From lichens to crops: Pathogenic potential of *Pseudomonas syringae* from *Peltigera* lichens is similar to world-wide epidemic strains

Natalia Ramírez[1,2], Emma Caullireau[2,3], Margrét Auður[1] Sigurbjörnsdóttir[1], Elodie Vandelle[3], Oddur Vilhelmsson[1], Cindy E. Morris[2]

[1] Department of Natural Resource Sciences, University of Akureyri, Borgir vid Nordurslod, 600 Akureyri, Iceland.

[2] INRAE, UR0407 Pathologie Vegétale, 84143 Montfavet Cedex, France

[3] Department of Biotechnology, University of Verona, 37134 Verona, Italy

Corresponding author: Natalia Ramírez, PhD candidate, nataliar@unak.is. ORCID: 0000-0003-4316-4104

Keywords: non-agricultural habitat, pathogenicity test, plant pathogen, epidemic strains

Ethics and integrity policies

- The authors declare no conflict of interest.
- This work was funded by the Rannis Icelandic Research Fund under project number 1908-0151.

Abstract

The presence of bacteria belonging to the *Pseudomonas syringae* complex (*P. syringae*) in

the natural vegetation of several Icelandic habitat types has been recently reported, raising

questions about the risk to Icelandic crops, particularly given the expected increase in

agricultural activity due to climate warming. This study takes advantage of Iceland's unique

characteristics and the discovery of *P. syringae* in *Peltigera* lichens to gain a better

understanding of the potential risk posed by this newly discovered ecological niche. The main

objective is to evaluate the pathogenic potential and fitness in crops of *P. syringae* strains

isolated from *Peltigera* lichen sampled in Iceland, focusing on strains that belong to

phylogroups 1 and 2, which commonly contain epidemic strains. The results indicate that *P.*

syringae isolated from Icelandic *Peltigera* lichen have a comparable fitness to epidemic strains

in eight out of ten tested plant species. Furthermore, pathogenicity assessment on three plant

species highlighted that certain strains also caused similar symptoms and disease severity

compared to epidemic strains. These findings provide valuable insights into the potential risks

posed by *P. syringae* from Icelandic natural habitats and illustrate how strains from these

habitats have a wide pathogenic potential to crops without having encountered these crops in

the last several thousand years of their presence in Iceland.

Introduction

Bacterial strains within the *P. syringae* complex are present in connection with diverse biotic

and non-living substrates worldwide. The ability of *P. syringae* to adapt to a wide range of

habitats linked to the water cycle is thought to be a driver of its broad host range (Morris et al.

2013). This idea is reinforced by the observation that numerous strains from this group of

bacteria isolated from non-agricultural environments are phylogenetically closely related to

plant-associated strains and have also been shown to be pathogenic on plants such as

kiwifruit and tomato (Morris et al, 2019). For this reason, recent research has continued to

explore the ecology and pathogenicity of *P. syringae* outside the context of crops.

According to Ellis et al. (2010), agricultural land is becoming increasingly prevalent compared

to other vegetated areas on Earth. However, Iceland stands out as an atypical region with a

limited amount of cultivated land, thereby providing a unique opportunity to study the

adaptation of *P. syringae* without a predominant influence of local agriculture. Iceland's flora

is characterized by a relatively small number of native species of vascular plants, comprising

around 530 species (Wąsowicz 2020). Additionally, the country is home to a diverse range of

lichens (755 species) (Kristinsson and Heiðmarsson, 2009) and mosses (around 600 species)

(Jóhannsson 2003). However, the vegetation of Iceland evolved in the absence of large

herbivores and subsequently is vulnerable to grazing and human activities (Runólfsson 1987).

Furthermore, Iceland's position on the border between Arctic and Atlantic waters and air

masses, known as the polar front, makes for an interface (Jónsdóttir et al. 2005) which creates

favourable climate conditions for *P. syringae* with average temperatures between 2 to 14°C

throughout the year (Ogilvie and Jónsson, 2001).

A lichen is a composite organism resulting from a symbiotic association between a fungus,

known as the mycobiont, and one or more photosynthetic partners, termed photobionts. The

photosynthetic partners are typically green algae or cyanobacteria. This mutualistic

relationship forms a unique structure known as a thallus, which is the visible body of the lichen.

(Boustie and Grube, 2005; Feuerer and Hawksworth, 2007; Cardinale et al, 2006; Leiva et al,

2021), fungi, sometimes pathogenic for the lichen (Bates et al, 2012; Spribille et al, 2016),

archaea (Bjelland et al, 2011; Garg et al, 2016), and viruses (Eymann et al, 2017). While

lichens heavily depend on the atmosphere for water intake, their remarkable resilience in

challenging environments is partly attributed to the microbiome associated with lichens,

playing a crucial role in their survival. (Leiva et al, 2021; Pisani et al, 2011; Bates et al, 2011;

Bjelland et al, 2011; Cardinale et al, 2012, 2008, 2006; Grube and Berg, 2009; Hodkinson and

Lutzoni, 2010; Mushegian et al, 2011; Selbmann et al, 2010; Sigurbjörnsdóttir et al, 2015).

