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IDENTIFICATION AND CHARACTERIZATION OF BACTERIA ISOLATED FROM GARLIC THRIPS (*Thrips tabaci* LINDEMAN) (Thysanoptera: Thripidae) IN THE PHILIPPINES

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ABSTRACT

Thrips tabaci Lindeman (Thysanoptera: Thripidae) is a serious insect pest of garlic and onion in the Philippines. This study sought to isolate and identify species of bacteria associated with thrips infesting garlic plants in La Trinidad, Benguet, Philippines, from March 2020 to March 2021. A total of 135 live adult female thrips attached to the leaves were picked under a dissecting microscope and isolated in nutrient agar plates. Purification of bacteria was done by single colony isolation using 10^{-3} serial dilution, and morphology was determined using the standard bacterial colony characterization chart. Out of the 135 thrips, 104 yielded bacteria (77.03%). Analysis of *16S ribosomal RNA* gene sequence revealed the following: *Bacillus amyloliquefaciens, Peribacillus frigoritolerans, Brevundimonas diminuta, Comamonas koreensis, Enterobacter hormaechei, Enterobacter ludwigii, Rosenbergiella epipactidis*, and *Staphylococcus sciuri*, all with > 99% nucleotide identity. Most of the bacterial colonies were round, entire margin, creamy white color, and a smooth colony surface. These are new records in the Philippines. The findings of this study provided baseline information on the microbiota of garlic-associated thrips and offer promising leads for the development of bacterial-based biocontrol agents, with broader implications for sustainable pest management and microbial ecological research in agroecosystems.

Key words: *Bacillus, Enterobacter, Brevundimonas, Rosenbergiella, Staphylococcus*

INTRODUCTION

Garlic (*Allium sativum* L.) is one of the main condiment crops planted in the Philippines with an estimate of 6 to 7 thousand metric tons annual production from 2016-2020 (PSA 2021). Despite the high market potential and demand, garlic production in the Philippines is still very low (PSA 2014). One of the factors contributing to the low production is the continuous ravaging of insect pests and diseases (Declaro-Ruedas 2020; PSA 2014). Garlic thrips (*Thrips tabaci* Lindeman*)* is a destructive insect pest that was recorded in Batanes, Davao, Ilocos Norte and Misamis Occidental, Philippines

(Reyes 2021) on various crops including garlic, onion, tobacco, banana, mango, tomato, melon, eggplant, potato, and pepper (Reyes 1994a; 2017b). These tiny phytophagous insects damage their hosts either by direct feeding in the plant tissues through their piercing-sucking mouthparts or indirect transmission of plant pathogens (Reyes et al. 2022). The nymphs and adults damage crops by sucking the leaf sap resulting in leaf scarring and streaking. At high levels of infestation, plants may wilt and eventually die or bulbs become severely damaged. Chemical control remains the primary strategy in managing insect pests in garlic (PSA 2014).

