

# Insights into plant-beneficial traits of probiotic *Pseudomonas chlororaphis* isolates

Anne J. Anderson<sup>1</sup> and Young Cheol Kim<sup>2,\*</sup>

## Abstract

*Pseudomonas chlororaphis* isolates have been studied intensively for their beneficial traits. *P. chlororaphis* species function as probiotics in plants and fish, offering plants protection against microbes, nematodes and insects. In this review, we discuss the classification of *P. chlororaphis* isolates within four subspecies; the shared traits include the production of coloured antimicrobial phenazines, high sequence identity between housekeeping genes and similar cellular fatty acid composition. The direct antimicrobial, insecticidal and nematocidal effects of *P. chlororaphis* isolates are correlated with known metabolites. Other metabolites prime the plants for stress tolerance and participate in microbial cell signalling events and biofilm formation among other things. Formulations of *P. chlororaphis* isolates and their metabolites are currently being commercialized for agricultural use.

## INTRODUCTION

*Pseudomonas chlororaphis* isolates exist worldwide. From the frequency of their detection, many isolates are plant colonizers. Interest in *P. chlororaphis* isolates is driven by the properties of their metabolites, which show potential for use in formulations beneficial to plant health [1]. The *P. chlororaphis* isolates associate with both mono- and dicotyledonous plants growing in commercialized and natural habitats. A recent review of *P. chlororaphis* isolates indicated that these bacteria colonize 11 different plant hosts grown on 4 different continents [1]. *P. chlororaphis* isolates from soils include: UFB2 [2] from soybean field soil; L19 [3] from coal-, heavy metal- and petroleum-contaminated saline soils [4]; and MCC2693, a psychrophile from a mountain ecosystem [5].

The aim of this review is to highlight the currently identified traits of *P. chlororaphis* isolates that would benefit from further study because of their potential agricultural value. The present scientific methods and technologies have provided extensive knowledge of the behaviour of *P. chlororaphis* isolates within the confines of the laboratory; however, studies are currently investigating the process that occur in the field to identify the traits of *P. chlororaphis* isolates that will aid the development of successful commercial products.

This review begins with a background of how microbial isolates are classified as belonging to the four subspecies of the

*P. chlororaphis* group. Isolates of this group have protective, 'probiotic-like' effects on their hosts. The arsenal of metabolites produced by *P. chlororaphis* group isolates are discussed to illustrate their protective roles for the plant hosts. Volatile organic compounds (VOCs) are significant because they allow the microbe to influence its environment in three dimensions (including through the atmosphere). Next, microbial survival mechanisms are addressed with a focus on biofilm formation and microbial nutrition. Although *P. chlororaphis* isolates are deemed nonpathogenic [6], isolates have the potential to kill plant-associated organisms such as nematodes and insects. Further, these isolates can be denitrifiers; therefore, their potential effects on ecosystem function should be carefully considered before their widespread use in the field. The final section of this review focuses on the potential commercial use of metabolites of *P. chlororaphis* isolates.

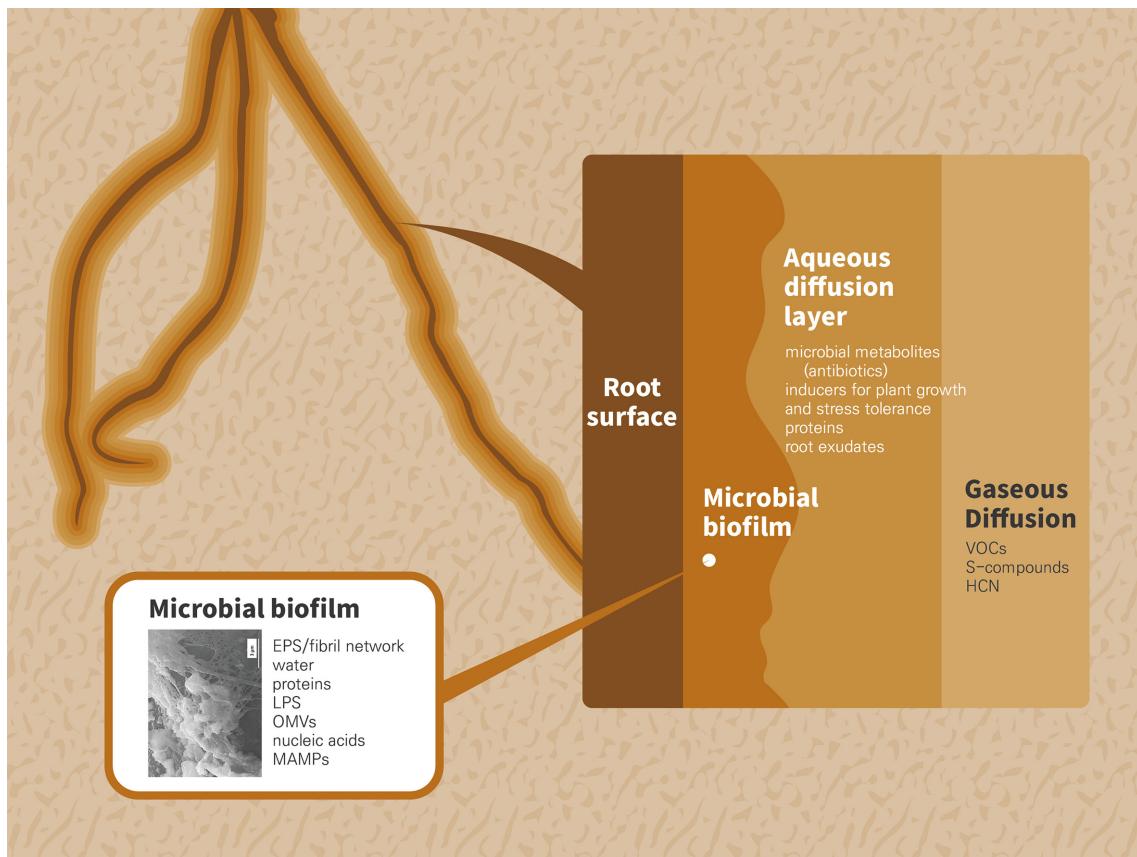
The information reviewed in these sections reveals the potential for *P. chlororaphis* isolates to provide plant protection that extends further than the intact cells. The model shown in Fig. 1 illustrates there are at least three overlapping layers and spheres of protection that arise from colonization of the root surface. Each of these layers offers different mechanisms with the potential to contribute to plant health. The mechanisms and traits of importance in the rhizosphere for the beneficial activities of *P. chlororaphis* isolates summarized in Fig. 1 are discussed in the subsequent sections.

Received 19 September 2019; Accepted 14 January 2020; Published 11 February 2020

Author affiliations: <sup>1</sup>Department of Biological Engineering, Utah State University, Logan UT84322, USA; <sup>2</sup>Department of Applied Biology, Chonnam National University, Gwangju 61186, Republic of Korea.

\*Correspondence: Young Cheol Kim, yckimyc@jnu.ac.kr

Keywords: acyl homoserine lactones; antimicrobial, insecticidal and nematocidal effects; biofilm; hydrogen cyanide; phenazines; pyrrolnitrin; resorcinols; siderophore; volatile organic compounds.



**Fig. 1.** The multilayered protective mechanisms pertinent to a root colonized by a *P. chlororaphis* isolate. The layers considered are at the root surface, the patchy biofilm of microbial cells, the sphere generated by aqueous diffusion of secreted metabolites and the extended volume in the rhizosphere impacted by volatile diffusion. At the root surface, metabolites/volatiles, including VOCs, released by root colonists could be transported in the plant upward apoplastically and/or by the plant vasculature (xylem/phloem) to initiate plant responses such as changes in growth and stress tolerance. Microbial products could also function in pathogenicity towards nematodes and insects. Growth of the bacterium as a biofilm offers protection to the bacterial cells and the ability to trap materials through charge-charge interactions (e.g. nucleic acids would provide negative charges to bind metal ions) and physically because of the fibrillar nature of the extracellular matrix. The presence within the EPSs and OMVs of discrete structures that act as microbially associated molecular patterns (MAMPs) would activate plant defences. The insert image is a scanning electron micrograph showing cells of strain O6 *P. chlororaphis* colonizing a 7 day-old wheat root from a seed inoculum; the methods are described by Jacobson *et al.* [72]. The diffusion of secreted metabolites and enzymatic proteins in the pore waters surrounding the root would extend their functions to a wider volume in the rhizosphere than just the root surface. Diffusion of the volatiles released from the colonized root through pore spaces in the soil and into the air would influence surrounding soil organisms and shoot tissues and neighbouring plants.

