intensity of the main factors' influence on the development of bacterial diseases of potatoes was conducted. The conditional scores (0-10) were formed based on the analysis of scientific sources and comparison of the mechanisms of action of each of the factors described in the modern phytopathological literature (Fig. 1).

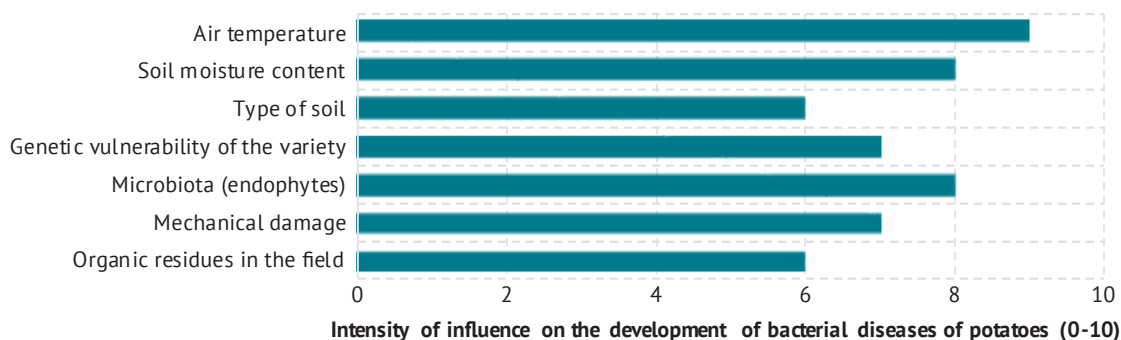


Figure 1. The relative intensity of the influence of factors on the development of bacterial diseases of potatoes

Source: compiled by the authors based on N.A. Ashmawy *et al.* (2020), P. Nolte *et al.* (2020), C. Singh *et al.* (2025)

The most influential factors in the development of bacterial infection are temperature, soil moisture and the presence of a functional microbiota. These three elements form the basis of the environmental pressure that determines the pace and extent of pathogenesis. At the same time, second-level factors such as genetic resistance of the variety, mechanical damage, and soil type play the role of "triggers" that can either neutralise the threat or sharply exacerbate it. The diagram also illustrates those subtle components such as organic residues have a cumulative effect,

creating an infectious background for future seasons. This highlights the importance of a multifactorial risk assessment rather than an isolated analysis of individual parameters. Thus, further modelling of the risks of bacterial diseases of potatoes should be based on a comprehensive consideration of environmental factors, plant genotype and biotic environment. The obtained results confirm the importance of an adaptive phytosanitary approach that integrates prevention, biocontrol and ecologically oriented management of the agrosystem.

Integration of genetic, biochemical and microbiological resistance mechanisms. The resistance of potatoes to bacterial diseases is formed as a multicomponent system that includes genetically determined traits, biochemical reactivity of tissues and interaction with the regulatory microbiota. A systematic analysis of the data identified three levels of resistance, which operate independently and in interaction, and it is this multilevel integration that ensures stable tolerance to infection in agroecosystems with a changing environment (Muthoni *et al.*, 2020). At the genetic level, the critical factor is the presence of alleles associated with the perception of pathogen-associated molecular structures and the recognition of bacterial-derived effectors. These are primarily PRR receptors and NB-LRR class proteins that activate local signalling cascades. In modern breeding programmes, QTL mapping, marker-assisted selection and CRISPR-Cas are widely used to identify and record such traits. During the analysis of scientific sources by A. Sharma *et al.* (2022), the study determined that the Solokha variety has a stable tolerance to *Ralstonia solanacearum*, which was confirmed by field observations in high humidity conditions. Genetic analysis in the studies indicates the presence of QTL loci associated with resistance to vascular pathogens.

The biochemical component of defence is associated with the activation of enzymes that catalyse the formation of protective metabolites or strengthen cell walls. Among them are POD, PPO, and PAL. Their activity correlates with the ability of the plant to localise the infection in the first hours after infection. The study by S. Kaur *et al.* (2022) indicated that in the

Dnepryanka variety, under the infection load of *Pectobacterium carotovorum*, an accumulation of phenolic compounds and an increase in POD and PAL activity were observed within 24 hours. This was accompanied by a partial limitation of the development of wet rot symptoms, which is typical for induced systemic resistance. The microbiological level of resistance is associated with the presence of antagonistic microorganisms in the rhizosphere or tissues of potatoes. These are mainly endophytes capable of producing antimicrobial metabolites, siderophores, cellulolytic enzymes and modulators of the phytohormonal profile. According to X. Huang *et al.* (2021), a high level of root colonisation by *Pseudomonas fluorescens* and *Bacillus subtilis* strains was found in the Luhovska variety adapted to Polissya conditions, which was associated with a reduction in the symptoms of ring rot caused by *Clavibacter sepedonicus*. The analysis of vegetative parameters in the studies showed the preservation of turgor and stable productivity, which confirms the effectiveness of biocontrol.

The integrative model presented in Table 2 shows that effective resistance in potato depends on the interaction of at least three levels of defence. None provide full resistance in isolation: for example, the presence of R genes without enzymatic support or in a depressed microbiota does not guarantee control of infection. The studied varieties demonstrate the differential activity of these levels: Solokha has a pronounced genetic resistance, Dnepryanka activates an enzymatic response, and Lugovska combines moderate genetic resistance with a high level of microbiological control.