Microbial communities associated with insects have long been recognized to have a significant role not only in the growth and survival of their host insects but also in its effect on the host plants and the spread of plant pathogens. Like other insects, thrips can also harbor numerous microorganisms such as bacteria, fungi and viruses (De Vries et al. 2008; Garcia-Rodriguez et al. 2014). Depending on their relationship, these microorganisms can be pathogenic to, symbiotic with, or vectored by insects (Sanchez-Contreras and Vlisidou 2008). Microorganisms that live in the insect without harming its host are called symbionts. Symbiotic microorganisms that live within their host are called endosymbionts while those that are located on the surface are called ectosymbionts (Douglas 2009). Meanwhile, insect pathogens or sometimes referred as entomopathogens, are microorganisms that destroy and kill their insect host. Some insects, however, play the role of vectors by carrying and spreading pathogens. The most intensively studied thrips-associated microorganism is probably the Tomato spotted wilt virus (TWSV), a pathogen spread by several thrips species including *Thrips tabaci*, *T. palmi*, *Frankliniella occidentalis*, and *F. fusca*, (de Assis et al. 2004; Wijkamp et al. 1993). Thrips are common vectors of plant viruses (Jones 2005) therefore, work on thrips-associated viruses are abundant. On the other hand, most research on thrips-associated fungi were mainly on screening and evaluation of potential entomopathogenic fungi such as *Metarhizium anisopliae, Peacilomyces* spp. and *Beauveria bassiana* against different species of thrips (Niassy et al. 2012; Sengonca et al. 2006). Records of fungi isolated from thrips are limited but a notable work was reported by Kirisik and Erler (2024) on the potential of *Beauveria bassiana, Isaria fumosorosea,* and *Lecanicillium psalliotae* isolated from western flower thrips (*Frankliniella occidentalis*) as entomopathogens that can cause significant mortality against pupae and adult females of *F. occidentalis*. In the Philippines, two endophytic fungi were reported from garlic thrips (*T. tabaci*), which are *Fusarium proliferatum* and *Aspergillus candidatus* based on its gene sequences and fungal morphology (Reyes et al. 2021). *F. proliferatum* is considered an entomopathogenic fungus of various insect pests and could have significance in biological control management utilizing fungal entomopathogens.

For thrips-associated bacteria, several studies had been conducted for onion thrips (*T. tabaci*), chili thrips (*Scirtothrips dorsalis*), Western flower thrips (*F. occidentalis*), avocado thrips (*S. hansoni, F. panamensis, F.* sp.), and tobacco thrips (*F. fusca*) (Cano-Calle et al. 2022; Dickey et al. 2014; Wells et al. 2002). Molecular identification using 16S gene sequencing showed *Pantoea agglomerans* and *Pantoea ananatis* as the most commonly associated bacteria in the majority of these thrips. Both of these *Pantoea* species are multifaceted bacteria that can cause rot disease in various crops including onion (Dutta et al. 2014) but can also be beneficial as biological control agents (Lorenzi et al. 2022). The association of a symbiont *Erwinia* under the family *Enterobacteriaceae* with western flower thrips, *F. occidentalis* (Pergande), was also reported, although its role as gut bacteria is still unclear (De Vries et al. 2012). Species of *Wolbachia* is another bacterial symbiont associated with several thrips species including *Aptinothrips rufus* Haliday*, Sciothrips cardamom* (Ramakrishna), *Suocerathrips linguis* Mound & Marullo*, Heliothrips haemorrhoidalis* (Bouche), *Echinothrips americanus* Morgan, *Caliothrips fasciatus* (Pergande), *Pezothrips kellyanus* (Bagnall), and *Thrips palmi* Karny (Saurav et al. 2016; Schausberger 2018). In garlic thrips and its associated bacteria, limited studies have been conducted in other countries, and no previous effort has been made yet in the Philippines.

Understanding the microbiota of thrips is crucial as it offers ecological insights into the insect with huge potential in pest management and biotechnological applications. In the present study, bacteria from garlic thrips, *Thrips tabaci* Lindeman was isolated and the identities were confirmed based on cultural and molecular characteristics. This study sought to provide information on the bacterial microbiota of garlic thrips in the Philippines that holds potential for multiple applications, especially in bacteria-based microbial pest management.

MATERIALS AND METHODS

Thrips collection and identification. Adult thrips were collected from infested 'Ilocos White" garlic plants grown in the experimental area of Benguet State University (BSU) in La Trinidad, Benguet, in March 2020 and March 2021. The thrips were brought to the laboratory, examined under dissecting microscope, and adult female thrips were identified using the comprehensive diagnostic keys of thrips in the Philippines (Reyes 1994), and online resources, Lucid Key Server – Lucid Central (Hoddle et al. 2019).