### What is in a name for these colourful bacteria?

*P. chlororaphis* isolates are Gram-negative, motile, green-/yellow-/orange-coloured gamma-proteobacteria that are now assigned to their own taxonomic group (*Pc*; NCBI Taxonomy Browser) among seven *Pseudomonas* spp. groups. Currently there are four subspecies designated as *P. chlororaphis* isolates: *chlororaphis*, *aurantiaca*, *aureofaciens* and *piscium*. Bacterial isolates were first identified as pseudomonads in the late 1800s by Miguela, and the opportunistic human pathogen, *Pseudomonas aeruginosa*, was designated as the first type culture. This early work on taxonomy is elegantly discussed by Palleroni [7], who comments that the complexity of classification of *P. chlororaphis* isolates is partly due to the extreme metabolic diversity of pseudomonads. Classification based on

16 s rRNA gene sequences, a tool first used in 1965, clarifies the predicted evolutionary relationships among *P. chlororaphis* isolates. In 2007, the *P. chlororaphis* group was split into subspecies (*P. chlororaphis* subsp. *aurantiaca*, *P. chlororaphis* subsp. *chlororaphis* and *P. chlororaphis* subsp. *aureofaciens*) based on genetic and phenotypic properties [8]. Alignment of 16S rRNA gene sequences grouped type cultures of the subspecies *aurantiaca*, *chlororaphis* and *aureofaciens* together and apart from other *Pseudomonas* species [8]. DNA–DNA hybridization values were 76 % for two *aurantiaca* type cultures, 67–81 % for three *chlororaphis* type cultures and 76–88 % for three *aureofaciens* type cultures [8]. These findings, as well as the observed variability in the sequences of the housekeeping genes *atpD*, *recA* and *carA*, while the fatty acid

**Table 1.** Correlation between colony pigmentation and *P. chlororaphis* isolate classification

Name of <i>P. chlororaphis</i> subspecies	Pigmentation colour/phenazines	Type culture
<i>chlororaphis</i>	Green PCA	ATCC 9446
<i>aureofaciens</i>	Gold PCA, 2-OH PCA, 2-OH PHZ	ATCC 13985
<i>aurantiaca</i>	Orange/yellow PCA, 2 OH PCA, 2 OH PHZ	ATCC 33663
<i>piscium</i>	Yellow/green. PCA and PCN	NCIMB 14478

These descriptions are based on publications by Biessy *et al.* 2018 [11], Burr *et al.* 2010 [9] and Peix *et al.* 2007 [8]. The abbreviations for phenazines are as follows: phenazine-1-carboxylic acid, (PCA); phenazine-1-carboxamide, PCN; 2-hydroxyphenazine-1-carboxylic acid, 2-OH PCA; 2-OH hydroxyphenazine, 2-OH PHZ.

compositions agree, support their designation as subspecies of *P. chlororaphis* [8].

In 2010, a new branch was added to the *P. chlororaphis* group: *P. chlororaphis* subsp. *piscium* [6, 9]. Burr *et al.* [9] characterized two isolates of this subspecies; both from fish intestines. However, a strain from a tomato rhizosphere, known as PCL 1391, which confers strong protection against tomato foot and root rot [10], was also classified as belonging to *P. chlororaphis* subsp. *piscium*. As discussed by Peix *et al.* [8], certain phenotypic traits are variable among the *P. chlororaphis* subspecies, such as the potential for denitrification and the use of arabinose or ketogluconate as C sources [8, 9]. A visually distinguishing feature for cells in the different *P. chlororaphis* subspecies is pigmentation when cultured on a rich medium [Table 1, [8]]. The pigmentation varies with the array of antifungal phenazines produced by the *P. chlororaphis* isolate. An analysis conducted by Biessy *et al.* [1] showed that each isolate in the *P. chlororaphis* group had unique singleton genes within their genomes, which ranged in size from 6.66 to 7.30 kbp. The isolates share a common core of 71 % of their genes with pseudomonads of different species that also produce phenazines. This common core of genes is increased to 87 % within each subspecies of the *P. chlororaphis* group. Despite these studies on classification, most published studies of *P. chlororaphis* isolates do not identify to the subspecies level.

### Beneficial traits of *P. chlororaphis* isolates in the rhizosphere: metabolites for direct antagonism of pathogens and systemic activation of plant defences

#### Phenazines

The intensity of colony pigmentation in *P. chlororaphis* strains, when grown on a rich medium, contributes to their ease of

isolation and detection during studies. This pigmentation is due to the production of three-ring nitrogen-containing phenazines, which have antimicrobial properties and affect cell signalling [11]. In a 1962 paper [12], the difficulty of identifying an isolate as *P. chlororaphis* or *P. aeruginosa* based solely on pigmentation is discussed, because cells of both these species can produce a green colouration. However, the correlation between phenazine structure and colour and isolate identity (Table 1) is discussed in more recent publications, and is strengthened by genome analysis and transcriptomics [1, 11].

The metabolic pathways that transform the product of the shikimic acid pathway, chorismate, to one of several phenazines produced by plant-beneficial pseudomonads, including those of the *P. chlororaphis* group [e.g. phenazine 1 carboxylic acid (PCA), phenazine 1-carboxamide (PCN), 2-hydroxyphenazine-1-carboxylic acid (2-OH PCA) and 2-OH hydroxyphenazine (2-OH PHZ)] are discussed by Biessy *et al.* [11]. The genes involved in the synthesis of the basic phenazine rings are clustered (genes *phzA*, *phzB*, *phzC* ... *phzG*) and the gene order is highly conserved among beneficial phenazine producers [11]. These clusters are preceded by the regulatory genes (e.g. *phzI* and *phzR*). The findings highlight how the genes in these beneficial phenazine-producing pseudomonads differ from those in other microbes (e.g. *Streptomyces*, *Burkholderia* and *Pectobacterium* spp.) that also synthesize phenazines but with different structures [13]. Comparisons among plant-beneficial phenazine-producing pseudomonads show that all isolates in the *P. chlororaphis* group generate PCA; the *P. chlororaphis* subspecies *aurantiaca* and *aureofaciens* do not produce PCN, whereas this phenazine is synthesized by all *P. chlororaphis* subspecies *piscium* [1]. Genes, such as *phzH* for PCN and *phzO* for 2-OH PCA, account for the variation in the side groups of the final phenazine products [1].

The mechanisms by which microbes regulate phenazine synthesis have been studied intensively in many *P. chlororaphis* isolates, revealing overall similarities and some differences. Synthesis is conditioned by environmental factors, including cell density, which, when above a threshold density, triggers global changes in gene expression through a quorum-sensing system. The quorum-sensing systems of *P. chlororaphis* isolates are governed by cell-signalling molecules called acyl homoserine lactones (AHSLs), which are produced under the control of a 'Gac' sensor kinase mechanism [11]. Both translational and transcriptional control measures condition the synthesis of AHSLs, although there are differences in the regulatory processes among pseudomonad isolates. For example, most *P. chlororaphis* isolates have two regulatory loci for AHSL synthesis; however, three have been reported in *P. chlororaphis* subsp. *aurantiaca* PB-St2 [14]. The knowledge of these pathways is the most detailed for isolates 30–84, due to the efforts of the Pierson group [15, 16], and PA23, from the work of deKievit's research team [17, 18]. Important findings include the fact that phenazines, such as PCA, regulate their own gene expression [19] and the discovery of overlap between Gac regulation and that of other global regulators,

such as RpoS and Anr [17, 20, 21]. Readers are referred to the review by Biessy and Filion [11] for details of the complex regulation of gene expression for phenazine synthesis.

The review by Biessy and Filion [11] also summarizes the properties of the phenazines that are important for plant interactions. The most widely researched is the direct inhibition of microbial growth by phenazines, a finding that suggests the potential for biological control of plant microbial pathogens by *P. chlororaphis* isolates. Fungal and bacterial growth inhibition is readily observed when these microbes are grown in medium adjacent to the *P. chlororaphis* isolates where the phenazines diffuse from the bacterial colonies. The presence of phenazine-producing microbes is correlated with soils that suppress certain pathogens, as in the classic example of take-all decline soils [22], in which the level of crop damage caused by a fungal pathogen declines with continuous cropping of wheat on the same fields [22].

In addition to direct growth antagonism of microbes, the phenazines also induce systemic resistance in plants such that protection against shoot pathogens is triggered by root colonization with *P. chlororaphis* isolates. Both PCN- and PCA/2-OH PHZ-producing microbes possess this ability [23–25]. Duke *et al.* [23] observed that aerial application of isolates induces both localized and systemic responses associated with resistance. Thus, the direct microbial antagonism caused by phenazine production is reinforced by the phenazine-mediated upregulation of plant defence mechanisms.