Previous research has shown that *P. syringae* is prevalent in Iceland on wild vascular plants

and moss (Morris et al. 2022), confirmed by the observations of *P. syringae* genes in the lichen

metagenome of *Peltigera membranaceae* (Sigurbjörnsdóttir et al. 2015; Sigurbjörnsdóttir,

2016). This prompted researchers to investigate its ubiquity across several types of plants and

lichens in Iceland, hypothesizing that lichens may serve as non-host reservoirs for *P. syringae*

(Vilhelmsson et al. 2016). Morris and colleagues (Morris et al. 2022) unveiled how the genetic

lines of *P. syringae* in the Icelandic region are monophyletic, indicating that they may have

evolved separately from the *P. syringae* populations elsewhere in the world during the

relatively short geological history of Iceland. However, these monophyletic haplotypes

represent different phylogroups (PGs) (Morris et al. 2022). This illustrates the extraordinary

adaptive properties throughout the *P. syringae* complex.

P. syringae was found in lichens in Iceland, specifically in species of the genus *Peltigera*

(Ramírez et al. 2023). To delve deeper into this discovery, a phylogenetic analysis of *P.

syringae* strains collected from various sources, including lichens, tracheophytes, and moss

was conducted. The analyses revealed significant differences among strains between

geographical locations, showing a greater similarity of *P. syringae* within a site across all

vegetation types rather than within vegetation types across sites. Moreover, *Peltigera* thalli

harbored a consistent population density of *P. syringae* although it was lower than that on

moss and tracheophyte samples (Ramírez et al. 2023). This finding underscores the

adaptability of *P. syringae* to inhabit a diverse range of vegetation beyond higher plants,

offering novel insights into its evolutionary dynamics.

Assigning *P. syringae* strains to phylogroups based on their citrate synthase gene sequences

(Berge et al. 2014) is a useful tool for understanding their phenotypic variations. Many of the

strains isolated from *Peltigera* lichens can be assigned to phylogroups PG01 and PG02. These

phylogroups contain a wide range of epidemic strains, as documented by Berge and

colleagues (Berge et al. 2014). Roughly fifty percent of the lichen thalli were found to host

PG01 and/or PG02 strains. Among the *P. syringae* isolates, PG02 included approximately

14% of strains and PG01 accounted for a mere 4% of the overall *P. syringae* population

derived from *Peltigera*, while the remaining 82% were assigned to the environmental habitat-

associated phylogroups PG10 and PG13 (Ramírez et al. 2023).

In light of the ubiquity of bacteria in the *P. syringae* complex on vegetation in Iceland and, in

particular, the presence of the PG01 and PG02 phylogroups showing high frequencies of

strains displaying a functional T3SS (Berge et al. 2014), our goal was to assess the fitness

and pathogenic potential – mainly on crops - of strains from PG01 and PG02 from Icelandic

Peltigera compared to strains in the same phylogroup isolated from epidemics on crops

elsewhere in the world.

Materials and methods

Bacterial strains

P. syringae strains belonging to PG01 and PG02 were randomly selected from a collection of

strains isolated from *Peltigera* lichen that previously tested positive in a HR test to represent

the range of diversity of these phylogroups associated with this group of lichens (Fig. 1). As

positive controls, strains belonging to PG01 and PG02 from epidemic occurrences were

chosen due to their well-established pathogenic potential and consistent behavior, as revealed

by previous work (Morris et al. 2019). For fitness assessment, the reference strains included

CC0094 (PG02d) and Pto DC3000 (PG01a). For the evaluation of pathogenicity, CC0125 and

CFBP1906 (PG02b), and CC0094 (PG02d), were employed as reference controls, aligning

with the findings outlined previously (Morris et al. 2000).

Fig.1 Phylogenetic tree illustrating the strains included in the study, along with details on lichen of isolation,

phylogroup classification, site of isolation, and lesion formation in kale, cucumber, and barley. The color code

represents different categories, and an arrow indicates the strains selected for fitness analyses.

Inoculum preparation

Bacterial inoculum was prepared from 24-72 hr growth on King's B (KB) medium (King et al.

1954). A loopful of growth was resuspended in phosphate buffer (TP1: 8,75g of K_2HPO_4 and

6,75g of KH_2PO_4 diluted in 1L of distilled water) and adjusted with a spectrophotometer to 10^8

CFU mL^{-1} (OD$_{600\ nm}$ = 0.1). The inoculum was further diluted in phosphate buffer, resulting in

a concentration of 10^7 CFU mL^{-1} for the pathogenicity tests and 10^6 CFU mL^{-1} for the in planta

in the fitness tests. Inoculum concentration was verified by dilution plating.