Isolation of bacteria from the thrips. Thrips-infested fresh garlic leaves collected from La Trinidad, Benguet, Philippines were brought to the laboratories of National Crop Protection Center, University of the Philippines Los Baños and Benguet State University, then examined under a dissecting microscope. Live, adult female thrips attached to fresh garlic leaves were picked individually inside the laminar flow hood using a very fine insect hairbrush with the aid of a dissecting microscope. Prior to isolation, adult thrips were surface sterilized with 10% bleach (sodium hypochlorite) and washed three times with sterile distilled water for at least two minutes for each wash and then blotted dry with sterile tissue paper inside a laminar flow hood to reduce possible external contamination. A total of 135 live and adult female thrips were plated in two batches: the macerated thrips and the individual thrips using nutrient agar (NA) with five thrips for each plate to ensure sufficient representation across replicates, maximize the likelihood of bacterial recovery, and allow for comparison between pooled and individual isolation methods. The plates were then sealed using parafilm and placed under room conditions to allow bacterial growth and then observed after 24 hours. Bacteria that directly grew from the isolated insects were individually isolated in separate plates of NA. After plating the bacterial colonies, serial dilution was done to purify the bacteria and to allow single colony formation. A loopful of individual bacterial isolates was placed in separate 1.5mL tubes containing 1mL sterile distilled water and incubated overnight for at least 12 hours at room temperature. After incubation, 100ul of bacterial solution was transferred into another tube containing 900ul of sterile distilled water which served as the 10^{-1} dilution, until higher dilutions were achieved. Samples were plated at 10^{-1} – 10^{-3} dilutions following the bacterial streak method on NA plates and then isolates were allowed to grow for at least 12 hours. As soon as single colonies grew, these were transferred individually to test tube slants for further processing. While single colonies are still growing, these were characterized under a microscope following the cultural and morphological characterization methods for bacteria (Ahern 2018; Breakwell et al. 2007). Colony morphology analysis was done 24 hours after isolation from serial dilution using a dissecting microscope. Colony characteristics such as shape, margin, elevation, appearance, color, opacity, and pigmentation were observed by visual assessment under a dissecting microscope.

Molecular identification of the bacterial isolates. Fresh isolates of the bacteria were prepared for molecular identification using nutrient broth and nutrient agar plates. Samples were sent to Macrogen, Inc., South Korea through Kinovett Scientific Solutions Company, Philippines for molecular analysis using *16S ribosomal RNA* gene. Genomic DNA was extracted by Macrogen, and sequencing was performed through capillary sequencing using standardized commercial protocols appropriate for bacterial samples. The 16S rRNA gene was amplified using universal primers 27F (5'-AGAGTTTGATCMTGGCTCAG-3') and 1492R (5'-TACGGYTACCTTGTTACGACTT-3') (Miller et al., 2013). The integrity of the extracted DNA was confirmed through agarose gel electrophoresis. The raw nucleotide sequence of each sample was checked, edited, and aligned to produce the consensus sequence using the software package Geneious Prime® 2023.0.2 (Biomatters Ltd., Auckland, New

Zealand). The consensus sequences were then compared with those deposited in GenBank to confirm bacterial species identity, obtaining the highest percentage genetic identity using NCBI BLASTN from https://blast.ncbi.nlm.nih.gov/Blast.cgi. A phylogenetic tree derived from 16S of the consensus sequences and twenty bacterial sequences obtained from GenBank was generated. The molecular phylogenetic analysis of the bacterial species isolated from *T. tabaci* was inferred using the Maximum Likelihood method based on the Tamura-Nei model with 1000 bootstraps. For evolutionary analyses, the software Geneious was used with 644 positions and an additional twenty GenBank sequences in the final dataset to make the phylogenetic tree more informative.

RESULTS AND DISCUSSION

Thrips identity and taxonomic classification. The thrips collected from the garlic were identified as *Thrips tabaci* Lindeman (Reyes 1994). Photomicrographs of the female garlic thrips are presented in Figure 1. *T. tabaci* belongs to Order Thysanoptera, Suborder Terebrantia, and family Thripidae. Adult female thrips had a yellowish brown body with dark setae, rounded and elongate mouth cone, pale grey forewings with four distal setae and an anterior vein, and yellow legs. The striae of pleurotergites had ciliate microtrichia (Hoddle et al. 2019; Reyes et al. 2021).