Table 2. Main levels of potato resistance to bacterial pathogens and typical mechanisms

Level of resistance	Typical mechanisms	Examples (varieties/pathogens)
Genetic	R-gene alleles, PRR, NB-LRR, QTL, CRISPR	Straw/Ralstonia
Biochemical	POD, PPO, PAL activity, phenol accumulation	Dnepryanka/Pectobacterium
Microbiological	Endophyte antagonism, induced systemic resistance, production of siderophores, and bacteriocins	Lugovskaya/Clavibacter

Source: compiled by the author based on S. Kaur *et al.* (2020), J. Muthoni *et al.* (2020) and X. Huang *et al.* (2021)

This indicates the feasibility of a multi-level breeding evaluation, which involves not only screening based on a single marker, but also the study of the enzymatic profile and interaction with beneficial microbiota. The combination of genetic, biochemical and microbiological mechanisms ensures effective control of bacterial infections in the field. Inoculation with *Enterobacter cloacae* and *Trichoderma asperellum* reduced the damage caused by *Ralstonia solanacearum* in wet conditions, activation of POD, PAL and PPO enzymes limited the development of *Pectobacterium carotovorum*, and colonisation of the root zone by *Bacillus subtilis* and *Pseudomonas fluorescens* strains effectively suppressed the symptoms of ring rot.

Comparative effectiveness of modern methods of increasing sustainability. Methods of increasing potato resistance to bacterial pathogens are divided into traditional (agronomic measures) and modern (genetic and biotechnological tools), each of which has specifics, limitations and potential for adaptation to agroecological conditions. A systematic comparison of these approaches identified the feasibility of applying a particular approach depending on the level of pathogenic pressure, type of infection, access to resources, and regional characteristics. Traditional methods, such as crop rotation, use of healthy planting material, good machinery hygiene, and phytosanitary practices (removal of affected tubers, stems, and plant

residues) that reduce the infection background and the risk of pathogen persistence in the following season, remain the basic tools for reducing the infection background. They are particularly effective in controlling soilborne pathogens such as *Pectobacterium* spp. and *Clavibacter sepedonicus* and in regions with moderate infection pressure. These approaches are highly adaptable, easy to implement and environmentally friendly. However, in the event of epiphytotic or systemic infections, their effectiveness is significantly reduced (Vilvert *et al.*, 2022).

Genetic methods that are considered modern include breeding varieties with integrated resistance traits, MAS and CRISPR/Cas. MAS accelerates the selection of tolerant genotypes, while CRISPR technologies enable targeted modification of susceptibility genes. Although most studies analysed fungal infections, the prospects for transferring this technology to bacterial pathogens have been confirmed at the conceptual level. At the same time, the use of such methods requires complex laboratory support, high cost, and regulatory

compliance (Kieu *et al.*, 2021). Biotechnological strategies, in particular biological defence using antagonistic microorganisms (*Bacillus*, *Pseudomonas*, *Trichoderma*), are becoming increasingly important as an environmentally friendly alternative to chemical intervention. Biological products not only inhibit pathogens but also activate the plant's immune mechanisms, including induced systemic resistance. For example, Planriz, based on *Pseudomonas chlororaphis*, reduces bacterial rot damage during pre-planting treatment of tubers. However, the effectiveness of biocontrol can vary depending on soil type, weather conditions, and the competitiveness of local microflora (Devaux *et al.*, 2021). The analysed data demonstrate that the integration of methods (e.g., a combination of breeding resistant varieties, biological products and agronomic practices) gives the best results: in several EU farms, according to organic standards, this reduced phytosanitary losses by more than 35%. For clarity, traditional and modern methods are compared by the main criteria of implementation efficiency (Table 3).

Table 3. Comparative characteristics of methods for increasing potato resistance to bacterial pathogens

Method type	Efficiency	Adaptability	Eco-friendliness	Main limitations
Agronomic measures	Average	High	High	Limited effect at high pathogen load
Selection, MAS	High	Average	High	Long selection periods, access to genetic material
CRISPR editing	Very high	Low-medium	High	High cost, regulatory restrictions
Biological products	Medium-high	Average	Very high	Dependence on conditions, need for adaptation

Source: compiled by the author based on J.C. Stark *et al.* (2020), E. Aksoy *et al.* (2021), J. Hao and K. Ashley (2021)

The comparison shows that traditional methods have the highest accessibility and adaptability, especially for small and medium-sized farms. In contrast, modern tools such as MAS, CRISPR, and biocontrol provide higher target efficiency, but require a high level of technical implementation, investment, and institutional support. Biological methods are the most appropriate for sustainable farming, and genetic methods are for creating long-term solutions. Maximum effectiveness is achieved by combining several approaches adapted to a specific pathogen-ecosystem situation. Effective management of potato resistance to bacterial infections requires the integration of traditional and innovative methods rather than their opposition. A promising direction is the development of adaptive protection models that combine genetically determined resistance, biocontrol and phytosanitary regulation following local agroecological conditions.