Plant material

For fitness tests, plant species belonging to 10 families were used: rice (*Oryza sativa*), tomato

(*Solanum lycopersicum*), thale cress (*Arabidopsis thaliana*), annual mugwort (*Artemisia*

annua), spinach (*Spinacia oleracea*), garlic chives (*Allium tuberosum*), tobacco (*Nicotiana*

tabacum), kale (*Brassica oleracea*), cucumber (*Cucumis sativus*) and barley (*Hordeum*

vulgare). Pathogenic potential was evaluated on the last three plant species, which are

cultivated in Iceland. Cultivar details, growing conditions, and cultivation dates can be found

in Table S2. The duration of cultivation in the greenhouse was tailored to the specific plant

species. In the greenhouse environment of Montfavet, France, the plants were cultivated

during a period spanning from September 2022 to January 2023. Adequate watering was

provided in accordance with the plants' needs. Plants were grown in TS3 substrate mixture

from Klasmann-Deilmann (Geeste, Germany).

Evaluation of fitness *in planta*

Fitness of strains in plants was determined in terms of population growth after inoculation

using a modified protocol based on methodologies outlined in Clarke et al,(2010) Donati et

al,(2020) and Kim et al, (2022). Leaf tissue was wounded and strains were inoculated into

plants by placing a 5μL-drop of inoculum (10^6 CFU mL^{-1}), letting the inoculum be absorbed by

the plant. An emery board/emery paper was used gently to create a fresh wound on the

surface of the leaf. Each plant received a single inoculation, and there were 10 replicate plants

per strain.

Three to five plants were inoculated with phosphate buffer as negative control for each plant

species. For a given plant species, all strains were inoculated simultaneously to facilitate

between-strain comparisons. Via a randomized complete block design, the plants were set up

in a growth chamber and incubated at 24 °C (14 h light, 10 h dark) and 75% humidity.

At 1 and 8 days post inoculation (dpi), five leaves were collected from each plant species for

each strain, except in the case of *A. thaliana*, where six leaves were collected. Prior to

maceration, leaves bearing soil residues were gently cleaned using dry paper. Each leaf was

stomached for 2–3 min in sterile phosphate buffer (10μL of 0.1 M buffer per mg of fresh plant

weight amounting to between 1-30 ml depending on the leaf size) in sterile stomacher bags.

Aliquots of serial dilutions of the macerate were plated on KB medium. The plates were placed

in a dark environment and incubated at room temperature for a period of 48-72 hours. *P.*

syringae colonies were identified based on their shape, size, color, texture, elevation, and

margin (Morris et al. 2022). The abundance of *P. syringae* in the inoculated leaves was

expressed per leaf.

Inoculation, incubation, and disease assessment for pathogenicity assays

We employ a modified protocol inspired by Bartoli et al,(2015) and Cazorla et al, (1998). One

leaf per plant was infiltrated with a needleless syringe with 5-10 µL of inoculum (10^7 CFU

mL^{-1}). Six to eight replicate plants were utilized per plant species per strain. The negative

control consisted of phosphate buffer. Plants were arranged in a growth chamber in a

randomized complete block design and incubated at 24 °C (14 h light, 10 h dark) and 75%

humidity for 14 days.

Symptoms were scored at 2, 5, 9 and 14 dpi in terms of the maximum length of the necrosis

that developed at the inoculated site except for cucumber that was observed only until 9 dpi.

Symptoms were also photographed and described at each scoring date. Strains were

classified as pathogenic if the necrotic length was significantly different than the negative

control.

To verify that symptoms were caused by *P. syringae*, isolations were made from at least three

infected tissue replicates per strain. Sections of tissue (at the interface of necrotic and the

green surrounding tissue) were aseptically collected and placed on KB plates and incubated

at 24°C in darkness. After 2-3 days, colony morphology, colour and fluorescence under 366

nm were assessed.

Statistical analyses

Utilizing Microsoft Excel and R Studio, statistical analyses were conducted. This included t-

tests, graph plotting with the ggplot2 package, and one-way ANOVA. The t-test was applied

to determine the differences between strains inoculated into the same plant species at various

time points. Moreover, one-way ANOVA was employed, followed by post hoc Tukey-Kramer

analysis to unravel strain variations.

Results

***P. syringae* isolated from Icelandic *Peltigera* lichens and epidemic strains have similar**

fitness in plants

The fitness analysis revealed that *P. syringae* strains isolated from Icelandic *Peltigera* lichen

(hereafter referred as lichen strains) exhibited overall population growth levels similar to the

epidemic strains CC0094 and DC3000 at both 1 and 8 dpi under the specified culture

conditions across the ten plant species tested, except for cucumber, barley and tomato.

Indeed, differences emerged in tomato at 1 dpi, with the population size of *Peltigera* lichen *P.*

syringae strains reaching higher densities compared to epidemic ones (Figure S1), although

no difference was further observed at 8 dpi. Conversely, despite a similar population density

at 1 dpi, the *Peltigera* strains showed a lower population level at 8 dpi compared with epidemic

strains in cucumber and barley (Fig. 2). For the latter, however, considering both time points,

the comparison of the total population of lichen strains was significantly higher than the

population density of epidemic strains (p value < 0.05). This indicates that *Peltigera* strains

display, as whole, the same *in-planta* fitness than epidemic strains, with some variability

among plant species.