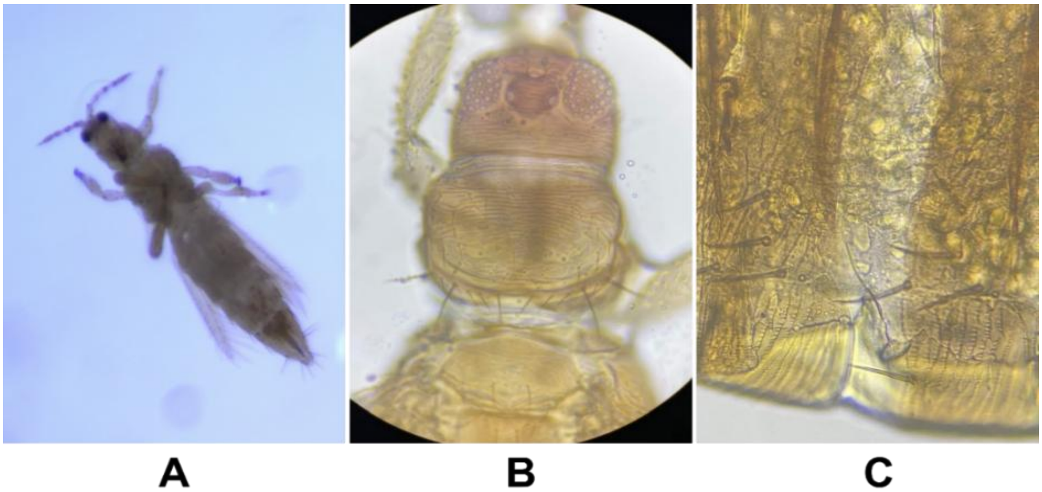

Figure 1. Photomicrograph of adult female *Thrips tabaci* Lindeman infesting garlic: (a) whole body (45x); (b) head and thorax (400x); (c) pleurotergites (400x)

Identity and phylogenetic tree of bacterial isolates. Molecular identification of bacteria is essential since morphological characterization often poses challenges to species resolution. Out of the 135 thrips plated in nutrient agar, 104 yielded bacteria (77.03%). Using the 16s rRNA gene marker, 8 species of bacteria isolated from *T. tabaci* were identified. Two of these belong to the genus *Enterobacter*, and one each from the *Bacillus, Peribacillus, Brevundimonas, Comamonas, Rosenbergiella* and *Staphylococcus* genera. Nucleotide sequence alignment using the NCBI BLASTN database showed that all the bacteria had at least 99% nucleotide identity (Table 1).

The phylogenetic tree (Fig. 2) reveals close genetic relationships between the following isolate-reference pairs: SBA6 and *E. ludwigii*, SBC3 and *E. hormaechei*, SBS5 and *R. epipactidis*, SBB01 and *B. amyloliquefaciens*, SBA7 and *P. frigoritolerans,* SBC1 and *S. sciuri*, SBS2 and *B. diminuta*, and SBA5 and *C. koreensis*. This analysis provides insights into genetic relatedness and divergence patterns among the bacterial species associated with garlic thrips. Six of these bacterial species were isolated from live thrips collected from fresh garlic leaves: *Enterobacter hormaechei,* *Comamonas koreensis, Enterobacter ludwigii, Peribacillus frigoritolerans, Bacillus amyloliquefaciens,* and *Staphylococcus sciuri*. Additionally, *Brevundimonas diminuta* and *Rosenbergiella epipactidis* were recovered from surface-sterilized, macerated thrips.