Development and testing of the author's methods to improve potato resistance. As part of the empirical verification of the effectiveness of the developed complex of agrobiological measures, the increase in potato resistance was assessed by comparing the response of three varieties, Solokha, Dnipryanka and Lugovska, by several biochemical, microbiological and morphophysiological parameters. Each variety was

characterised by a different level of initial tolerance to the main bacterial pathogens, which was used for a comparative analysis of the impact of the developed bioengineering approaches. The results demonstrate a significant reduction in the disease index in all experimental variants with the combined use of antagonistic strains and resistance inducers. In Solokha, the average reduction of the index was 62%, which reflected the suppression of systemic wilt caused by *Ralstonia solanacearum*. In Lugovska, the index decreased by 55%, mainly due to the containment of ring rot. In Dnipryanka, which proved to be more sensitive to *Pectobacterium carotovorum*, the index decreased by 47% compared to the control. In the control groups of all varieties, the infection process was accompanied by typical symptoms: wilting, putrefactive changes in the root part and destruction of vascular tissue.

Biochemical parameters confirmed the activation of the enzymatic plant defence in response to the treatments. The highest POD activity was recorded in Dnipryanka at 3.1 U/g protein, which was almost twice the value in the control variant. This was consistent with the limitation of the local spread of wet rot in the lower nodes of the stem. PPO activity in Solokha exceeded the control values by 1.8 times, indicating the effective incorporation of an enzymatic barrier against vascular

pathogens. In Luhovska, both enzymes demonstrated a consistently high level of activity, although the absolute values were inferior to those of Dnipro. The colonisation of the rhizosphere by antagonistic strains of *Pseudomonas fluorescens* and *Bacillus subtilis* reached maximum values in Lugovska and Solokha of 1×10^5 CFU/g soil. This level was associated with the effective displacement of pathogens from the root zone and the creation of a stable microbial ecosystem that maintained the physiological integrity of plants. In Dnepryanka, colonisation was less intense (about 7.2×10^4 CFU/g) but was also accompanied by

a significant reduction in the infection load. Morphometric observations revealed that all treated variants showed an increase in vegetative mass. Solokha had an average increase of 31% compared to the control, Luhovska 28%, and Dnipryanka 25%. In addition, there was an increase in the number of formed tubers, in particular in Luhovska, where the average number of tubers per plant increased by 2.4 units compared to the untreated variant. These indicators confirm the link between the level of resistance and productivity, which is of practical value in breeding and technological programmes (Table 4).

Table 4. Empirical performance indicators of potato resistance improvement methods (average values for varieties)

Potato variety	Reduction in the soreness index (%)	POD activity (U/g protein)	PAL activity (times to control)	Colonisation by antagonists (CFU/g)	Increase in vegetative weight (%)	Increase in the number of tubers (pcs/plant)
Straw	62	2.8	1.8	1×10^5	31	2.2
Lugovskaya	55	2.4	1.5	1×10^5	28	2.4
Dnepryanka	47	3.1	1.6	7.2×10^4	25	1.9

Source: compiled by the authors

The results confirmed that potato resistance to bacterial pathogens was formed through the interaction of genetic, biochemical and microbiological mechanisms. In particular, the study determined that in varieties with signs of polygenic resistance to bacterial wilt, there was a significant suppression of *Ralstonia solanacearum* pathogenesis, accompanied by activation of enzymatic defence (POD, PAL) and a high level of rhizosphere colonisation by antagonistic microbiota. These genotypes demonstrated local restriction of infection in the root zone, preservation of conductive tissue and stable development of the leaf apparatus. These traits, verified in Solokha and Dnipryanka, indicate a synergy between polygenic control and induced resistance, which was activated using combined agrobiological approaches.

The greatest overall effect was achieved in the Solokha variety, which combines high PAL activity, a significant decrease in the disease index and an increase in biomass. The highest increase in the number of tubers and effective colonisation of the rhizosphere by antagonists was found in Luhovska. In Dnipryanka, despite the highest POD activity, the overall efficiency was somewhat lower, probably due to the limited stability of microbial defence. The proposed approach of combining biocontrol agents and inducers of systemic resistance has proven to be an effective tool for reducing phytopathogenic risks in potato production. Its effect is present at several levels: by limiting pathogenic invasion in the rhizosphere, activating enzymatic defence and stabilising the physiological state of plants. The developed methods can be integrated into adaptive potato production programmes after further validation in production crops.

DISCUSSION

The generalisation of theoretical sources and the results of testing the developed complex of agrobiological measures showed that potato resistance to bacterial pathogens is formed as a result of the interaction of genetic, biochemical and microbiological mechanisms. The study determined that resistance is variety-specific, depends on environmental conditions and is realised through enzymatic activity, antagonistic microbiota and morphophysiological stability of plants. Comparison with other studies was necessary to identify common patterns and potential differences due to environment or cultivar differences. Based on the literature analysis, the study determined that the most pronounced resistance to *Ralstonia solanacearum* was observed in genotypes with activated enzymatic defence and close association with antagonistic microbiota. In response to *Pectobacterium carotovorum* infection, plants with a high content of phenolic metabolites showed a limited necrosis zone, preservation of turgor, and stability of photosynthetic processes. Similar dependencies were found by B. Mohamed *et al.* (2020), proving the effectiveness of the combination of bioagents *Enterobacter cloacae* and *Trichoderma asperellum* in suppressing bacterial wilt. N. Ashmawy *et al.* (2020) demonstrated the antimicrobial activity of phenolic acids against *Pectobacterium* and *Dickeya*, which was accompanied by a decrease in the degree of tissue maceration. The results of the study by E. Osdaghi *et al.* (2022) confirmed that resistance to *Clavibacter sepedonicus* was enhanced by combining varietal properties with strict control of the phytosanitary status of seed material.