### Pyrrolnitrin and resorcinols

Phenazines are not the only metabolites synthesized by *P. chlororaphis* isolates that offer plants protection against microbial pathogens. As shown by Biessy *et al.* [1], *P. chlororaphis* group isolates synthesize other antimicrobials, including the chlorinated product, pyrrolnitrin, and the alkyl resorcinols. These compounds have different importance in plant pathosystems, depending on the identities of the plant, pathogen and pseudomonad. Mutational analysis of *P. chlororaphis* subsp. *piscium* PCL 1391 revealed that the phenazine PCN was a key metabolite for controlling fusarium root rot in tomato [26]; however, although isolate PCL 1606 produces PCN, the synthesis of 2-hexyl-5-propyl resorcinol, from the *dar* gene cluster, is more important for combatting the white rot fungus in avocado [27]. However, pyrrolnitrin, rather than phenazines, is the key antimicrobial produced by *P. chlororaphis* subsp. *aureofaciens* PA23 that controls white rot on canola [28]. Pyrrolnitrin is also the key metabolite in the inhibition of fusarium head blight by *P. chlororaphis* G05 [29]. Whether these observations are influenced by the nutrients available to the pseudomonad awaits resolution. The synthesis of phenazines predominates over pyrrolnitrin in *P. chlororaphis* isolate O6 in medium with abundant glucose [30]. Thus, the question arises of the role of the composition and concentrations of plant metabolites in the root exudates in regulating the production of antimicrobials by *P. chlororaphis* isolates in the rhizosphere. The phenazine PCA is detected in soils harbouring phenazine-producing pseudomonad isolates [31]; however, the extent to which this phenazine originates from

*P. chlororaphis* group isolates or from other bacteria, such as *P. synxantha* detected in the soils, is unknown.

### Hydrogen cyanide (HCN)

HCN, a very simple, soluble and volatile compound formed from glycine, is another part of the *P. chlororaphis* group's toxic arsenal because of its ability to bind to structures containing heme groups. The nematocidal activity of *P. chlororaphis* isolate PA23 is correlated with both pyrrolnitrin and HCN [32]. An isolate of *P. putida* also kills nematodes via multiple mechanisms involving volatiles [33]. In addition, Flury *et al.* [34], working with *P. chlororaphis* isolate PCL 1391 and other pseudomonads, show that HCN, rather than phenazines or pyrrolnitrin, is the active component responsible for nematode larval death. The production of HCN by *P. chlororaphis* isolate O6 causes cell death in both nematodes [35] and aphid nymphs [36]. HCN is detected in the air space of tomato plants growing with roots colonized by *P. chlororaphis* O6 [35]. The successful control of root-lesion nematodes by the *P. chlororaphis* Sm3 is reported in greenhouse-grown strawberries; however, no studies on the underlying mechanism are discussed in this work [37]. Similarly, under commercial greenhouse conditions, the application of *P. chlororaphis* O6 formulations results in the control of nematodes on pepper plants [38].

### Volatile organic compounds (VOCs)

Much interest is currently directed towards microbially produced VOCs [39–43] that protect the plant in three dimensions through gaseous diffusion. This process is independent of water flux and aqueous diffusion, processes that would distribute the metabolites such as the phenazines. Generally, VOC activity is assessed by growth of the organisms (i.e. plants and microbes) separately on media in enclosed vessels where only the air space is in common. These dual but separate culture systems are made possible, for example, by the presence of a solid barrier across an agar plate separating media, but not the air space. When the VOC composition is analysed by sampling this air space from dual cultures with *P. chlororaphis* isolates, an array of metabolites with compositions that change with the growth medium is reported. It is possible that VOCs that are not found in nature are released from the medium used for microbial growth. In addition, medium components not found in nature may be metabolically transformed into VOCs due to the versatility of microbial metabolism, i.e. these VOCs would not be produced on a colonized root. Dual culture assays only containing microbes also negate the detection of any VOCs generated by the plant in response to contact with microbial cells or secreted metabolites. The composition of the VOCs from microbially colonized plants has not yet been comprehensively studied. Another process important in understanding the role of VOCs is that diseased plants alter their VOC patterns and it is suggested that some of these compounds will attract soil microbes with antifungal properties [44].

For *P. chlororaphis* O6, VOC production with growth on two different media is reduced by mutations in the Gac system,

which eliminates regulation by the acyl homoserine lactones involved in quorum sensing. Similarly, the reduction in VOC emissions observed in *gacS* mutants of *P. fluorescens* isolates [45] suggests that Gac dependence is a common trait among the plant-associated pseudomonads. One of these Gac-regulated metabolites with marginal volatility, 2R,3R-butanediol, is produced by the microbial fermentation of pyruvate by the *P. chlororaphis* strains O6 and M71 [46, 47]. The plant responds to the butanediol with narrowed stomatal openings and the induction of systemic responses, changes that are involved in drought and pathogen tolerance [24, 48]. Butanediol also promotes plant growth, a response that is partly attributed to the activation of genes encoding plant cell wall-modifying enzymes and enhanced C metabolism [49]. In addition, the composition of plant root exudates is altered in plants exposed to this VOC, a process that modifies microbial root colonization [50]. Thus, 2R,3R-butanediol induces an array of responses in the plant that benefit plant health.

Another class of plant-active compounds with low volatility are the polyamines. Polyamine production in *P. chlororaphis* O6 has implications for biocontrol [51]. In plants, polyamine oxidases generate reactive oxygen species (ROS), which are involved in defence system signalling [51]. Consequently, the production of polyamines by bacterial cells may stimulate signalling in the host plant cells.

Many additional simple volatiles are detected from *P. chlororaphis* group isolates. For the *P. subsp. aureofaciens* SPS-41 [52], the production of 3-methyl butanol, 2-methyl butanol and phenylethyl alcohol is associated with direct growth antagonism towards the fungus causing black rot in sweet potato tubers. The hydrocarbon, undecane, is detected from *P. subsp. aurantiaca* KNU17Pc1 [53] and *P. chlororaphis* O6 (unpublished) when isolates are grown on rich medium. Other VOCs detected in both O6 (unpublished) and M71 [46] isolates include S-containing compounds, such as hydrogen sulfide, dimethyl sulfide and methanethiol. These metabolites may be correlated with induced plant defence responses. There are a wide variety of VOCs for which the production by *P. chlororaphis* isolates needs to be clarified under field conditions where the microbe is colonizing a plant or other host. Moreover, their modes of action as a single compound or within a 'VOC cocktail' should be established.

## SURVIVAL STRATEGIES OF BACTERIAL ISOLATES

### Sources of nutrients

The isolation of *P. chlororaphis* group strains from many soils, rhizospheres and plants indicates that they have strong survival mechanisms in nature. Their association with plant roots provides them with diverse C and N sources from the metabolites in root exudates. The catabolism of these metabolites is indicated by alterations in root exudate composition for colonized plants [54]. For example, citrate is one of the organic acids in wheat root exudates that is preferentially utilized by a *P. chlororaphis* isolate [54]. The various catabolic

pathways of pseudomonads enhance their abilities to process an array of organic molecules into biomass. The *P. chlororaphis* isolate O3 degrades lignin-like structures [55] and genes conferring tolerance to toluene are present in other *P. chlororaphis* isolates [56]. These traits raise the possibility that some *P. chlororaphis* isolates may be of commercial use in recycling and environmental remediation.

The ability of *P. chlororaphis* isolates to kill other soil organisms, such as nematodes, insects, algae [57] and other microbes would provide copious and varied nutrients for microbes to augment those available from the plant. The role of volatile HCN and organic metabolites produced by *P. chlororaphis* isolates in killing insects and nematodes has already been discussed. However, members of the *Pc* group also produce insecticidal peptides. One gene cluster involved is the set of 'fit' genes, most thoroughly studied in *P. fluorescens* isolates [58]. Loci for the 'fit ABCDEFGH' cluster are found in *P. chlororaphis* isolates O6 and 30–84 [59] and these microbes cause death in tobacco hornworm when injected or ingested [60]. However, the 'fit' system may be augmented by other insecticidal peptides, for example the peptide IPD072Aa, produced by *P. chlororaphis* isolates. The expression of the *P. chlororaphis* gene encoding this peptide in maize results in plants that are toxic to the rootworm pest [61]. Inspection of the *P. chlororaphis* O6 genome reveals an analogue to this gene; thus, this trait may be widespread among *P. chlororaphis* isolates. These examples show the array of traits within the *P. chlororaphis* group of pseudomonads that can achieve the same goals, such as insecticidal activity.

The aggressiveness of the *P. chlororaphis* isolates as root colonizers [62] may also be enhanced by a completely different mechanism, that is, the killing of competing bacteria by the production of bacteriocins, called tailocins, as demonstrated for *P. chlororaphis* isolate 30–84 [63, 64]. Tailocins are related to the pyocins of *P. aeruginosa* [65] and were first implicated in isolate 30–84 in connection with phenazine promotion in the biofilm structure [19]. The tailocins promote colonization of the root surface by isolate 30–84 by killing other potential colonizers that are sensitive, i.e. other pseudomonads and bacterial genera. This mechanism is effective for colonization of the isolate 30–84 at the root surface but not for bulk soil colonization [64].