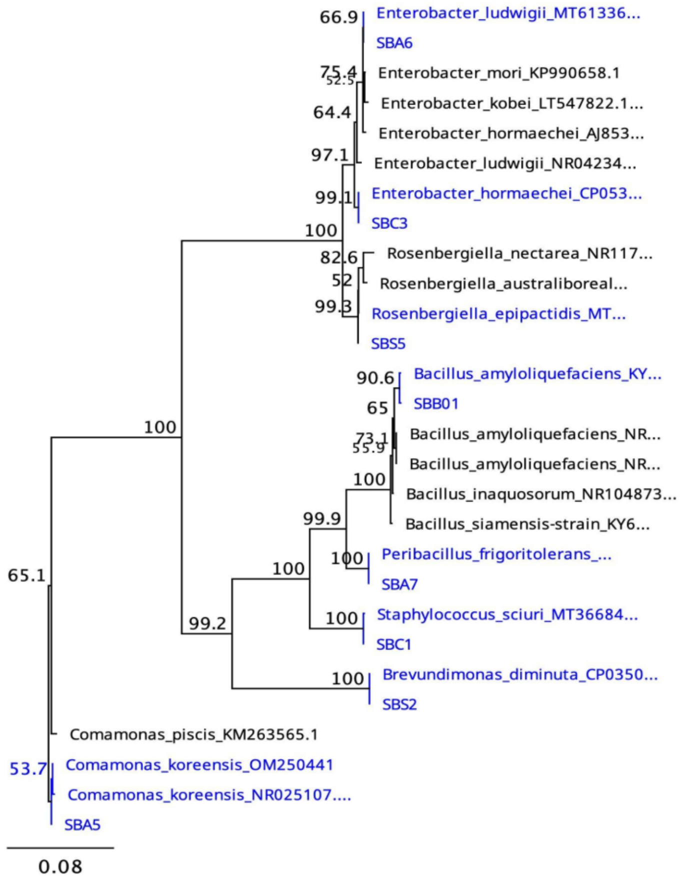

Figure 2. Maximum Likelihood phylogenetic tree based on 16S rRNA gene sequences showing the relationship of selected bacterial isolates (SBA5–SBA7, SBC1–SBC3, SBB01, SBSS2, SBSS5) with closely related reference strains. Bootstrap values (>50%) based on 1000 replicates are shown at the nodes. The scale bar signifies the number of substitutions per site.

Table 1. Molecular identity of the bacteria from garlic thrips (*T. tabaci*) based on 16s rRNA full sequence.

No.	Isolate code	Query Sequences	Scientific name	Percent identity	GenBank Accession number
1	SBB01	OR437230	*Bacillus amyloliquefaciens*	100	JX316756
2	SBA7	OR437229	*Peribacillus frigoritolerans*	99	CP128118
3	SBS2	OR437233	*Brevundimonas diminuta*	100	LC420060
4	SBA5	OR437227	*Comamonas koreensis*	99	NR_025107

No.	Isolate code	Query Sequences	Scientific name	Percent identity	GenBank Accession number
5	SBC3	OR437232	*Enterobacter hormaechei*	100	CP059422
6	SBA6-1	OR437228	*Enterobacter ludwigii*	99	MG602668
7	SBS5	OR437234	*Rosenbergiella epipactidis*	99	MT341879
8	SBC1	OR437231	*Staphylococcus sciuri*	100	MT366845

Colony characteristics of the bacteria. Colonies of the bacterial isolates in the nutrient agar plate at 24 hours after isolation are presented in Figure 3. Most of the isolates were punctiform (less than 1mm in diameter) except for *P. frigoritolerans* with colony size of at least 1 mm in diameter. The shapes and margins of the colonies were difficult to assess using the naked eye due to their tiny sizes, but under a dissecting microscope, the distinction of each bacterial colony became more apparent. *C. koreensis* was distinguishable among the isolates due to its undulate margin. *P. frigoritolerans* appears to be slightly filiform with convex elevation. The rest had an entire margin with a smooth colony surface. In terms of color and pigmentation, all the isolates were consistently creamy white and without pigmentation. All the bacteria grew fast and well in NA at room temperature, except for *Rosenbergiella epipactidis,* which had much slower growth. The colony of *R. epipactidis* was also difficult to isolate due to its strong adherence to the agar medium. The rest can be easily isolated due to their non-sticky characteristics when transferred using a bacterial loop. A summary of the colony characteristics is presented in Table 2.