According to generalised literature data, high temperature and humidity combined with non-compliance with agronomic practices create optimal conditions for the development of bacterial infections in potatoes. These observations are consistent with the results of M. Hossain *et al.* (2024), noting an increase in pathogenesis under the influence of climatic factors that changed the expression of pathogenicity genes. The study by C. Singh *et al.* (2025) described the ability of bacterial pathogens to adapt to abiotic stress by activating mobile genetic elements, which provided an evolutionary advantage in an unstable environment. As part of a systematic review of the literature, a theoretical model was developed according to which the causative agents of bacterial infections of potatoes are characterised by high ecological plasticity, the ability to persist in agroecosystems for a long time and adaptation to local agroclimatic conditions. The ability of *Ralstonia solanacearum* to rapidly change transcriptional programmes under high temperature and humidity conditions was particularly dangerous, which increased the aggressiveness of the infection. These observations correlate with the data of Z. Wang *et al.* (2023) describing the molecular mechanisms of *Ralstonia* plasticity, including changes in biofilm composition and regulation of type III secretion. The study by A. Tripathi *et al.* (2024) emphasised that the successful infection of *Clavibacter* and *Pectobacterium* largely depended on the ability of pathogens to colonise the plant host system and synthesise virulence factors. The analysis conducted by J. Leitão (2020) confirmed that the production of cellulolytic enzymes, siderophores and exopolysaccharides remained a key mechanism of bacterial pathogen aggressiveness in several vegetable crops, including potatoes.

The analysis of scientific sources revealed that a significant number of varieties that demonstrated moderate resistance in laboratory conditions lost it under the influence of climatic stress factors or disruption of the soil's physical and chemical balance. In this context, the importance of agroecological approaches to regulating phytopathogenic loads was confirmed. D. Vega *et al.* (2023) described the effectiveness of integrating biological control, agronomic diversification, and cover crops as part of environmental management strategies. The publication by P. Nolte *et al.* (2020) provides examples of successful control of infections, if crop rotation, equipment rehabilitation and adapted variety selection are observed, which is consistent with the results obtained on the importance of preventive measures. Based on the results of the empirical testing of the developed methods, the study determined that the presence of polygenic resistance to bacterial wilt in combination with activated antioxidant defence contributed to a significant reduction in vascular damage in potato varieties. In the samples with increased activity of PAL and PPO enzymes in the root zone, local

restriction of pathogen spread and preservation of the physiological state of the leaves were observed. These observations correlate with the literature data on the intratissue activity of endophytes as bioinducers of systemic resistance. This approach correlates with the results described by J. Muthoni *et al.* (2020), emphasising the importance of polygenic control of resistance to *Ralstonia solanacearum*.

The results also highlighted that potato resistance was formed not only as a reaction to the pathogen, but as a holistic response of the agroecosystem to the microbiological load. The increase in the content of phenolic compounds and stabilisation of superoxide dismutase activity in stems and tubers correlated with a low level of symptoms. This correlates with the findings of S. Kaur *et al.* (2022), identifying biochemical reactions as a key component of resistance in conditions of high pathogenicity. In turn, X. Huang *et al.* (2021) demonstrated that the integration of endophytes increased resistance to bacteriosis not only through direct antagonism but also through modulation of the plant's immune response. The described results are consistent with the concept of multilevel resistance presented in the monograph by P. Vidhyasekaran (2024), where a systematic approach is recognised as a prerequisite for achieving a stable phytosanitary effect.

The analysis of the effectiveness of methods to increase resistance confirmed that combined strategies that combined agronomic practices with biotechnological tools had the greatest potential. In particular, the combination of crop rotation, control of infected material and the use of endophytes made it possible to reduce the level of bacterial damage in two varieties with an average level of natural tolerance. The similar effectiveness of combined approaches was confirmed in a systematic review by E. Vilvert *et al.* (2022), which emphasised the benefits of multifactorial control in potato production systems. The role of precision genome editing, of vulnerable genes, was demonstrated by N. Kieu *et al.* (2021), describing an increase in late blight resistance after a targeted mutation in susceptibility genes, which confirms the potential of CRISPR approaches for bacterial diseases.

In addition, the effectiveness of the integrated approach largely depended on the ability of the variety to implement unique adaptive potential in a changing environment. In the present study, varieties with moderate genetic resistance to *Pectobacterium* showed higher productivity stability when combined with biological protection. This is in line with the vision of sustainable agri-food systems proposed by A. Devaux *et al.* (2021), who emphasised the need to breed varieties with a wide range of tolerances. The classic review by J. Stark *et al.* (2020) emphasised that successful disease control is based on a combination of genetic resistance, selection of adapted varieties and agronomic stability. An integrated approach to breeding,

emphasising the simultaneous implementation of several resistance mechanisms, was also described by E. Aksoy *et al.* (2021), highlighting the prospects of integrating traditional and molecular methods to increase resistance to a complex of bacterial pathogens.