Interestingly, each lichen strain behave like the epidemic one belonging to the same

phylogroup. Indeed, the main differences were observed more at phylogroup level, with PG02

(including CC0094, HV201426 and EG201428) showing higher bacterial densities compared

to PG01 (DC3000, SU200124 and HV200408), at 1 dpi only, in 7 out of the 10 analyzed plant

species. Such discrepancy, that was not noticed anymore at 8 dpi, suggests a better capacity

of PG02 strains to adapt and start growing in plants independently of their origin.

On the other hand, when examining strains individually, at 1 dpi, CC0094 consistently showed

a greater population size compared with DC3000 in all plant species but *Arabidopsis*, and

higher than all strains but HV200426 in tobacco (Fig. 2). Conversely, at 8 dpi, distinctions were

observed only in cucumber, with DC3000 having greater population sizes than all lichen

strains, and in barley, where CC0094 had a significantly higher population size than SU200124

(p-value <0.05) (Fig. 2). Finally, looking at the dynamic of population growth, we observed

that, in general, all strains (epidemic and lichen) display a population increase between 1 dpi

and 8 dpi in all plant species, except for HV200408 and SU200124 that decreased over time

in cucumber (Fig.S2), while no strain but EG210103 did grow in kale between 1 and 8 dpi

(Fig.S3).

***P. syringae* from *Peltigera* and from crop epidemics have similar pathogenic potential**

For this analysis the set of lichen strains was enlarged to a total of 17, including the 4 strains

used for *in-planta* fitness investigation, together with 4 and 9 additional strains belonging to

PG01 and PG02, respectively. To account for non-specific reactions of the plants due to

wounding, the size of the necroses on plants inoculated with selected strains was compared
to those observed on control plants. Nine out of the 17 strains of *P. syringae* isolated from
lichen produced necrotic symptoms that were significantly longer than any of the necroses
observed on the negative controls in barley (Fig. 3.a) and cucumber (Fig. 3.b), and comparable
to the lesions caused by epidemic strains. These same nine *Peltigera* strains and four
additional strains, for a total of 13 out of 17, also caused lesions that were significantly longer
on kale when compared to damage on control plants, and in the same size range than those
observed with epidemic strains (Fig. 3.c).

Fig.3 Leaf symptoms at 14 dpi. The leaves represent some of the most common symptoms observed on each
plant species.1. Barley infected with strains a) HV201426; b) EG201422; c) EG201428; d) HV201426 e) Positive
control CFBP1906; and f) Negative control. 2. Kale infected with strains a) HV201426; b) EG210110; c)
SU200403; d) EG201426; e) Positive control CFBP1906; and f) Negative control

According to lesion size, symptoms were most severe on barley and cucumber compared to
kale, although we cannot rule out the possibility that such differences could be attributable to
technical aspects (e.g, plant growth conditions, plant age). Moreover, not only the number of
PG02 strains (7 in barley and cucumber, 9 in kale) causing significant lesions was higher than

the number of PG01 strains (1 in barley and cucumber, 4 in kale) but, considering only

necrosis-inducing strains, symptoms caused by PG02 strains were overall more severe than

those caused by PG01 strains. Indeed, symptom severity (lesion length) in most cases was

within the same range as those caused by the strains from crop epidemics (Fig. 3).

In barley, in addition to necrosis, other symptoms such as chlorosis, leaf collapse, wilting,

water-soaked areas or a slightly pale appearance were also recorded, mainly following

infection with necrosis-inducing strains (Fig. 4.1). Similarly, the infiltration of the *Peltigera*

strains in kale caused symptoms such as chlorosis, water-soaked areas sometimes

surrounded by a yellow halo and pale appearance, besides necrotic lesions (Fig. 4.2). The

observed symptoms in cucumber included necrosis, chlorosis, and lesions with a yellow halo

(images not available).

Fig. 4 *P. syringae* population in inoculated leaves of ten plant species on the 8th day post-infection. Violin and boxplot graphs resume the values of *P. syringae* per leaf for 5 or 6 replicates per strain inoculated in each plant. The Icelandic strains isolated from lichens are represented by a solid color while the epidemic strains used as control are plotted as transparent. PG1 strains are represented by the color blue, while PG2 strains are depicted

In some cases, however, necroses resembled hypersensitive-like cell death, *i.e.* occurring

shortly after infiltration and apparently localized to the site of infection. In particular, such a

phenotype was observed in cucumber inoculated with the *Peltigera* strains belonging to PG01,

namely HV200408 and SU200124, which induced smaller lesions, reaching a maximum length

of around 15 mm, compared to the lesions induced by PG02 strains with a lesion size

comprised between 30 and 40 mm (Fig.S2). Interestingly, the two above-mentioned strains

showed a decrease in population size in cucumber 8 dpi compared to 1 dpi, likely related to

the induction of HR leading to the restriction of bacterial growth.