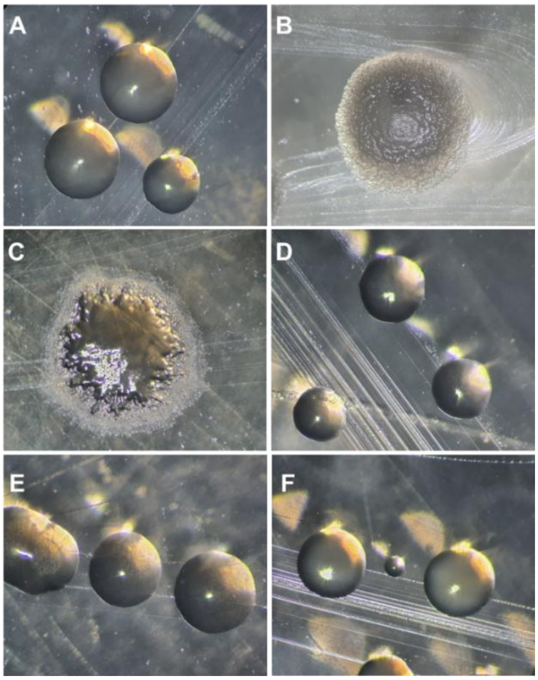

Figure 3. Colonies of bacteria on nutrient agar plate 24 hours after isolation. Photos taken under dissecting microscope at 3x-4x magnification. A-*Bacillus amyloliquefaciens*, B- *B. frigoritolerans*, C- *Comamonas koreensis* , D- *Enterobacter kobei*, E- *E. roggenkampii*, F- *Staphylococcus sciuri*.

Table 2. Colony characteristics of the bacteria isolated from *T. tabaci* in nutrient agar 24 hours after isolation under room temperature.

Scientific name	Shape	Size	Margin	Elevation	Appearance	Color	Opacity	Surface Texture	Pigmentation
Bacillus amyloliquefaciens	punctiform	0.6-0.7 mm	entire	convex	glistening	creamy white	translucent	smooth	Non-pigmented
Peribacillus frigoritolerans	round	1-1.2 mm	slightly filiform	convex	dull	creamy white	opaque	rough with concentric ring	Non-pigmented
Comamonas koreensis	punctiform	0.6-0.8 mm	undulate	convex	glistening	creamy white	translucent	wrinkled	Non-pigmented
Enterobacter hormaechei	punctiform	0.3-0.6 mm	entire	convex	glistening	creamy white	translucent	smooth	Non-pigmented
Enterobacter ludwigii	punctiform	0.5-0.8 mm	entire	convex	glistening	creamy white	translucent	smooth	Non-pigmented
Staphylococcus sciuri	punctiform	0.5-0.7 mm	entire	convex	glistening	creamy white	translucent	smooth	Non-pigmented