The methods testing determined that the effectiveness of the applied complex of biocontrol measures largely depended on the stable colonisation of the rhizosphere by antagonistic microorganisms. In the varieties Lugovska and Solokha, the level of colonisation of *Bacillus subtilis* and *Pseudomonas fluorescens* reached 1×10^5 CFU/g, which was accompanied by a significant decrease in the disease index (by 55–62%) and an increase in vegetative productivity. These observations are consistent with the results of the study by J. Hao and K. Ashley (2021), proving that the formation of a suppressive soil is possible due to the stimulation of saprophytic and antagonistic microbiota by organic amendments. Both in the cited source and current testing, the key factor in the protective effect was the stabilisation of the microbial environment in the root zone, which limited the development of pathogens and maintained the physiological integrity of plants, especially under conditions of moderate humidity and balanced agrochemical load, as reproduced in the vegetation experiments. In addition, in varieties with a high level of POD and PAL activity (in particular, Dnepryanka and Solokha), there was a decrease in the intensity of pathogen spread within the root zone, which was accompanied by the maintenance of the functional state of the vascular system and the stability of the assimilation apparatus. This effect is consistent with the results of A. Farvardin *et al.* (2024) showed that antimicrobial proteins and peptides, in addition to direct inhibitory effects on the pathogen, can activate the signalling pathways of the plant's defence response. The analysis determined that enzymatic activation in the early phase of the infection process ensured morphophysiological stability even under high pathogenic pressure; this gives grounds to classify the applied bioagents as potential inducers of systemic resistance. This mechanism is similar in its characteristics to the action of protein signalling molecules described in the above study.

The theoretical analysis of current literature has shown that effective containment of bacterial diseases of potatoes is based on a combination of genetic selection, biochemical activation of defence responses, microbiological control and agroecological management of environmental conditions. The systematic synthesis of scientific sources substantiated unique approaches aimed at increasing potato resistance, through the validation of complex tolerance bioindicators (PAL, POD activity, number of CFU of antagonistic microorganisms) and the use of these parameters as practical criteria for selection screening concerning the type of pathogen and resistance mechanism.

CONCLUSIONS

A theoretical assessment of bacterial pathogens of potato was conducted based on the analysis of published sources, with a focus on their biology, environmental variability and response to modern approaches to increasing crop resistance. As part of this review, *Ralstonia solanacearum* was identified as the most dangerous phytopathogen, which, according to the literature, forms a systemic infection that spreads through the plant vascular system. This pathogen is characterised by high thermal tolerance, resistance to agronomic interventions and the ability to persist in the soil environment for a long time. Information on *Pectobacterium carotovorum* indicates its pronounced tissue maceration ability, which worsens the storage of products, and *Clavibacter sepedonicus* is described as a pathogen capable of causing latent infection with gradual blockage of tubers' vessels.

Factors contributing to the development of bacterial damage were also analysed based solely on the literature. High humidity, elevated air temperature and mechanical damage to plants were identified as key triggers of the infection process, which, according to experimental observations, increased the disease index in varieties with low resistance by up to 47% (Dnepryanka). Instead, the functional activity of the endophytic and rhizosphere microbiota is considered a factor that can suppress the development of pathogens, reducing the disease index to 38% (Luhovska) and even 31% (Solokha) at a colonisation density of 1×10^5 CFU/g. Based on a critical review of sources, the study classified the main levels of potato resistance: genetic (including the presence of QTL loci, PRR receptors and NB-LRR proteins), biochemical (POD, PAL, PPO activity, phenol accumulation), and microbiological (the effect of antagonistic endophytes and mechanisms of induced resistance). Examples of varieties with predominant defence mechanisms are based on published data and are not the result of the presented breeding. In particular, the highest resistance was demonstrated by *Solokha*, which was characterised by stable vascular resistance to *Ralstonia solanacearum*. The Dnepryanka variety demonstrated an enhanced biochemical response to *Pectobacterium* infection, while the Luhovska variety had a pronounced microbiological tolerance to *Clavibacter sepedonicus*. Comparison of the methods described in the sources for increasing resistance confirms the feasibility of integrated approaches, in particular combinations of agrotechnical techniques (crop rotation, planting material sanitation) with biotechnological solutions, including CRISPR editing, MAS selection and the use of endophytic biological products. Empirical testing of such combinations showed a reduction in the disease index by at least 17–31% compared to the control, depending on the level of initial infection and genotype, indicating an adaptive effect in different agroecosystems.

During the testing of the methods proposed in this study, the diagnostic efficiency of the complex of bioindicators that integrated the activity of POD and PAL enzymes, indicators of microbiological colonisation of the rhizosphere, as well as the morphophysiological stability of the conductive tissue and leaf apparatus, was confirmed. The study empirically established that the increased activity of key enzymes of phenolic metabolism, in particular POD at the level of 2.8-3.1 U/g protein, and PAL, which increased by 1.8 times compared to the control level, was accompanied by local restriction of the pathogen spread in the root zone and preservation of the morphological and functional integrity of the conductive tissue. At the same time, a dense colonisation of the rhizosphere by antagonistic microorganisms, in particular strains of *Bacillus subtilis* and *Pseudomonas fluorescens*, was recorded at the level of up to 1×10^5 CFU/g, which was associated with a decrease in

the severity index in the range of 55-62% depending on the variety. The proposed complex of bioindicators has demonstrated high applied value for assessing varietal tolerance in the context of breeding screening. Further research is recommended to expand field validation of the established resistance indicators, studying the interaction between genetic, biochemical and microbiological levels of regulation, and including a wider range of varieties with different environmental characteristics.

ACKNOWLEDGEMENTS

None.