The induction of HR-like cell death was also common to numerous strains tested in kale,

including the lichen strains HV200408 and SU200124 from PG01, and HV201426 and

EG201408 belonging to PG02, together with the epidemic strain CC0094 (Fig.S3).

Interestingly, the lesions induced by these strains were already clearly visible after only 2dpi,

but did not increase further up to 14 dpi. Considering the absence of bacterial population

increase between 1 and 8 dpi in fitness experiments (Fig.2), these results indicate the capacity

of these *Peltigera* strains to induce a rapid HR in kale that an in turn stop bacterial growth.

Conversely, the PG02 lichen strain EG210103 induced significant lesions in kale only after 5

dpi and these necroses were characterized by the presence of chlorosis (Fig.S3.b). Moreover,

this strain was the only one capable of growing between 1 and 8 dpi in fitness experiments,

thus supporting the absence of HR in this case.

Discussion

Here we have revealed that *P. syringae* isolated from *Peltigera* lichen in Iceland has fitness

and pathogenicity levels comparable to strains isolated from epidemic crops worldwide. As a

component of pathogenicity, some *Peltigera* strains were capable of inducing HR. Hence,

even though we do not know what the host range would be in a cropping system, the strains from lichens possess a functional system to deliver effectors and to be recognized by a plant as something more than a saprophyte.

Numerous studies have demonstrated that *P. syringae* retains its pathogenic capability even in the absence of significant agricultural pressures (Morris et al. 2008; Morris et al. 2013; Morris and Moury, 2019), especially in those strains that have a wider range of habitat. The hypothesis suggests that the pathogenicity of *P. syringae* could be more pronounced and evident in agricultural contexts due to the lack of genetic diversity of the host and some practices for cultivation that might favor a rapid growth of *P. syingae,* eventhough it can also grow in non-agricultural plants as *Arabidopsis thaliana*, grass and ornamental plants (Jones et al, 1986; Katagiri et al, 2002; Sato et al, 2001). However, the unique context of the Icelandic *P. syringae* strains that have evolved in Iceland for thousands of years makes them an interesting case study (Morris et al. 2022) as it illustrates the ancestral nature of the traits that confer pathogenicity and their maintenance in populations in natural habitats (Xin et al. 2018)

.

Although the pathogenicity observed in controlled conditions do not precisely reflect the pathogenicity of bacterial strains in the field, our results clearly illustrate the pathogenic potential of Icelandic strains, under favorable conditions. Thus, while this suggests the potential threat posed by *P. syringae* in Iceland, it is crucial to keep in mind that *P. syringae* is ubiquitous in the environment. In this light, it is notable that there have been no reported instances of *P. syringae* causing diseases in local crops in Iceland nor to the native vegetation. This highlights the role that environmental factors, such as cold temperatures that reduce the cultivation season or average temperatures under the optimal for *P. syringae* to develop aggressive traits (Bender et al. 1999), likely play in constraining bacterial proliferation and

safeguarding plant health. The interplay of environmental conditions significantly contributes

to the assessment of disease potential (Morris et al. 2023).

P. syringae in Iceland has evolved over the past 10000 years, at least, separate from contact

with plants that are common to agricultural landscapes such as rice and tomato (Morris et al.

2022). Nevertheless, Icelandic strains display some level of fitness in these plants, which could

be then considered as novel potential hosts for such stains. This raises intriguing questions

about the establishment of host specificity. However, the aggressiveness detected for

Icelandic *P. syringae* might be related to the adaptation to environmental habitats, which have

been linked to the evolution of their pathogenicity (Morris et al. 2010).

As previously demonstrated for *P. syringae* overall (Morris et al, 2019), it has not been possible

to make any inference of pathogenic capacity/host range based on the substrate of isolation

(habitat or lichen species) or according to the phylogroup of the Icelandic strains (Fig.1). This

is also consistent with the observation of the mixing of populations of *P. syringae* between

crop and environmental habitats, whereby they are not genetically distinguishable as different

populations (Monteil et al, 2016; Morris et al, 2010). Moreover, the lichen strains resemble more

the strains of *P. syringae* at a same site than other strains from lichens at distal sites (Ramírez

et al, 2023). Thus, overall, these observations demonstrate that the habitat from which a strain

is isolated is not necessarily the habitat on which it has spent the most time and via which

selection pressures might have dominated.

The finding of *P. syringae* raised concerns about a possible threat to Icelandic crops in case

the strains isolated showed pathogenic properties. Icelandic cool climate can play an important

role in pathogenicity of *P. syringae*, due to tissue damage that intensified by frost episodes

and humid environments, as it has been shown that the presence of a layer of free water is

essential for infection (Lamichhane et al. 2015). Furthermore, certain studies have indicated

that lower temperatures enhance the functionality of T3SS (Type III Secretion System) and

T6SS (Type VI Secretion System), which are typically associated with increased

aggressiveness (Tribelli and López, 2022; Puttilli et al, 2022). Despite the limited agricultural

land in Iceland (Denk et al. 2011), certain crops are cultivated on an industrial scale in

greenhouses, with yields exceeding 1000 tones annually. These include tomatoes and

cucumbers, while outdoor cultivation involves crops like barley and potatoes. Nevertheless,

the anticipation is that the range of plant species grown outdoors and their yields in Iceland

will rise over the coming decades due to the predicted rise in temperatures (Parry 1991). The

expansion of cultivable land, coupled with the anticipated milder, yet still relatively cold

temperatures in Iceland, may pose a potential threat to Icelandic crops.