The information that was obtained in this study provides insights into the bacterial microbiota associated with garlic thrips (*Thrips tabaci* Lindeman) and can be useful for the development of appropriate management strategies. In the Philippines, this is the first report of bacteria isolated from *T. tabaci* of garlic identified using *16S ribosomal RNA* gene sequencing. The association of these bacteria with *T. tabaci* is still unclear; however, just like other insect-microbe relationships, these bacteria can be antagonistic or symbiotic with their host insect, pathogenic to the thrips and its host plant, or vectored by the insect. The most interesting bacterial isolate obtained from this study was the genus *Bacillus,* which was also reported in onion thrips (Gawande et al. 2019) and avocado thrips. *Bacillus amyloliquefaciens* was specifically reported in avocado thrips (Cano-Calle et al. 2022). *Bacillus* are gram-positive bacteria that are known to produce toxins and other secondary metabolites that can kill their hosts (Vairagkar et al. 2021). Numerous *Bacillus* species, including the broadly adopted *B. thuringiensis,* are used as biological control agents (BCA) against various agricultural insect pests. *B. amyloliquefaciens* is a common bacterial endophyte of many plants (Sun et al. 2006; White et al. 2014). Intensive studies were already conducted using various strains of *B. amyloliquefaciens* due to their numerous benefits not only in bioremediation (Xie et al. 2013) and biofertilization (Luo et al. 2022) but also in controlling agricultural pests. Some studies have demonstrated the insecticidal activity of *B. amyloliquefaciens* against *Myzus persicae* (López-Isasmendi et al. 2019) and *Tuta absoluta* (Ben Khedher et al. 2015). Interestingly, *B. amyloliquefaciens* is also used as a biopesticide against *Fusarium oxysporum, Ralstonia solanacearum, Colletotrichum truncatum* (Huang et. al. 2014; López-Isasmendi et al. 2019; Singh et al. 2021). In contrast, a rare case of *B. amyloliquefaciens* was reported in Korea causing bacterial rot in onion bulbs (Hwang et al. 2012). This means that *B. amyloliquefaciens* can have potential as a biological control agent, or it can be a disease-causing pathogen carried by garlic thrips. The pathogenicity test of this *B. amyloliquefaciens* from *T. tabaci* against insect pests and pathogens, including tests for garlic and onion, could therefore provide new knowledge and information for pest management of onion and garlic in the Philippines. Other thrips-associated *Bacillus* species that were reported include *B. cereus, B. thuringiensis, B. safensis,* and *B. velezensis* from a pooled population of avocado thrips (*Frankliniella* sp., *Frankliniella panamensis* and *Scirtothrips hansoni*) in Colombia (Cano-Calle et al. 2022).

Furthermore, *Peribacillus frigoritolerans* (formerly *Bacillus frigoritolerans*) has been reported to have numerous benefits, just like other species of *Bacillus*. Several strains of this species have potential as plant growth promoter (Batool et al. 2019), as post-harvest biocontrol agents against plant pathogens (Chacón-López et al. 2021), and as entomopathogens of coleopterans (Selvakumar et al. 2011). The association of *P. frigoritolerans* in thrips and other pathogens of garlic, and the assessment of its insecticidal and antimicrobial potential, are also interesting areas for future research to address pest management issues.

Additionally, two of the bacteria obtained in this study were identified as *Enterobacter hormaechei* and *E. ludwigii*. Currently, no local studies on the association of these bacteria with thrips or garlic plants have been conducted yet. However, the genus *Enterobacter* was included in the report of Cano-Calle et al. (2022) as one of the genera of bacteria associated with avocado thrips, *S. hansoni* and *F. panamensis,* but more abundant in *Frankliniella* sp. This genus was also found in onion thrips *T. tabaci* in India (Gawande et al. 2019) and in chili thrips *Scirtothrips dorsalis* (Dickey et al. 2014). Currently, these two *Enterobacter* species belong to *Enterobacter cloacae* complex (ECC) causing animal and human infections (Kosako et al. 1996; Zhou et al. 2017). Although considered as human and animal pathogens, some studies suggested that both *E. hormaechei* and *E. ludwigii* are excellent plant growth promoter that can help boost plant vigor, induce disease resistance, and increase yield by enhancing plant nutrient uptake of tomato, cotton, and other crops (Ranawat et al. 2021; Wang et al. 2025).