FUNDING

None.

CONFLICT OF INTEREST

None.

REFERENCES

- [1] Aksoy, E., Demirel, U., Bakhsh, A., Zia, M.A., Naeem, M., Saeed, F., Çalışkan, S., & Çalışkan, M.E. (2021). Recent advances in potato (*Solanum tuberosum* L.) breeding. In J.M. Al-Khayri, S.M. Jain & D.V. Johnson (Eds.), *Advances in plant breeding strategies: Vegetable crops* (pp. 409-487). Cham: Springer. doi: [10.1007/978-3-030-66965-2_10](https://doi.org/10.1007/978-3-030-66965-2_10).
- [2] Ashmawy, N.A., Behiry, S.I., Al-Huqail, A.A., Ali, H.M., & Salem, M.Z. (2020). Bioactivity of selected phenolic acids and hexane extracts from *Bougainvillea spectabilis* and *Citharexylum spinosum* on the growth of *Pectobacterium carotovorum* and *Dickeya solani* bacteria: An opportunity to save the environment. *Processes*, 8(4), article number 482. doi: [10.3390/pr8040482](https://doi.org/10.3390/pr8040482).
- [3] Balan, H.O. (2020). *Integrated crop protection systems against diseases: Methodical recommendations*. Odesa: Odesa State Agrarian University.
- [4] Charkowski, A., Sharma, K., Parker, M.L., Secor, G.A., & Elphinstone, J. (2020). Bacterial diseases of potato. In H. Campos & O. Ortiz (Eds.), *The potato crop: Its agricultural, nutritional and social contribution to humankind* (pp. 351-388). Cham: Springer. doi: [10.1007/978-3-030-28683-5_10](https://doi.org/10.1007/978-3-030-28683-5_10).
- [5] Convention on Biological Diversity. (1992, May). Retrieved from <https://www.cbd.int/convention>.
- [6] Devaux, A., Goffart, J.P., Kromann, P., Andrade-Piedra, J., Polar, V., & Hareau, G. (2021). The potato of the future: Opportunities and challenges in sustainable agri-food systems. *Potato Research*, 64(4), 681-720. doi: [10.1007/s11540-021-09501-4](https://doi.org/10.1007/s11540-021-09501-4).
- [7] European Food Safety Authority. (2019). *Pest survey card on potato brown rot, Ralstonia solanacearum*. Retrieved from <https://www.efsa.europa.eu/en/supporting/pub/en-1567>.
- [8] Farvardin, A., González-Hernández, A.I., Llorens, E., Camañes, G., Scalschi, L., & Vicedo, B. (2024). The dual role of antimicrobial proteins and peptides: Exploring their direct impact and plant defense-enhancing abilities. *Plants*, 13(15), article number 2059. doi: [10.3390/plants13152059](https://doi.org/10.3390/plants13152059).
- [9] Hao, J., & Ashley, K. (2021). Irreplaceable role of amendment-based strategies to enhance soil health and disease suppression in potato production. *Microorganisms*, 9(8), article number 1660. doi: [10.3390/microorganisms9081660](https://doi.org/10.3390/microorganisms9081660).
- [10] Hossain, M.M., et al. (2024). Plant disease dynamics in a changing climate: Impacts, molecular mechanisms, and climate-informed strategies for sustainable management. *Discover Agriculture*, 2, article number 132. doi: [10.1007/s44279-024-00144-w](https://doi.org/10.1007/s44279-024-00144-w).
- [11] Huang, X., Ren, J., Li, P., Feng, S., Dong, P., & Ren, M. (2021). Potential of microbial endophytes to enhance the resistance to postharvest diseases of fruit and vegetables. *Journal of the Science of Food and Agriculture*, 101(5), 1744-1757. doi: [10.1002/jsfa.10829](https://doi.org/10.1002/jsfa.10829).
- [12] Ismail, S., Jiang, B., Nasimi, Z., Inam-ul-Haq, M., Yamamoto, N., Danso Ofori, A., Khan, N., Arshad, M., Abbas, K., & Zheng, A. (2020). Investigation of *Streptomyces scabies* causing potato scab by various detection techniques, its pathogenicity and determination of host-disease resistance in potato germplasm. *Pathogens*, 9(9), article number 760. doi: [10.3390/pathogens9090760](https://doi.org/10.3390/pathogens9090760).
- [13] Kaur, S., Samota, M.K., Choudhary, M., Choudhary, M., Pandey, A.K., Sharma, A., & Thakur, J. (2022). How do plants defend themselves against pathogens – biochemical mechanisms and genetic interventions. *Physiology and Molecular Biology of Plants*, 28(2), 485-504. doi: [10.1007/s12298-022-01146-y](https://doi.org/10.1007/s12298-022-01146-y).