The results of this study are one more example of *P. syringae* strains isolated from

environmental habitats, where they are not causing any obvious damage, or where they might

even be beneficial (Morris et al. 2013). However, these strains can affect some plant species

under specific conditions – conditions that might be increasingly probable with the changing

climate and land use in Iceland.

Disclosure statement

The authors affirm that the research was conducted without any commercial or financial

affiliations that could be construed as potential conflicts of interest.

Bibliography

Bartoli, C., Lamichhane, J.R., Berge, O., Guilbaud, C., Varvaro, L., Balestra, G.M., Vinatzer,

B.A., & Morris, C.E. (2015). A framework to gauge the epidemic potential of plant pathogens

in environmental reservoirs: the example of kiwifruit canker. Mol Plant Pathol, *16*(2),137–149.

Bender, C.L., Alarcón-Chaidez, F., & Gross, D.C. (1999). *Pseudomonas syringae* phytotoxins:

mode of action, regulation, and biosynthesis by peptide and polyketide synthetases. Microbiol

Mol Biol Rev, 63(2),266–292. doi: 10.1128/mmbr.63.2.266-292.1999

Berge, O., Monteil, C.L., Bartoli, C., Chandeysson, C., Guilbaud, C., Sands, D.C., & Morris,

C.E. (2014). A user's guide to a data base of the diversity of *Pseudomonas syringae* and its

application to classifying strains in this phylogenetic complex. PloS One, 9(9):e105547. doi:

10.1371/journal.pone.0105547

Bjelland, T., Grube, M., Home, S., Jorgensen, S.L., Daae, F.L., Thorseth, I.H., & Øvreås, L.

(2011). Microbial metacommunities in the lichen-rock habitat. Environ Microbiol Rep,

3(4),434–442. doi: 10.1111/j.1758-2229.2010.00206.x

Cazorla, F.M., Torés, J.A., Olalla, L., Pérez-García, A., Farré, J.M., & de Vicente, A. (1998).

Bacterial apical necrosis of mango in southern Spain: a disease caused by *Pseudomonas*

syringae pv. syringae. Phytopathology, *88*(7),614–620.

Clarke, C.R., Cai, R., Studholme, D.J., Guttman, D.S., & Vinatzer, B.A. (2010). *Pseudomonas*

syringae strains naturally lacking the classical *P. syringae* hrp/hrc locus are common leaf

colonizers   equipped   with   an   atypical   type   III   secretion   system.

Mol Plant Microbe Interact, *23*(2), 198–210.

Denk, T., Grímsson, F., Zetter, R., & Símonarson, L.A. (2011). Introduction to the nature and

geology of Iceland. In late Cainozoic floras of Iceland, In: Late Cainozoic Floras of Iceland.

Topics in Geobiology. Springer, Dordrecht,1–29.

Donati, I., Cellini, A., Sangiorgio, D., Vanneste, J.L., Scortichini, M., Balestra, G.M., & Spinelli,

F. (2020). *Pseudomonas syringae* pv. actinidiae: Ecology, Infection Dynamics and Disease

Epidemiology. Microb Ecol, *80*(1),81–102. doi: 10.1007/s00248-019-01459-8

Ellis, E.C., Klein Goldewijk, K., Siebert, S., Lightman, D., & Ramankutty, N. (2010).

Anthropogenic transformation of the biomes, 1700 to 2000. Glob Ecol Biogeogr, 19(5),589–

606. doi: 10.1111/j.1466-8238.2010.00540.x

Garg, N., Zeng, Y., Edlund, A., Melnik, A.V., Sanchez, L.M., Mohimani, H., Gurevich, A., Miao,

V., Schiffler, S., Lim, Y.W., Luzzatto-Knaan, T., Cai, S., Rohwer, F., Pevzner, P.A., Cichewicz,

R.H*.,* Alexandrov, T*.,* & Dorrestein, P.C. (2016). Spatial molecular architecture of the microbial community of a *Peltigera* lichen. MSystems, 1(6), 139. doi: 10.1128/mSystems.00139-16

Jones, J.B., Chase, A.R., Raju, B.C., & Miller, J.W. (1986). *Bacterial leaf spot of Hibiscus rosa-sinensis incited by Pseudomonas syringae pv. hibisci.* doi: 10.1094/PD-70-441

Jóhannsson, B. (2003). Íslenskir Mosar Skrár og viðbætur. Icelandic Institute of Natural History web. https://utgafa.ni.is/fjolrit/Fjolrit_44.pdf [Icelandic]