In addition to obtaining nutrition from plants and prey organisms, *P. chlororaphis* cells can also glean essential elements from the soil. Isolates of the *P. chlororaphis* group are termed 'fluorescent' pseudomonads because, under iron-deficient growth conditions, they synthesize effective pyoverdine (PVD)-like siderophores that mine Fe in the environment to be taken up by the bacterial cell. Fe is an essential element for microbes. PVD siderophores exhibit characteristic blue-green fluorescence when non-chelated. The transfer of Fe from loaded PVDs to the plant shows yet another way in which the plants benefit from their associations with these pseudomonads. These siderophores, which extract Fe from soil minerals, may also scavenge other metals, such as Cu, because these ions also bind in the active pocket of the PVD

structure [66]. Indeed, PVDs from the *P. chlororaphis* isolate ATCC 9446 are implicated in the breakdown of organotin antifouling paints, presumably by binding the tin ion and dissolution of the paint solution [56]. Similarly, the release of vanadium from Fe-containing soil minerals observed for *P. chlororaphis* isolate L19 in coal-contaminated soil [3] could be due to selective ion binding by the microbial siderophores. Such observations expand the potential usefulness of the *P. chlororaphis* isolates in commercial remediation ventures.

PVD is not the only type of siderophore produced by *P. chlororaphis* isolates. Genetic loci that allow the synthesis of citrate-based siderophores, called achromobactins [1], are detected in *P. chlororaphis* genomes. Currently, little is known about the ecological significance of these iron-chelators. In *P. chlororaphis* subsp. *chlororaphis*, mutants that overproduce PCN show upregulation of genes for both PVD and achromobactin production [67]. Consequently, there is potential for the genes of both siderophores to be expressed simultaneously by a *P. chlororaphis* isolate. An isolate of *P. chlororaphis* subsp. *piscium* also expands its potential sources of Fe using heme, a trait possibly associated with the isolation of these strains from fish that possess heme in the blood supply. The heme becomes associated with secreted hematophores before being loaded into the cell by special receptors [1]. Finally, phenazines may play yet another role in Fe bioavailability. Dissolution of the Fe-containing minerals, ferrite and hematite, occurs under low-oxygen conditions when exposed to phenazines; 2-OH PHZ is found to be more effective than PCA in mediating Fe release from these minerals [68].

In addition to the chelation of Fe, *P. chlororaphis* isolates subsp. *chlororaphis* and *aurantiaca* solubilize insoluble Zn minerals, such as ZnO and Zn carbonate [69]. The underlying mechanisms are not yet known, and the question of whether the released Zn is bioavailable to plants has not yet been answered. The microbial secretion of organic acids, such as gluconic acid, may be involved in metal solubilization, because these acids also chelate several metals [54]. Gluconate production by other microbes is linked to phosphate solubilization from rock phosphate [48]. Phosphate solubilization by *P. chlororaphis* isolates is a variable trait, occurring in the high-mountain *P. chlororaphis* isolate MCC2693 [5] but not in several other *P. chlororaphis* isolates, as studied by Shahid *et al.* [69]. Genetic analyses reveal that all *P. chlororaphis* isolates have genes for synthesizing PQQ, the cofactor for glucose dehydrogenase. This enzyme oxidizes glucose to gluconate as an alternative mechanism for glucose catabolism [1, 48]. This finding suggests that gluconate is a common metabolite for all *P. chlororaphis* isolates.

Nitrogen metabolism by *P. chlororaphis* isolates can involve denitrification. *P. chlororaphis* isolates use inorganic nitrate as an external electron acceptor when oxygen is limited, causing the production of nitrite. This process may be very important for the maintenance of metabolic flux when there is insufficient oxygen to act as a terminal electron acceptor, such as for the bacterial cells encased within a biofilm matrix. Nitrate flux in the denitrifying pathway is connected to phosphate

metabolism through the common regulator protein, Dnr, in *P. aeruginosa* [70]. The regulator, Anr, is involved in sensing low oxygen and activating Dnr, which stimulates the expression of genes involved in the denitrification pathway. However, high phosphate content in pseudomonad cells inhibits the activation potential of Dnr, and thus limits the conversion of nitrate to nitrogen [70]. The extent to which such pathways occur in all *P. chlororaphis* group isolates has not yet been clarified, but is of importance because of the fate of soil nitrate, such as that added purposely as a fertilizer.

The nitrite generated from nitrate can be further metabolized to gaseous nitric oxide (NO). NO is a significant signalling component in plants that is associated with several functions, including the activation of plant defences to biotic and abiotic stressors [71]. The extent to which microbial NO production from *P. chlororaphis* cells within biofilms on plant roots is involved in plant defence activation and remodelling of root morphology remains unclear. The accumulation of NO on *P. chlororaphis* O6-colonized wheat roots is visualized by using fluorescence staining [72]; however, H<sub>2</sub>O<sub>2</sub> accumulation is not detected [73]. Further reduction to nitrous oxide (N<sub>2</sub>O) followed by its conversion to nitrogen gas completes the denitrification pathway in some pseudomonads. Laboratory studies of *P. chlororaphis* and *P. fluorescens* isolates find that certain microbes only produce N<sub>2</sub>O, whereas others also generate N<sub>2</sub> [74]. Two isolates designated as *P. chlororaphis* subsp. *aureofaciens* and *chlororaphis* lack nitrous oxide reductase genes, and the pathway ends with N<sub>2</sub>O generation. These isolates possess different nitrite reductases (NIRs): the *aureofaciens* isolate possesses a Cu-NIR and the *chlororaphis* strain possesses a cd<sub>1</sub>-NIR. In addition, the two strains in these studies differ in the effectiveness of succinate versus citrate as the reductant substrate [75]. The overall process of denitrification is viewed negatively because it destroys nitrate added to the soil as a plant fertilizer by converting it to nonnutritive gaseous products. It generates a more toxic anion, nitrite, and the released N<sub>2</sub>O, which may exacerbate global warming. However, the pathway offers an alternative for *P. chlororaphis* isolates under conditions of hypoxia to maintain cellular function without generating acidic fermentation products.

## Biofilm formation

The growth of microbial cells on plant roots is seen as patchy biofilms. Work with *P. chlororaphis* O6 (72) shows that the biofilm cells on plant roots are embedded in a complex extracellular matrix (Fig. 1). This biofilm habitat likely contributes to the survival of isolates in the rhizosphere and soil, as well as their potency in plant protection. The potential beneficial effects of biofilm formation in the rhizosphere, summarized in Fig. 1, are discussed in this section.

Biofilm formation is associated with cell resistance to doses of external antibiotics and hydrogen peroxide that would be lethal to planktonic cells [76]. However, the matrix that embeds the bacterial cells also limits the diffusion of metabolites through the fibrous mass. The concentration of any

antimicrobial products synthesized by the biofilm cells, such as phenazines, pyrrolnitrin and HCN, would better restrict the growth of other microbes sensitive to these chemicals. In addition, biofilm cells would outcompete other microbes, insects and nematodes for the metabolites released as plant root exudates; thus, the potential colonization of a plant by pathogens would be reduced. Biofilm formation by *P. chlororaphis* isolates PA23 and 30–84 is differentially enhanced by phenazines [19, 28]. Phenazines, such as 2-OH PCA, promote the release of extracellular (e-) DNA [19, 77], which can bind cations and modify the biofilm structure, as discussed by Yu *et al.* [77].

Biofilms are observed on the roots of soil-grown plants. Greater biofilm production is observed on wheat roots in dry soil than on those in wet soil for the PCA-producer, *P. synxantha* 2–79 [78]. This greater microbial biomass in dry soil correlates with higher stability and enhanced association of N with the plant roots. Thus, biofilms contribute to the health of both the plant and the soil. The PCA-producing pseudomonads are more dominant in non-irrigated soils than in irrigated soils [79, 80]. The production of water-holding extracellular polysaccharide matrices by microbes promotes healthier soils by mediating soil particle aggregation [81]. The aggregation limits soil run off and loss from wind and rain. The higher level of hydration of the gel-like biofilms on root surfaces is proposed to contribute to drought protection of the plant [82, 83].

