Differences in Microbiota Between Two Multilocus Lineages of the Sugarcane Aphid (Melanaphis sacchari) in the Continental United States

Differences in Microbiota between Two Multilocus Lineages of the Sugarcane Aphid (*Melanaphis sacchari*) in the Continental US

Authors

Jocelyn R. Holt[1], Alex Styer[2], Jennifer A. White[2], J. Scott Armstrong[3], Samuel Nibouche[4], Laurent Costet[4], Antonino Malacrinò[5], Josephine B. Antwi[6], Jason Wulff[1], Gary Peterson[7], Neal McLaren[8], and Raul F. Medina[1]

[1]Texas A&M University, College Station, TX; [2]University of Kentucky, Lexington, KY; [3]USDA – ARS, Stillwater, OK; [4]CIRAD, UMR PVBMT, Saint-Pierre, La Réunion, France; [5]Department of Evolution, Ecology and Organismal Biology, The Ohio State University, Columbus, OH; [6]University of Mary Washington, VA; [7]Texas A&M AgriLife Research and Extension Center, Lubbock, TX; [8]University of the Free State, Bloemfontein, South Africa

Journal: Annals of the Entomological Society of America

DOI: 10.1093/aesa/saaa003

Article available at: https://academic.oup.com/aesa/article/113/4/257/5805417

Please, cite as:

Jocelyn R Holt, Alex Styer, Jennifer A White, J Scott Armstrong, Samuel Nibouche, Laurent Costet, Antonino Malacrinò, Josephine B Antwi, Jason Wulff, Gary Peterson, Neal McLaren, Raul F Medina, Differences in Microbiota Between Two Multilocus Lineages of the Sugarcane Aphid (*Melanaphis sacchari*) in the Continental United States, Annals of the Entomological Society of America, Volume 113, Issue 4, July 2020, Pages 257–265, https://doi.org/10.1093/aesa/saaa003

Abstract

The sugarcane aphid (SCA), *Melanaphis sacchari* (Zehntner), has been considered an invasive pest of sugarcane in the continental US since 1977. Then, in 2013, SCA abruptly became a serious pest of US sorghum and is now a sorghum pest in twenty-two states across the continental US. Changes in insect-associated microbial community composition are known to influence host-plant range in aphids. In this study, we assessed whether changes in microbiota composition may explain the SCA outbreak in US sorghum. We characterized the SCA bacterial microbiota on sugarcane and grain sorghum in four US states, using a metabarcoding approach. In addition, we used taxon-specific PCR primers to screen for bacteria commonly reported in aphid species. As anticipated, all SCA harbored the primary aphid endosymbiont *Buchnera aphidicola,* an obligate mutualistic bacterial symbiont. Interestingly, none of the secondary symbionts, facultative bacteria typically associated with aphids, (e.g., *Arsenophonus*, *Hamiltonella*, *Regiella*), were present in either the metabarcoding data or PCR screens (with the exception of *Rickettsiella* and *Serratia,* which were detected by metabarcoding at low abundances <1%). However, our metabarcoding detected bacteria not previously identified in aphids (*Arcobacter*, *Bifidobacterium*, *Citrobacter*). Lastly, we found microbial host-associated differentiation in aphids that seems to correspond to genetically distinct aphid lineages that prefer to feed on grain sorghum (MLL-F) versus sugarcane (MLL-D).

Keywords: bacterial host-associated differentiation, bacterial symbiont, high-throughput sequencing, invasive insect, metabarcoding

Introduction

The sugarcane aphid (SCA), *Melanaphis sacchari* (Zehntner), is a globally distributed species that feeds on members of Poaceae including sugarcane, sorghum, rice, millet, corn and wild grasses (Singh et al. 2004). In most parts of the world (e.g., Asia, Australia, the Americas and Africa), SCA is considered a pest of sorghum (Singh et al. 2004). Its center of origin is currently unknown, but it is hypothesized to be either in central or northern Africa or in Asia (Nibouche et al. 2014). In regions of the world where both sugarcane (*Saccharum officinarum* L. and *Saccharum* spp.) and grain sorghum (*Sorghum bicolor* (L.) Moench) are grown, SCA is reported to have higher abundances on grain sorghum than on sugarcane and exhibits preference for sorghum over sugarcane (Nibouche et al. 2015). SCA was first reported on sugarcane in the continental US in Florida during 1977 (Mead 1978) and in Louisiana during 1999 (White et al. 2001). Despite the presence of SCA on commercial sugarcane, SCA was not a sorghum pest in the continental US (Mead 1978, Hall 1987, Denmark 1988, Armstrong et al. 2015, Medina et al. 2017) until spring 2013 when SCA was reported on grain sorghum (Bowling et al. 2016). SCA damage to sorghum is caused by feeding activity and honeydew production, which combined can decrease crop yields and harvesting efficiency (Bowling et al. 2016, Zapata et al. 2016). Damage estimates in US grain sorghum range from 20% to 100% crop loss (Villanueva et al. 2014, Kerns 2015, Zapata et al. 2016) plus the additional financial burden incurred by pest management efforts (Zapata et al. 2016).