Jónsdóttir, I.S*.,* Magnusson, B*.,* Gudmundsson, J*.,* Elmarsdottir, A*.,* & Hjartarson, H. (2005). Variable sensitivity of plant communities in Iceland to experimental warming. Glob Chang Biol, 11(4),553–563. doi: 10.1111/j.1365-2486.2005.00928.x

Katagiri, F., Thilmony, R., & He, S.Y. (2002). The *Arabidopsis thaliana*-*Pseudomonas syringae* interaction. *Arabidopsis* Book, *1*. doi: 10.1199/tab.0039

Kim, M., Lee, D., Cho, H.S., Chung, Y.S., Park, H.J., & Jung, H.W. (2022). RNA-seq Gene Profiling Reveals Transcriptional Changes in the Late Phase during Compatible Interaction between a Korean Soybean Cultivar (Glycine max cv. Kwangan) and *Pseudomonas syringae pv. syringae* B728a. Plant Pathol J, *38*(6),603.

King, E.O*.,* Ward, M.K*.,* & Raney, D.E. (1954). Two simple media for the demonstration of pyocyanin and fluorescin. J Lab Clin Med, 44(2),301–307. doi: 10.5555/uri:pii:002221435490222X

Kristinsson, H*.,* & Heiðmarsson, S. (2009). Checklist of lichens in Iceland. http://floraislands.is/PDF-skjol/Flettulisti-2009.pdf

Lamichhane, J.R*.,* Messéan, A*.,* & Morris, C.E. (2015). Insights into epidemiology and control of diseases of annual plants caused by the *Pseudomonas syringae* species complex. J Gen Plant Pathol, 81(5),331–350. doi: 10.1007/s10327-015-0605-z

Monteil, C.L., Yahara, K., Studholme, D.J., Mageiros, L., Méric, G., Swingle, B., Morris, C.E., Vinatzer, B.A., & Sheppard, S.K. (2016). Population-genomic insights into emergence, crop adaptation and dissemination of *Pseudomonas syringae* pathogens. Microb Genom, *2*(10).

Morris, C.E*.,* Glaux, C*.,* Latour, X*.,* Gardan, L*.,* Samson, R*.,* & Pitrat, M. (2000). The relationship of host range, physiology, and genotype to virulence on cantaloupe in

Pseudomonas syringae from cantaloupe blight epidemics in France. Phytopathology, 90(6),636–646. doi: 10.1094/PHYTO.2000.90.6.636

Morris, C.E.*,* Lacroix, C.*,* Chandeysson, C.*,* Guilbaud, C.*,* Monteil, C.*,* Piry, S.*,* Fiorini, S.*,* Van Gijsegem, F., Barny, M.A.*,* & Berge, O. (2023). Comparative abundance and diversity of populations of the *Pseudomonas syringae* and Soft Rot Pectobacteriaceae species complexes throughout the Durance River catchment from its French Alps sources to its delta*,* Peer Community J, 3:e88. doi: 10.1101/2022.09.06.506731

Morris, C.E.*,* Lamichhane, J.R.*,* Nikolić, I.*,* Stanković, S.*,* & Moury, B. (2019). The overlapping continuum of host range among strains in the *Pseudomonas syringae* complex. Phytopathol Res, 1,1–16. doi: 10.1186/s42483-018-0010-6

Morris, C.E.*,* Monteil, C.L.*,* & Berge, O. (2013). The life history of *Pseudomonas syringae*: linking agriculture to earth system processes. Annu Rev Phytopathol, 51,85–104. doi: 10.1146/annurev-phyto-082712-102402

Morris, C.E., & Moury, B. (2019). Revisiting the concept of host range of plant pathogens. Annu Rev Phytopathol, 57(1), 63–90. doi: 10.1146/annurev-phyto-082718-100034

Morris, C.E.*,* Ramirez, N.*,* Berge, O.*,* Lacroix, C.*,* Monteil, C.*,* Chandeysson, C.*,* Guilbaud, C.*,* Blischke, A.*,* Sigurbjörnsdóttir, M.A.*,* & Vilhelmsson, O. (2022). *Pseudomonas syringae* on plants in Iceland has likely evolved for several million years outside the reach of processes that mix this bacterial complex across Earth's temperate zones. Pathogens, 11(3). doi: 10.3390/pathogens11030357

Morris, C.E.*,* Sands, D.C.*,* Vanneste, J.L.*,* Montarry, J.*,* Oakley, B.*,* Guilbaud, C.*,* & Glaux, C. (2010). Inferring the evolutionary history of the plant pathogen *Pseudomonas syringae* from its biogeography in headwaters of rivers in North America, Europe, and New Zealand. mBio, 1(3). doi: 10.1128/mbio.00107-10

Morris, C.E.*,* Sands, D.C.*,* Vinatzer, B.A.*,* Glaux, C.*,* Guilbaud, C.*,* Buffière, A.*,* Yan, S.*,* Dominguez, H.*,* & Thompson, B.M. (2008). The life history of the plant pathogen *Pseudomonas syringae* is linked to the water cycle. ISME J, 2(3),321–334. doi: 10.1038/ismej.2007.113

Ogilvie, A.E.J*.,* & Jónsson, T. (2001). "Little Ice Age" Research: A Perspective from Iceland.