- [14] Khairy, A.M., Tohamy, M.R., Zayed, M.A., & Ali, M.A. (2021). Detecting pathogenic bacterial wilt disease of potato using biochemical markers and evaluate resistant in some cultivars. *Saudi Journal of Biological Sciences*, 28(9), 5193-5203. doi: [10.1016/j.sjbs.2021.05.045](https://doi.org/10.1016/j.sjbs.2021.05.045).
- [15] Khomenko, T., Tonkha, O., Puzniak, O., & Havryliuk, O. (2023). Assessment of the complex influence of biopreparations on the process of chlorophyll fluorescence induction in potato leaves by organic cultivation technology. *Scientific Reports of the National University of Life and Environmental Sciences of Ukraine*, 19(6). doi: [10.31548/dopovid6\(106\).2023.006](https://doi.org/10.31548/dopovid6(106).2023.006).
- [16] Kieu, N.P., Lenman, M., Wang, E.S., Petersen, B.L., & Andreasson, E. (2021). Mutations introduced in susceptibility genes through CRISPR/Cas9 genome editing confer increased late blight resistance in potatoes. *Scientific Reports*, 11(1), article number 4487. doi: [10.1038/s41598-021-83972-w](https://doi.org/10.1038/s41598-021-83972-w).
- [17] Leitão, J.H. (2020). Microbial virulence factors. *International Journal of Molecular Sciences*, 21(15), article number 5320. doi: [10.3390/ijms21155320](https://doi.org/10.3390/ijms21155320).
- [18] Liu, J.-M., Wang, S.-S., Zheng, X., Jin, N., Lu, J., Huang, Y.-T., Fan, B., & Wang, F.Z. (2020). Antimicrobial activity against phytopathogens and inhibitory activity on solanine in potatoes of the endophytic bacteria isolated from potato tubers. *Frontiers in Microbiology*, 11, article number 570926. doi: [10.3389/fmicb.2020.570926](https://doi.org/10.3389/fmicb.2020.570926).
- [19] Manda, R.R., Addanki, V.A., & Srivastava, S. (2020). Bacterial wilt of solanaceous crops. *International Journal of Chemical Studies*, 8(6), 1048-1057. doi: [10.22271/chemi.2020.v8.i6o.10903](https://doi.org/10.22271/chemi.2020.v8.i6o.10903).
- [20] Mohamed, B.F., Sallam, N.M., Alamri, S.A., Abo-Elyousr, K.A., Mostafa, Y.S., & Hashem, M. (2020). Approving the biocontrol method of potato wilt caused by *Ralstonia solanacearum* (Smith) using *Enterobacter cloacae* PS14 and *Trichoderma asperellum* T34. *Egyptian Journal of Biological Pest Control*, 30, article number 61. doi: [10.1186/s41938-020-00262-9](https://doi.org/10.1186/s41938-020-00262-9).
- [21] Muthoni, J., Shimelis, H., & Melis, R. (2020). Conventional breeding of potatoes for resistance to bacterial wilt (*Ralstonia solanacearum*): Any light in the horizon? *Australian Journal of Crop Science*, 14(3), 485-494. doi: [10.21475/ajcs.20.14.03.p2144](https://doi.org/10.21475/ajcs.20.14.03.p2144).
- [22] Nolte, P., Miller, J., Duellman, K.M., Gevens, A.J., & Banks, E. (2020). Disease management. In J.C. Stark, M. Thornton & P. Nolte (Eds.), *Potato production systems* (pp. 203-257). Cham: Springer. doi: [10.1007/978-3-030-39157-7_9](https://doi.org/10.1007/978-3-030-39157-7_9).
- [23] Osdaghi, E., van der Wolf, J.M., Abachi, H., Li, X., De Boer, S.H., & Ishimaru, C.A. (2022). Bacterial ring rot of potato caused by *Clavibacter sepedonicus*: A successful example of defeating the enemy under international regulations. *Molecular Plant Pathology*, 23(7), 911-932. doi: [10.1111/mpp.13191](https://doi.org/10.1111/mpp.13191).
- [24] Paluchowska, P., Śliwka, J., & Yin, Z. (2022). Late blight resistance genes in potato breeding. *Planta*, 255(6), article number 127. doi: [10.1007/s00425-022-03910-6](https://doi.org/10.1007/s00425-022-03910-6).
- [25] Rolot, J.-L. (2012). *The potato diseases: An overview*. Yerevan: Food and Agriculture Organization.
- [26] Sharma, A., Abrahamian, P., Carvalho, R., Choudhary, M., Paret, M.L., Vallad, G.E., & Jones, J.B. (2022). Future of bacterial disease management in crop production. *Annual Review of Phytopathology*, 60(1), 259-282. doi: [10.1146/annurev-phyto-021621-121806](https://doi.org/10.1146/annurev-phyto-021621-121806).
- [27] Singh, C., Pandey, S., Rahmani, U., Chaudhary, M., Chauhan, A., Semwal, A., & Singh, A.K. (2025). Molecular basis of the evolution of pathogens under changing climate conditions. In A. Singh, S. Pandey & A. Kumar (Eds.), *Climate change and biotic factors: A molecular approach* (pp. 143-180). New York: Apple Academic Press. doi: [10.1201/9781003568704-6](https://doi.org/10.1201/9781003568704-6).
- [28] Stark, J.C., Thornton, M., & Nolte, P. (2020). *Potato production systems*. Cham: Springer. doi: [10.1007/978-3-030-39157-7](https://doi.org/10.1007/978-3-030-39157-7).
- [29] Tripathi, A.N., Tiwari, S.K., Sharma, S.K., Sharma, P.K., & Behera, T.K. (2024). Current status of bacterial diseases of vegetable crops. *Vegetable Science*, 51, 106-117. doi: [10.61180/vegsci.2024.v51.spl.10](https://doi.org/10.61180/vegsci.2024.v51.spl.10).
- [30] Vega, D., Ibarra, S., Varela Pardo, R.A., & Poggio, S.L. (2023). Agroecological management of crop diseases: A review. *Agroecology and Sustainable Food Systems*, 47(7), 919-949. doi: [10.1080/21683565.2023.2216149](https://doi.org/10.1080/21683565.2023.2216149).
- [31] Vidhyasekaran, P. (2024). *Bacterial disease resistance in plants: Molecular biology and biotechnological applications*. London: CRC Press.
- [32] Vilvert, E., Stridh, L., Andersson, B., Olson, Å., Aldén, L., & Berlin, A. (2022). Evidence based disease control methods in potato production: A systematic map protocol. *Environmental Evidence*, 11(1), article number 6. doi: [10.1186/s13750-022-00259-x](https://doi.org/10.1186/s13750-022-00259-x).
- [33] Wang, Z., Luo, W., Cheng, S., Zhang, H., Zong, J., & Zhang, Z. (2023). *Ralstonia solanacearum* – a soil borne hidden enemy of plants: research development in management strategies, their action mechanism and challenges. *Frontiers in Plant Science*, 14, article number 1141902. doi: [10.3389/fpls.2023.1141902](https://doi.org/10.3389/fpls.2023.1141902).
- [34] Yarema, N.M. (2023). *Comparative study of nematode-resistant potato varieties as a means of protecting against harmful phytohelminths under the conditions of the Educational and Scientific Center of Lviv National Environmental University*. Dubliany: Lviv National Environmental University.