In a related study, performed in autoclaved soil, wheat survival under conditions of drought is promoted by colonization with the phenazine-producing *P. chlororaphis* 30–84 [84]. Improved root formation by the colonized wheat is observed and is proposed to enhance water uptake. Induced drought tolerance by the biofilm-former *P. chlororaphis* O6 also occurs in wheat seedlings [72] due to several potential factors: priming by the bacterium to stimulate transcription of a large array of genes associated with drought tolerance [85], alteration of root morphology through the proliferation of root hairs connected to bacterial IAA production [72], butanediol-stimulated stomatal closure [47], NO production elicited by microbial colonization and water-withholding in the bacterial biofilm due to its polysaccharide components [72]. Analysis of priming for drought tolerance in tomato by *P. chlororaphis* M71 [46] also revealed that the induction of antioxidant mechanisms in the plant and the accumulation of the protectant osmolyte proline are important processes in resistance to drought.

Priming of the protective responses in the plant could, in part, involve induction by components of the biofilm matrix. Isolated extracellular polymeric substances (EPSs) protect plants from drought [86]. The EPSs from both planktonic and biofilm cells contain nano-sized outer-membrane vesicles (OMVs), which are released in greater quantities from bacterial cell surfaces under conditions of stress [87]. Atomic force microscope imaging of live *P. chlororaphis* O6 cells subjected to oxidative stress show released OMVs [88]. Studies on other Gram-negative pathogenic bacteria find

that OMVs harbour toxins that interact with the host and thereby become part of the pathogen virulence mechanism [89]. However, OMVs also contain lipopolysaccharides and flagellar proteins perceived as ‘microbe-associated molecular patterns’ (MAMPs) to activate immune responses in plants, a process akin to that observed in animals [90, 91].

Biofilm formation protects microbial cells from water-deficit stress due to its high moisture content and ability to reduce diffusion of toxic materials. Other underlying mechanisms for drought resistance include osmolyte accumulation within microbial cells and their potential secretion. Likely metabolites include proline, glycine, betaine and trehalose, because the genes required for synthesis of these osmolytes are present in *P. chlororaphis* genomes. Trehalose formation is reported for the *P. chlororaphis* subsp. *aurantiaca* G5 and, like many other traits of the *P. chlororaphis* group isolates, this activity is under Gac sensor kinase global control [92]. Thus, the cells in the biofilm contribute to an extended protectant hydrated layer on the root surface to improve plant and microbial survival to drought and salinity.

The importance of the biofilm habitat to bacterial cells in the *P. chlororaphis* group is supported by the finding that another antifungal metabolite, 2-hexyl-5-propyl resorcinol, stimulates biofilm formation, and that the *dar* genes required for resorcinol synthesis are common to all *P. chlororaphis* isolates [1]. 2-Hexyl-5-propyl resorcinol is essential for the biocontrol action of *P. chlororaphis* isolate PCL 1606 [93] and the production of several additional resorcinol family members is found for *P. chlororaphis* isolate O6 (unpublished). Mutants of *P. chlororaphis* PCL 1606 lacking resorcinol formation are impaired in adhesion, which would limit microbial cell-to-cell interactions involved in biofilm formation [94]. For another bacterium, *Photorhabdus asymbiotica*, the diakyl resorcinols act as cell-signalling molecules [95], suggesting similar roles to the AHSs for *P. chlororaphis* isolates. Thus, we again observe that, for the *P. chlororaphis* isolates, a single metabolite may have multiple roles.

The above studies indicate that biofilm formation is a dynamic part of the association between *P. chlororaphis* isolates and plants and plays vital roles in both microbe and plant protection. Currently, the nature of the embedding matrix and how its composition may vary with time and between plants and isolates require further examination to identify the chemistry of the matrix and the array of genes, both structural and regulatory, that are involved.

### Use of *P. chlororaphis* isolates in commercial agricultural products

The commercial use of the *P. chlororaphis* group of biocontrol agents has two branches: the application of specialized metabolites and the formulation of live cell preparations. Genomics, transcriptomics and metabolomics enable the genomic modification of bacteria to target the production of defined metabolites. Phenazines are antibiotics that may have potential as anticancer drugs [96]. The transfer of a *phz*

cluster to a nodulation nitrogen-fixing strain of *Rhizobium etli* correlated a novel antifungal trait with phenazine production, but this modification also destroyed functional nodule formation [97]. A different approach to genetic modification is to transfer the beneficial properties of the microbe to the host. This has been successful in maize, in which the expression of an insecticidal protein reduces insect pest damage [61]. Another example is the expression of a gene from the *P. chlororaphis* isolate G65 to control ethylene production in transformed plants, as summarized in the discussion by Anderson *et al.* [98]. Carlson *et al.* [99] have covered the extensive testing required to demonstrate that genetic modifications are not likely to adversely affect human health. For example, the 'safety' criteria for plant expression of the insecticidal protein, IPD072Aa, included the findings that this protein neither had any similarities to known allergens nor caused morbidity or weight loss in tested animals [99].

Shen *et al.* [100] used genome reduction as a tool to boost 2-OH PHZ production in *P. chlororaphis* isolate GP72, a sequenced biocontrol microbe isolated from green pepper [101]. Overproduction is greatest in a mutant defective in the production of pyoverdine-like siderophores, because the synthesis of this Fe-binding metabolite is an energy- and N-expensive process. Mutants with altered ratios of phenazines exhibit different colony growth patterns to the parental strain, suggesting cell-surface modifications [100]. These observations align with the findings that phenazines modify biofilm structures [19, 28]. The characterization of another mutant with enhanced PCN production also provides information on the traits associated with phenazine formation. Studies of the *P. chlororaphis* isolate HT66 demonstrate that a mutant with increased PCN production had alterations in over 400 proteins [67] and showed increased N metabolism and Fe uptake. An additional finding is that PCN production is influenced by the phosphate supply: a 50 % reduction in phosphate in the growth medium enhances phenazine production. This observation illustrates the importance of the growth medium in generating effective formulations of commercial value.

Studies performed to EPA standards indicate that *P. chlororaphis* isolates pose limited risks to humans and the environment [98]. The supporting evidence includes the absence of pathogenicity islands and type III/IV transfer systems in bacterial pathogens and that no genes required for the production of toxins characterized from pseudomonad plant pathogens are found in *P. chlororaphis* isolates. Indeed the literature has few reports of *P. chlororaphis* isolates from diseased human tissues [102, 103]. Moreover, no disadvantageous effects of *P. chlororaphis* isolate application to field-grown plants are known.

Currently, as reviewed by Anderson *et al.* [98], there are several commercial formulations of different *P. chlororaphis* isolates for agriculture: AtEze for greenhouse use, Cedemon and Cerall for use in cereals, and Howler formulations sold as fungicides. An additional *P. chlororaphis* formulation based on *P. chlororaphis* subsp. *aurantiaca* SR1 is available for use in Argentina to promote the growth of a variety of crops

[104]. It is likely that, as the need for 'green' regenerative and sustainable agriculture increases, there will be greater demand for products employing live cells and those based on bioactive metabolites from such microbes, such as *P. chlororaphis* isolates.

## SUMMARY OF BENEFICIAL TRAITS

The *P. chlororaphis* group of isolates is a topic of interest because of the biocontrol potential of these bacteria for commercially significant plant pests, such as microbes, insects and nematodes. A model showing the overlapping layers of protection resulting from microbial colonization of a plant root surface is presented in Fig. 1. The multifunctional effects of the interactions between *P. chlororaphis* isolates and the host plant are consistent with their functions as plant probiotics. Indeed, as discussed earlier, *P. chlororaphis* subsp. *piscium* isolates are termed fish probiotics because their presence in the intestine improves fish health.

Several metabolites of isolates from the *P. chlororaphis* group, first identified because of their antifungal activities, are multifunctional. These metabolites participate in metal chelation, insecticidal and nematocidal activities, biofilm formation, induction of priming for plant tolerance to stress and microbial cell signalling. Evidence has accumulated to show that the formation of a biofilm on a plant's surface plays a more important role than just securing an environment for bacterial cells. Instead, the biofilm presence on the root surface aids plant performance and resilience to stress. The beneficial effects of the *P. chlororaphis* group isolates on plants suggests that the use of these traits in commercial formulations for green and regenerative agriculture will be expanded.

### Funding information

This work was financially supported by Chonnam National University (grant number: 2018-3305).

### Conflicts of interest

The authors declare that there are no conflicts of interest.