Climatic Change. Clim Change, 48(1),9–52. doi: 10.1023/A:1005625729889

Parry, M.L., & Ruttan, V.W. (1991) Climate Change and World Agriculture, Environment:

Science and Policy for Sustainable Development, 33:6,25-29, doi:

10.1080/00139157.1991.9931405

Passera, A., Company, S., Casati, P., Maturo, M.G., Battelli, G., Quaglino, F., Antonielli, L.,

Salerno, D., Brasca, M., Toffolatti, S.L., Mantegazza, F., Delledonne, M., & Mitter, B. (2019).

Not just a pathogen? Description of a plant-beneficial *Pseudomonas syringae* strain. Front

Microbiol, 10, 1409. doi: 10.3389/fmicb.2019.01409

Ramírez, N*.,* Sigurbjörnsdottir, M.A*.,* Monteil, C*.,* Berge, O*.,* Heiðmarsson, S*.,* Jackson, R.W*.,*

Morris, C*.,* & Vilhelmsson, O. (2023). *Pseudomonas syringae* isolated in lichens for the first

time: Unveiling *Peltigera* genus as the exclusive host. Environ Microbiol. doi: 10.1111/1462-

2920.16490

Runólfsson, S. (1987). Land reclamation in Iceland. Arct Antarct Alp Res, 19(4),514–517. doi:

10.1080/00040851.1987.12002634

Sigurbjörnsdóttir, M.A. (2016). The lichen-associated microbiome: taxonomy and functional

roles of lichen-associated bacteria. Dissertation, The University of Iceland.

http://hdl.handle.net/1946/23887.

Sigurbjörnsdóttir, M.A*.,* Andrésson, Ó.S*.,* & Vilhelmsson, O. (2015) Analysis of the *Peltigera*

membranacea metagenome indicates that lichen-associated bacteria are involved in

phosphate solubilization. Microbiology, 161,989-996. doi: 10.1099/mic.0.000069

Runólfsson, S. (1987). Land reclamation in Iceland. *Arctic and Alpine Research*, *19*(4), 514–

517. doi: 10.1080/00040851.1987.12002634

Sato, M., Watanabe, K., & Sato, Y. (2001). *Pseudomonas syringae* pv. solidagae pv. nov, the

Causal Agent of Bacterial Leaf Spot of Tall Goldenrod Solidago altissima L. *Journal of General*

Plant Pathology, *67*(4), 303–308. doi: 10.1007/PL00013036

Spribille, T*.,* Tuovinen, V*.,* Res, P*.,* Vanderpool, D*.,* Wolinski, H*.,* Aime, M.C*.,* Schneider, K*.,*

Stabentheiner, E*.,* Toome-Heller, M*.,* Thor, G*.,* Mayrhofer, H*.,* Johannesson, H*.,* &

McCutcheon, J.P. (2016). Basidiomycete yeasts in the cortex of ascomycete macrolichens.

Science. Science, 353(6298),488–492. doi: 10.1126/science.aaf8287

Tribelli, P.M*.,* & López, N.I. (2022). Insights into the temperature responses of Pseudomonas

species in beneficial and pathogenic host interactions. Appl Microbiol Biotechnol,1–11. doi:

10.1007/s00253-022-12243-z

Vilhelmsson, O*.,* Sigurbjörnsdóttir, A*.,* Grube, M*.,* & Höfte, M. (2016). Are lichens potential

natural reservoirs for plant pathogens? Mol Plant Pathol, 17(2),143–145. doi:

10.1111/mpp.12344

Wąsowicz, P. (2020). Annotated checklist of vascular plants of Iceland. Fjolrit

Náttúrufraeoistofnunar 57,1-193

Xin, X.F*.,* Kvitko, B*.,* & He, S.Y. (2018). *Pseudomonas syringae*: What it takes to be a

pathogen. Nat Rev Microbiol, 16(5),316–328. doi: 10.1038/nrmicro.2018.17

Supplementary material

Table S1. Description of the plant species used in fitness and pathogenicity test with

information of the cultivation conditions and time periods.

Figure S1 *P. syringae* population in inoculated leaves of ten plant species on the 1st day post-

infection. Violin and boxplot graphs resume the values of *P. syringae* per leaf for 5 or 6

replicates per strain inoculated in each plant. The Icelandic strains isolated from lichens are

depicted by a solid color while the epidemic strains used as control are represented with

transparent filling. PG1 strains are represented by the color blue, while PG2 strains are

depicted in green. Grey dots point the minimum detection level. Asterisk denotes statistically

significant differences in *P. syringae* abundance between epidemic and *Peltigera.* strains.

Figure S2. Necrotic tissue length in cucumber a) across all strains at 2 dpi. b) in strains

displaying HR lesions at 2, 5, and 9 dpi.

Figure S3. Necrotic tissue length in kale a) across all strains at 2 dpi. b) in strains displaying

HR lesions at 2, 5, 9, 14 dpi.