Other bacteria from garlic thrips are *Staphylococcus sciuri, Brevundimonas diminuta, Rosenbergiella epipactidis,* and *Comamonas koreensis.* The genus *Staphylococcus* was reported in onion thrips (*T. tabaci*) in India (Gawande et al. 2019) and in gall-inducing thrips (*Gynaikothrips uzeli*) including *Brevundimonas* and *Enterobacter* (Tyagi et al. 2022). Currently, reports on *B. diminuta* and *S. sciuri* as human pathogens (Hu et al. 2015; Lupande-Mwenebitu et al. 2021) and animal pathogens (Beims et al. 2016) are the only available data. *Rosenbergiella epipactidis*, on the other hand, belongs to the family *Erwinianeae* formerly *Enterobacteriaceae* and was isolated from the nectar of flowers (Lenaerts et al. 2014) and also a common insect microbiota (Álvarez-Pérez et al. 2023). The genus *Rosenbergiella* is one of the bacteria associated with onion thrips (*T. tabaci*), avocado thrips (*S. hansoni*), and it was reported to be easily dispersed by western flower thrips (*F. occidentalis*) (Cano-Calle et al. 2022; Gawande et al. 2019; Vannette et al. 2021). Although the previous reports did not specify the species of *Rosenbergiella* obtained, the results of this study complement the previous studies and confirm the association of *Rosenbergiella* sp. with thrips. For *Comamonas koreensis,* limited studies were available on their properties, characteristics, habitat, hosts and significance.

Compared to the previous works of De Vries et al. (2008) and Jin et al. (2023) on the bacterial microbiota of *T. tabaci* in onion, the bacteria reported in this study are not the same and not even closely related to the ones they found. Based on the biochemical and 16S rDNA analysis they conducted, the three bacterial species isolated from the larvae of *T. tabaci* were identified as *Serratia marscens, Pseudomonas sp.* and *Erwinia herbicola,* which is synonymous with *Pantoea agglomerants* (De Vries et al. 2008). *P. agglomerans* in adult onion thrips (*T. tabaci*) has been reported in Korea (Jin et al. 2023). However, a study on microbiome profiling of adult *T. tabaci* in onion using 16S rRNA gene sequencing provided a more comprehensive list of bacterial genera associated (Gawande et al. 2019). From their report, five genera were found similar to the ones obtained from *T. tabaci* of garlic and these are *Bacillus, Enterobacter, Rosenbergiella, Brevundimonas*, and *Staphylococcus.* Therefore, the results of this study complement the previous works on the associated bacteria of *T. tabaci* in onion and other thrips species in other crops.

CONCLUSION

Eight bacterial species were obtained from 104 out of 135 live (77.03%) adult female thrips (*T. tabaci*) collected from "Ilocos White" garlic in La Trinidad, Benguet. The bacteria were identified as the following: *Bacillus amyloliquefaciens, Peribacillus frigoritolerans, Brevundimonas diminuta, Comamonas koreensis, Enterobacter hormaechei, Enterobacter ludwigii, Rosenbergiella epipactidis*, and *Staphylococcus sciuri.* All of the isolates were consistently nonpigmented and most were punctiform with entire margin and smooth surface except for *P. frigoritolerans* and *C. koreensis.* From the seven bacterial genera obtained from garlic thrips, five were also found in *T. tabaci* of onion and other species of thrips infesting other crops. Findings of this study provided insights into the bacterial microbiota of adult *T. tabaci* in garlic. A study on the association of these bacterial species with garlic thrips is an interesting area for future studies. A thorough investigation on the specific roles of these bacteria in disease spread, pathogenicity, and biological control could provide opportunities for better pest management. Scientific evidence showing the vectoring relationship between the thrips and the identified bacteria may provide new insights on the spread of bacterial pathogens. Moreover, knowledge on host specificity, whether the identified bacteria can infect limited species of host plants (specialist) or variety of hosts (generalist), can have numerous applications in disease diagnosis, management practices, breeding of resistant varieties, and biosecurity. Furthermore, exploring the biological control potential of the identified bacteria against insect pests such as thrips and other plant pathogens can also provide opportunities for the development of better pest management solutions.

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