### References

1. Biessy A, Novinscak A, Blom J, Leger G, Thomashow LS *et al.* Diversity of phytobeneficial traits revealed by whole-genome analysis of worldwide-isolated phenazine-producing *Pseudomonas* spp. *Environ Microbiol* 2019;21:437–455.
2. Deng P, Wang X, Baird SM, SE L. Complete genome of *Pseudomonas chlororaphis* strain UFB2, a soil bacterium with antibacterial activity against bacterial canker pathogen of tomato. *Stand Genomic Sci* 2015;10:117.
3. Peng Q, Yi L, Zhou L, Peng Q. Draft genome sequence of the vanadium-leaching bacterium *Pseudomonas chlororaphis* strain L19. *Genome Announc* 2018;6:e00966-17.
4. Wang X, Mavrodi DV, Ke L, Mavrodi OV, Yang M *et al.* Biocontrol and plant growth-promoting activity of rhizobacteria from Chinese fields with contaminated soils. *Microb Biotechnol* 2015;8:404–418.
5. Jain R, Pandey A. A phenazine-1-carboxylic acid producing polyextremophilic *Pseudomonas chlororaphis* (MCC2693) strain, isolated from mountain ecosystem, possesses biocontrol and plant growth promotion abilities. *Microbiol Res* 2016;190:63–71.

6. Al Baki MA, Jung JK, Maharjan R, Yi H, Ahn JJ et al. Application of insulin signaling to predict insect growth rate in *Maruca vitrata* (Lepidoptera: Crambidae). *PLoS One* 2018;13:e0204935.
7. Palleroni NJ. The *Pseudomonas* story. *Environ Microbiol* 2010;12:1377–1383.
8. Peix A, Valverde A, Rivas R, Igual JM, Ramirez-Bahena MH et al. Reclassification of *Pseudomonas aurantiaca* as a synonym of *Pseudomonas chlororaphis* and proposal of three subspecies, *P. chlororaphis* subsp. *chlororaphis* subsp. nov., *P. chlororaphis* subsp. *aureofaciens* subsp. nov., comb. nov. and *P. chlororaphis* subsp. *aurantiaca* subsp. nov., comb. nov. *Int J Syst Evol Microbiol* 2007;57:1286–1290.
9. Burr SE, Gobeli S, Kuhnert P, Goldschmidt-Clermont E, Frey J. *Pseudomonas chlororaphis* subsp. *piscium* subsp. nov., isolated from freshwater fish. *Int J Syst Evol Microbiol* 2010;60:2753–2757.
10. van Rij ET, Wesselink M, Chin A, Bloemberg GV, Lugtenberg BJ. Influence of environmental conditions on the production of phenazine-1-carboxamide by *Pseudomonas chlororaphis* PCL1391. *Mol Plant Microbe Interact* 2004;17:557–566.
11. Biessy A, Filion M. Phenazines in plant-beneficial *Pseudomonas* spp.: biosynthesis, regulation, function and genomics. *Environ Microbiol* 2018;20:3905–3917.
12. Haynes WC, Rhodes LJ. Comparative taxonomy of crystallogenic strains of *Pseudomonas aeruginosa* and *Pseudomonas chlororaphis*. *J Bacteriol* 1962;84:1080–1084.
13. Guttenberger N, Blankenfeldt W, Breinbauer R. Recent developments in the isolation, biological function, biosynthesis, and synthesis of phenazine natural products. *Bioorg Med Chem* 2017;25:6149–6166.
14. Bauer JS, Hauck N, Christof L, Mehnaz S, Gust B et al. The systematic investigation of the quorum sensing system of the biocontrol strain *Pseudomonas chlororaphis* subsp. *aurantiaca* PB-St2 unveils *aurl* to be a biosynthetic origin for 3-oxo-homoserine lactones. *Plos One* 2016;11:e0167002.
15. Wang D, Lee SH, Seeve C, JM Y, Pierson LS 3rd et al. Roles of the Gac-Rsm pathway in the regulation of phenazine biosynthesis in *Pseudomonas chlororaphis* 30-84. *MicrobiologyOpen* 2013;2:505–524.
16. JM Y, Wang D, Ries TR, Pierson LS 3rd, Pierson EA. An upstream sequence modulates phenazine production at the level of transcription and translation in the biological control strain *Pseudomonas chlororaphis* 30-84. *PLoS One* 2018;13:e0193063.
17. Nandi M, Selin C, Brawerman G, Fernando WG, de Kievit TR. The global regulator ANR is essential for *Pseudomonas chlororaphis* strain PA23 biocontrol. *Microbiology* 2016;162:2159–2169.
18. Shah N, Klaponski N, Selin C, Rudney R, Fernando WG et al. PtrA is functionally intertwined with GacS in regulating the biocontrol activity of *Pseudomonas chlororaphis* PA23. *Front Microbiol* 2016;7:1512.
19. Wang D, JM Y, Dorosky RJ, Pierson LS 3rd, Pierson EA. The phenazine 2-hydroxy-phenazine-1-carboxylic acid promotes extracellular DNA release and has broad transcriptomic consequences in *Pseudomonas chlororaphis* 30-84. *PLoS One* 2016;11:e0148003.
20. Manuel J, Selin C, Fernando WG, de Kievit T. Stringent response mutants of *Pseudomonas chlororaphis* PA23 exhibit enhanced antifungal activity against *Sclerotinia sclerotiorum* in vitro. *Microbiology* 2012;158:207–216.
21. Selin C, Fernando WG, de Kievit T. The PhzL/PhzR quorum-sensing system is required for pyrrolnitrin and phenazine production, and exhibits cross-regulation with RpoS in *Pseudomonas chlororaphis* PA23. *Microbiology* 2012;158:896–907.
22. Thomashow LS, Weller DM. Role of a phenazine antibiotic from *Pseudomonas fluorescens* in biological control of *Gaeumannomyces graminis* var. *tritici*. *J Bacteriol* 1988;170:3499–3508.
23. Duke KA, Becker MG, Girard IJ, Millar JL, Dilantha Fernando WG et al. The biocontrol agent *Pseudomonas chlororaphis* PA23 primes *Brassica napus* defenses through distinct gene networks. *BMC Genomics* 2017;18:467.
24. Han SH, Lee SJ, Moon JH, Park KH, Yang KY et al. GacS-dependent production of 2R, 3R-butanediol by *Pseudomonas chlororaphis* O6 is a major determinant for eliciting systemic resistance against *Erwinia carotovora* but not against *Pseudomonas syringae* pv. *tabaci* in tobacco. *Mol Plant Microbe Interact* 2006;19:924–930.
25. Ma Z, GKH H, Ongena M, Höfte M. Role of phenazines and cyclic lipopeptides produced by *pseudomonas* sp. CMR12a in induced systemic resistance on rice and bean. *Environ Microbiol Rep* 2016;8:896–904.
26. Chin A, Bloemberg GV, Mulders IH, Dekkers LC, Lugtenberg BJ. Root colonization by phenazine-1-carboxamide-producing bacterium *Pseudomonas chlororaphis* PCL1391 is essential for biocontrol of tomato foot and root rot. *Mol Plant Microbe Interact* 2000;13:1340–1345.
27. Cazorla FM, Duckett SB, Bergstrom ET, Noreen S, Odijk R et al. Biocontrol of avocado dematophora root rot by antagonistic *Pseudomonas fluorescens* PCL1606 correlates with the production of 2-hexyl 5-propyl resorcinol. *Mol Plant Microbe Interact* 2006;19:418–428.
28. Selin C, Habibian R, Poritsanos N, Athukorala SN, Fernando D et al. Phenazines are not essential for *Pseudomonas chlororaphis* PA23 biocontrol of *Sclerotinia sclerotiorum*, but do play a role in biofilm formation. *FEMS Microbiol Ecol* 2010;71:73–83.
29. Huang R, Feng Z, Chi X, Sun X, Lu Y et al. Pyrrolnitrin is more essential than phenazines for *Pseudomonas chlororaphis* G05 in its suppression of *Fusarium graminearum*. *Microbiol Res* 2018;215:55–64.
30. Park JY, SA O, Anderson AJ, Neiswender J, Kim JC et al. Production of the antifungal compounds phenazine and pyrrolnitrin from *Pseudomonas chlororaphis* O6 is differentially regulated by glucose. *Lett Appl Microbiol* 2011;52:532–537.
31. Mavrodi DV, Mavrodi OV, Parejko JA, Bonsall RF, Kwak YS et al. Accumulation of the antibiotic phenazine-1-carboxylic acid in the rhizosphere of dryland cereals. *Appl Environ Microbiol* 2012;78:804–812.
32. Nandi M, Selin C, Brassinga AK, Belmonte MF, Fernando WG et al. Pyrrolnitrin and hydrogen cyanide production by *Pseudomonas chlororaphis* Strain PA23 exhibits nematicidal and repellent activity against *Caenorhabditis elegans*. *PLoS One* 2015;10:e0123184.
33. Zhai Y, Shao Z, Cai M, Zheng L, Li G et al. Multiple modes of nematode control by volatiles of *Pseudomonas putida* 1A00316 from antarctic soil against *Meloidogyne incognita*. *Front Microbiol* 2018;9:253.
34. Flury P, Vesga P, Pechy-Tarr M, Aellen N, Dennert F et al. Antimicrobial and insecticidal: Cyclic lipopeptides and hydrogencyanide produced by plant-beneficial *Pseudomonas* strains CHAO, CMR12a, and PCL1391 contribute to insect killing. *Front Microbiol* 2017;8:100.
35. Kang BR, Anderson AJ, Kim YC. Hydrogen cyanide produced by *Pseudomonas chlororaphis* O6 exhibits nematicidal activity against *Meloidogyne hapla*. *Plant Pathol J* 2018;34:35–43.
36. Kang BR, Anderson AJ, Kim YC. Hydrogen cyanide produced by *Pseudomonas chlororaphis* O6 is a key aphicidal metabolite. *Can J Microbiol* 2019;65:185–190.
37. Hackenberg C, Muehlkchen A, Forge T, Vrain T. *Pseudomonas chlororaphis* strain Sm3, bacterial antagonist of *Pratylenchus penetrans*. *J Nematol* 2000;32:183–189.
38. Nam HS, Anderson AJ, Kim YC. Biocontrol efficacy of formulated *Pseudomonas chlororaphis* O6 against plant diseases and root-knot nematodes. *Plant Pathol J* 2018;34:241–249.
39. Audrain B, Farag MA, Ryu CM, Ghigo JM. Role of bacterial volatile compounds in bacterial biology. *FEMS Microbiol Rev* 2015;39:222–233.
40. Aziz M, Nadipalli RK, Xie X, Sun Y, Surowiec K et al. Augmenting sulfur metabolism and herbivore defense in *Arabidopsis* by bacterial volatile signaling. *Front Plant Sci* 2016;7:458.