- [35] Yuan, J., Bizimungu, B., De Koeber, D., Rosyara, U., Wen, Z., & Lagüe, M. (2020). Genome-wide association study of resistance to potato common scab. *Potato Research*, 63, 253-266. doi: [10.1007/s11540-019-09437-w](https://doi.org/10.1007/s11540-019-09437-w).

Комплексна оцінка бактеріальних збудників картоплі та розробка методів підвищення її стійкості

Севіндж Магеррамова

Доктор філософії, доцент
Азербайджанський державний економічний університет (UNEC)
AZ1001, вул. Істікляліят, 6, м. Баку, Азербайджан
<https://orcid.org/0000-0002-1599-7013>

Мар'ям Мамедалієва

Доктор філософії, викладач
Азербайджанський державний економічний університет (UNEC)
AZ1001, вул. Істікляліят, 6, м. Баку, Азербайджан
<https://orcid.org/0000-0002-4351-8286>

Мехрібан Юсіфова

Доктор філософії, доцент
Азербайджанський державний економічний університет (UNEC)
AZ1001, вул. Істікляліят, 6, м. Баку, Азербайджан
<https://orcid.org/0000-0001-7608-5950>

Гюнаш Насруллаєва

Доктор філософії, доцент
Азербайджанський державний економічний університет (UNEC)
AZ1001, вул. Істікляліят, 6, м. Баку, Азербайджан
<https://orcid.org/0000-0003-2661-8354>

Юлія Коломієць

Доктор сільськогосподарських наук, професор
Національний університет біоресурсів і природокористування України
03041, вул. Героїв Оборони, 15, м. Київ, Україна
<https://orcid.org/0000-0002-1919-6336>

Анотація. Це дослідження зосереджувалося на вивченні складу бактеріальних збудників картоплі та ефективності різних стратегій формування резистентності культури в агроєкосистемах. В роботі було поєднано теоретичний аналіз літературних джерел щодо властивостей збудників і механізмів резистентності з експериментальною апробацією власних агробіологічних методів у вегетаційних умовах для порівняльної оцінки ефективності контролю бактеріальних хвороб картоплі. У результаті встановлено, що найвищу патогенну активність в умовах дослідження виявляла *Ralstonia solanacearum*, яка спричиняла системне в'янення рослин. *Pectobacterium carotovorum* переважно уражала бульби, формуючи осередки мокрої гнилі, тоді як *Clavibacter sepedonicus* проявляв повільний інфекційний процес, що частіше діагностувався на стадії зберігання. Розвиток бактеріальних хвороб картоплі інтенсифікувався за умов надмірної вологості ґрунту, температури вище 27°C, механічних ушкоджень та накопичення органічних решток. Формування стабільної ризосферної мікробіоти, зокрема за участі представників родів *Pseudomonas* і *Bacillus*, сприяло зниженню індексу хворобливості на 47-62 % та підвищенню вегетативної маси на 25-31 % порівняно з контролем. У досліджуваних сортів домінували різні механізми толерантності: у Солохи – судинна резистентність, що забезпечила 62 % зниження ураження, 31 % приріст маси та 2,2 додаткові бульби на рослину. У Дніпрянки – біохімічна відповідь, з підвищенням активності пероксидази у 3,1 раз та фенілаланінамоніак-ліази у 1,6 раз, а у Луговської – мікробіологічний контроль, з щільністю колонізації ризосфери до 1×10^5 колонієутворювальних одиниць на грам ґрунту та приростом кількості бульб на 24 штуки. Отримані результати мають практичне значення для розробки інтегрованих схем захисту картоплі, що передбачають використання біоагентів і індукторів резистентності як ефективну альтернативу хімічним засобам, а також для впровадження системи раннього діагностичного моніторингу на основі біоіндикаторів у селекційних та агропродовольчих технологіях.

Ключові слова: мікробіота; ґрунт; вологість; резистентність; агроєкосистема; ендofіти; в'янення