41. Lemfack MC, Nickel J, Dunkel M, Preissner R, Piechulla B. mVOC: a database of microbial volatiles. *Nucleic Acids Res* 2014;42:D744–748.
42. Liu XM, Zhang H. The effects of bacterial volatile emissions on plant abiotic stress tolerance. *Front Plant Sci* 2015;6:774.
43. Zhang H, Kim MS, Krishnamachari V, Payton P, Sun Y et al. Rhizobacterial volatile emissions regulate auxin homeostasis and cell expansion in *Arabidopsis*. *Planta* 2007;226:839–851.
44. Schulz-Bohm K, Gerards S, Hundscheid M, Melenhorst J, de Boer W et al. Calling from distance: attraction of soil bacteria by plant root volatiles. *Isme J* 2018;12:1252–1262.
45. Cheng X, Cordovez V, Etalo DW, van der Voort M, Raaijmakers JM. Role of the GacS sensor kinase in the regulation of volatile production by plant growth-promoting *Pseudomonas fluorescens* SBW25. *Front Plant Sci* 2016;7:1706.
46. Brilli F, Pollastri S, Raio A, Baraldi R, Neri L et al. Root colonization by *Pseudomonas chlororaphis* primes tomato (*Lycopersicum esculentum*) plants for enhanced tolerance to water stress. *J Plant Physiol* 2019;232:82–93.
47. Cho SM, Kang BR, Han SH, Anderson AJ, Park JY et al. 2R,3R-butanediol, a bacterial volatile produced by *Pseudomonas chlororaphis* O6, is involved in induction of systemic tolerance to drought in *Arabidopsis thaliana*. *Mol Plant Microbe Interact* 2008;21:1067–1075.
48. An R, Moe LA. Regulation of pyrroloquinoline quinone-dependent glucose dehydrogenase activity in the model rhizosphere-dwelling bacterium *Pseudomonas putida* KT2440. *Appl Environ Microbiol* 2016;82:4955–4964.
49. Ryu CM, Farag MA, CH H, Reddy MS, Wei HX et al. Bacterial volatiles promote growth in *Arabidopsis*. *Proc Natl Acad Sci USA* 2003;100:4927–4932.
50. HS Y, Ahn YR, Song GC, Ghim SY, Lee S et al. Impact of a bacterial volatile 2,3-butanediol on *Bacillus subtilis* rhizosphere robustness. *Front Microbiol* 2016;7:979.
51. Park JY, Kang BR, Ryu CM, Anderson AJ, Kim YC. Polyamine is a critical determinant of *Pseudomonas chlororaphis* O6 for GacS-dependent bacterial cell growth and biocontrol capacity. *Mol Plant Pathol* 2018;19:1257–1266.
52. Zhang Y, Li T, Liu Y, Li X, Zhang C et al. Volatile organic compounds produced by *Pseudomonas chlororaphis* subsp. *aureofaciens* SPS-41 as biological fumigants to control *Ceratocystis fimbriata* in postharvest sweet potatoes. *J Agric Food Chem* 2019;67:3702–3710.
53. Tagele SB, Lee HG, Kim SW, Lee YS. Phenazine and 1-undecene producing *Pseudomonas chlororaphis* subsp. *aurantiaca* strain KN17Pc1 for growth promotion and disease suppression in Korean maize cultivars. *J Microbiol Biotechnol* 2019;29:66–78.
54. McManus P, Hortin J, Anderson AJ, Jacobson AR, Britt DW et al. Rhizosphere interactions between copper oxide nanoparticles and wheat root exudates in a sand matrix: influences on copper bioavailability and uptake. *Environ Toxicol Chem* 2018;37:2619–2632.
55. Tian JH, Pourcher AM, Peu P. Isolation of bacterial strains able to metabolize lignin and lignin-related compounds. *Lett Appl Microbiol* 2016;63:30–37.
56. Moreno-Avitia F, Lozano L, Utrilla J, Bolívar F, Escalante A. Draft genome sequence of *Pseudomonas chlororaphis* ATCC 9446, a nonpathogenic bacterium with bioremediation and industrial potential. *Genome Announc* 2017;5.
57. Kim YC, Anderson AJ. Rhizosphere pseudomonads as probiotics improving plant health. *Mol Plant Pathol* 2018;19:2349–2359.
58. Pechy-Tarr M, Bruck DJ, Maurhofer M, Fischer E, Vogne C et al. Molecular analysis of a novel gene cluster encoding an insect toxin in plant-associated strains of *Pseudomonas fluorescens*. *Environ Microbiol* 2008;10:2368–2386.
59. Loper JE, Hassan KA, Mavrodin DV, Davis EW 2nd, Lim CK et al. Comparative genomics of plant-associated *Pseudomonas* spp.: insights into diversity and inheritance of traits involved in multi-trophic interactions. *PLoS Genet* 2012;8:e1002784.
60. Rangel LI, Henkels MD, Shaffer BT, Walker FL, Davis EW 2nd et al. Characterization of toxin complex gene clusters and insect toxicity of bacteria representing four subgroups of *Pseudomonas fluorescens*. *PLoS One* 2016;11:e0161120.
61. Schellenberger U, Oral J, Rosen BA, Wei JZ, Zhu G et al. A selective insecticidal protein from *Pseudomonas* for controlling corn rootworms. *Science* 2016;354:634–637.
62. Spencer M, Ryu C-M, Yang K-Y, Kim YC, Kloepper JW et al. Induced defence in tobacco by *Pseudomonas chlororaphis* strain O6 involves at least the ethylene pathway. *Physiol Mol Plant Pathol* 2003;63:27–34.
63. Dorosky RJ, Pierson LS 3rd, Pierson EA. *Pseudomonas chlororaphis* produces multiple R-tailocin particles that broaden the killing spectrum and contribute to persistence in rhizosphere communities. *Appl Environ Microbiol* 2018;84:e01230–18.
64. Dorosky RJ, JM Y, Pierson LS 3rd, Pierson EA. *Pseudomonas chlororaphis* produces two distinct R-tailocins that contribute to bacterial competition in biofilms and on roots. *Appl Environ Microbiol* 2017;83:e00706–00717.
65. Ghequire MG, De Mot R. Ribosomally encoded antibacterial proteins and peptides from *Pseudomonas*. *FEMS Microbiol Rev* 2014;38:523–568.
66. Dimkpa CO, McLean JE, Britt DW, Anderson AJ. CuO and ZnO nanoparticles differently affect the secretion of fluorescent siderophores in the beneficial root colonizer, *Pseudomonas chlororaphis* O6. *Nanotoxicology* 2012;6:635–642.
67. Jin XJ, Peng HS, HB H, Huang XQ, Wang W et al. iTRAQ-based quantitative proteomic analysis reveals potential factors associated with the enhancement of phenazine-1-carboxamide production in *Pseudomonas chlororaphis* P3. *Sci Rep* 2016;6:27393.
68. Wang Y, Newman DK. Redox reactions of phenazine antibiotics with ferric (hydr)oxides and molecular oxygen. *Environ Sci Technol* 2008;42:2380–2386.
69. Shahid I, Rizwan M, Baig DN, Saleem RS, Malik KA et al. Secondary metabolites production and plant growth promotion by *Pseudomonas chlororaphis* and *P. aurantiaca* strains isolated from cactus, cotton, and para grass. *J Microbiol Biotechnol* 2017;27:480–491.
70. Arat S, Bullerjahn GS, Laubenbacher R. A network biology approach to denitrification in *Pseudomonas aeruginosa*. *PLoS One* 2015;10:e0118235.
71. Domingos P, Prado AM, Wong A, Gehring C, Feijo JA. Nitric oxide: a multitasked signaling gas in plants. *Mol Plant* 2015;8:506–520.
72. Jacobson A, Doxey S, Potter M, Adams J, Britt D et al. Interactions between a plant probiotic and nanoparticles on plant responses related to drought tolerance. *Industrial Biotechnology* 2018;14:148–156.
73. Wright M, Adams J, Yang K, McManus P, Jacobson A et al. A root-colonizing pseudomonad lessens stress responses in wheat imposed by CuO nanoparticles. *PLoS One* 2016;11:e0164635.
74. Greenberg EP, Becker GE. Nitrous oxide as end product of denitrification by strains of fluorescent pseudomonads. *Can J Microbiol* 1977;23:903–907.
75. Haslun JA, Ostrom NE, Hegg EL, Ostrom PH. Estimation of isotope variation of  $N_2O$  during denitrification by *Pseudomonas aureofaciens* and *Pseudomonas chlororaphis*: implications for  $N_2O$  source apportionment. *Biogeosciences* 2018;15:3873–3882.
76. Costerton JW, Stewart PS, Greenberg EP. Bacterial biofilms: a common cause of persistent infections. *Science* 1999;284:1318–1322.
77. JM Y, Wang D, Pierson LS 3rd, Pierson EA. Effect of producing different phenazines on bacterial fitness and biological control in *Pseudomonas chlororaphis* 30-84. *Plant Pathol J* 2018;34:44–58.
78. LeTourneau MK, Marshall MJ, Cliff JB, Bonsall RF, Dohnalkova AC et al. Phenazine-1-Carboxylic acid and soil moisture influence biofilm development and turnover of rhizobacterial biomass on wheat root surfaces. *Environ Microbiol* 2018;20:2178–2194.

79. Mavrodi DV, Mavrodi OV, Elbourne LDH, Tetu S, Bonsall RF *et al.* Long-term irrigation affects the dynamics and activity of the wheat rhizosphere microbiome. *Front Plant Sci* 2018;9:345.

80. Mavrodi OV, Mavrodi DV, Parejko JA, Thomashow LS, Weller DM. Irrigation differentially impacts populations of indigenous antibiotic-producing *pseudomonas* spp. in the rhizosphere of wheat. *Appl Environ Microbiol* 2012;78:3214–3220.

81. Costa OYA, Raaijmakers JM, Kuramae EE. Microbial extracellular polymeric substances: ecological function and impact on soil aggregation. *Front Microbiol* 2018;9:1636.

82. Naseem H, Ahsan M, Shahid MA, Khan N. Exopolysaccharides producing rhizobacteria and their role in plant growth and drought tolerance. *J Basic Microbiol* 2018;58:1009–1022.

83. Timmusk S, Kim SB, Nevo E, Daim AE I, Ek B *et al.* Sfp-type PPTase inactivation promotes bacterial biofilm formation and ability to enhance wheat drought tolerance. *Front Microbiol* 2015;6:387.

84. Mahmoudi TR, JM Y, Liu S, Pierson LS 3rd, Pierson EA. Drought-stress tolerance in wheat seedlings conferred by phenazine-producing rhizobacteria. *Front Microbiol* 2019;10:1590.

85. Yang K-Y, Doxey S, McLean JE, Britt D, Watson A *et al.* Remodeling of root morphology by CuO and ZnO nanoparticles: effects on drought tolerance for plants colonized by a beneficial *pseudomonad*. *Botany* 2017;96:175–186.

86. Cho SM, Anderson AJ, Kim YC. Extracellular polymeric substances of *Pseudomonas chlororaphis* O6 induce systemic drought tolerance in plants. *Res Plant Dis* 2018;24:242–247.

87. Couto N, Schooling SR, Dutcher JR, Barber J. Proteome profiles of outer membrane vesicles and extracellular matrix of *Pseudomonas aeruginosa* biofilms. *J Proteome Res* 2015;14:4207–4222.

88. Gade A, Adams J, Britt DW, Shen FA, McLean JE *et al.* Ag nanoparticles generated using bio-reduction and -coating cause microbial killing without cell lysis. *Biometals* 2016;29:211–223.

89. Schertzer JW, Whiteley M. Bacterial outer membrane vesicles in trafficking, communication and the host-pathogen interaction. *J Mol Microbiol Biotechnol* 2013;23:118–130.

90. Satarian F, Nejadsattari T, Vaziri F, Siadat SD. Comparative study of immune responses elicited by outer membrane vesicles of different *Pseudomonas aeruginosa* strains. *Comp Immunol Microbiol Infect Dis* 2019;66:101328.

91. Choi HW, Klessig DF. Damps, MAMPs, and NAMPs in plant innate immunity. *BMC Plant Biol* 2016;16:232.

92. Li J, Yang Y, Dubern JF, Li H, Halliday N *et al.* Regulation of GacA in *Pseudomonas chlororaphis* strains shows a niche specificity. *PLoS One* 2015;10:e0137553.

93. Calderon CE, Ramos C, de Vicente A, Cazorla FM. Comparative genomic analysis of *Pseudomonas chlororaphis* PCL1606 reveals new insight into antifungal compounds involved in biocontrol. *Mol Plant Microbe Interact* 2015;28:249–260.

94. Calderon CE, Tienda S, Heredia-Ponce Z, Arrebola E, Carcamo-Oyarce G *et al.* The compound 2-hexyl, 5-propyl resorcinol has a key role in biofilm formation by the biocontrol rhizobacterium *Pseudomonas chlororaphis* PCL1606. *Front Microbiol* 2019;10:396.

95. Brameyer S, Kresovic D, Bode HB, Heermann R. Dialkylresorcinols as bacterial signaling molecules. *Proc Natl Acad Sci USA* 2015;112:572–577.

96. Cimmino A, Evidente A, Mathieu V, Andolfi A, Lefranc F *et al.* Phenazines and cancer. *Nat Prod Rep* 2012;29:487–501.

97. Krishnan HB, Kang BR, Hari Krishnan A, Kim KY, Kim YC. *Rhizobium etli* USDA9032 engineered to produce a phenazine antibiotic inhibits the growth of fungal pathogens but is impaired in symbiotic performance. *Appl Environ Microbiol* 2007;73:327–330.

98. Anderson JA, Staley J, Challender M, Heuton J. Safety of *Pseudomonas chlororaphis* as a gene source for genetically modified crops. *Transgenic Res* 2018;27:103–113.

99. Carlson AB, Mathesius CA, Ballou S, Boeckman CJ, Gunderson TA *et al.* Safety assessment of coleopteran active IPD072Aa protein from *Pseudomonas chlororaphis*. *Food Chem Toxicol* 2019;129:376–381.

100. Shen X, Wang Z, Huang X, Hu H, Wang W *et al.* Developing genome-reduced *Pseudomonas chlororaphis* strains for the production of secondary metabolites. *BMC Genomics* 2017;18:715.

101. Shen X, Chen M, Hu H, Wang W, Peng H *et al.* Genome sequence of *Pseudomonas chlororaphis* GP72, a root-colonizing biocontrol strain. *J Bacteriol* 2012;194:1269–1270.

102. Faccone D, Pasteran F, Albornoz E, Gonzalez L, Veliz O *et al.* Human infections due to *Pseudomonas chlororaphis* and *Pseudomonas oleovorans* harboring new blaVIM-2-borne integrons. *Infect Genet Evol* 2014;28:276–277.

103. Monta S, Lazzaro T, Uong S, Place K, Iriarte A *et al.* Genomics helps to decipher the resistance mechanisms present in a *Pseudomonas chlororaphis* strain recovered in an HIV patient. *New Microbes and New Infections* 2018;25:45–47.

104. Rosas SB. *Pseudomonas chlororaphis* subsp. *aurantiaca* SR1: isolated from rhizosphere and its return as inoculant. A review. *International Biology Review* 2017;1:1–19.

### Five reasons to publish your next article with a Microbiology Society journal

1. The Microbiology Society is a not-for-profit organization.
2. We offer fast and rigorous peer review – average time to first decision is 4–6 weeks.
3. Our journals have a global readership with subscriptions held in research institutions around the world.
4. 80% of our authors rate our submission process as 'excellent' or 'very good'.
5. Your article will be published on an interactive journal platform with advanced metrics.

Find out more and submit your article at [microbiologyresearch.org](http://microbiologyresearch.org).