Considering the fact that SCA was already present in US sugarcane, a host-switch could have occurred due to a change in SCA's symbiotic bacteria. Symbiotic bacteria are a part of an insect's microbiota defined as a collection of microorganisms (e.g. bacteria, fungi, protists, viruses)

contained within and on the surface of an insect host. Similar to the important role microbiomes play in humans (Hartstra et al. 2015, Findley et al. 2016, Marchesi et al. 2016), the bacterial composition in aphids can influence their health, resource use, and vector potential (Oliver et al. 2003, Oliver et al. 2010, Lukasik et al. 2013). Symbiotic bacteria may influence insect host-range through nutritional supplementation (Hosokawa et al. 2007) or by helping their insect hosts withstand plant defenses (Adams et al. 2013, Ceja-Navarro et al. 2015, Hammer and Bowers 2015). For example, when the kudzu bug (*Megacopta cribraria*) invaded the US, it was able to switch from kudzu to soybean because of its association with a bacterial strain of the obligate symbiont (one required for the insect's survival) Candidatus *Ishikawaella capsulata* (Hosokawa et al. 2007, Brown et al. 2014). Similarly, facultative bacteria (potentially beneficial to the insect, but not essential for survival) in the genus *Arsenophonus* improve cowpea aphids' (*Aphis craccivora*) fitness on locust plants (Wagner et al. 2015) while *Regiella insecticola* increases pea aphid fecundity on clover (Leonardo and Muiru 2003, Tsuchida et al. 2004).

Most research on aphid bacterial composition has been conducted on a few well studied species, such as the pea aphid and cowpea aphid through the use of PCR with taxon-specific primers (Chen et al. 1996, Darby et al. 2001, Simon et al. 2003, Brady and White 2013, Brady et al. 2014). However, it is important to understand the bacterial composition of non-model organisms as they may differ in symbiont composition and those symbionts' biological functions. Although the use of PCR to detect specific taxa remains an effective method for detection of well-known symbionts (e.g. *Hamiltonella defensa*, *Serratia symbiotica* and *Regiella insecticola*), it requires prior knowledge of the bacterial taxa and taxon-specific DNA sequences to be used for detection (Munson et al. 1991, Sandstrom et al. 2001, Russell et al. 2003, Oliver et al. 2006). Another approach called barcoding uses general or universal PCR primers to amplify common regions from

a variety of organisms. After using barcoding to sequence single fragments of DNA or RNA, the nucleotide composition can be used as a proxy for organism identification. The advent of High Throughput Sequencing (HTS) technologies (sometimes referred to as Next Generation Sequencing (NGS)) allows for the massive parallel sequencing of short DNA fragments pushing the boundaries of DNA barcoding and allowing the reconstruction of entire communities of organisms (Abdelfattah et al. 2018). With metabarcoding, a combination of PCR identification and high throughput sequencing, most of the bacteria harbored by an insect can be identified without any prior knowledge of what an insect may harbor and without the need to cultivate thousands of bacterial colonies or to clone thousands of DNA fragments (Mardis 2008, Malacrinò 2018).

Some of the earliest studies of aphids using 454 pyrosequencing were done on the microbial symbionts in cowpea aphids (Brady and White 2013), soybean aphid (Bansal et al. 2014) and pea aphids (Russell et al. 2013, Gauthier et al. 2015). Recently, metabarcoding has been used to identify bacteria that were not previously associated with aphids. Metabarcoding has allowed for the identification of potential symbionts that might otherwise go unnoticed with the screening of only specific symbionts (Bansal et al. 2014, Gauthier et al. 2015, Jousselin et al. 2016, Fakhour et al. 2018, Guyomar et al. 2018).

The objective of our study was to characterize the SCA microbiota from aphids collected from sorghum and sugarcane using PCR and metabarcoding**.** In addition, we sought to determine whether a change in SCA microbiota supports a host-plant shift, from sugarcane to grain sorghum.

Materials and Methods

Field Collections

Specimens of sugarcane aphid were collected from grain sorghum and sugarcane in 4 different states (i.e. Florida, Alabama, Louisiana, and Texas) in the US between 2014 and 2015 and from sorghum in South Africa in 2014 (Figure 1, Table 1). Aphids within each state were collected on both grain sorghum and sugarcane from as many counties as possible, collecting specimens from fields at least 1km apart from each other to minimize the chance of sampling siblings. We also added SCA samples from Louisiana sugarcane collected between 2007 and 2009, before the 2013 SCA invasion on sorghum in US (Table 1). Aphids were killed in 95% ethanol and stored at 4°C.

DNA Extraction

Nymphs and apterous adults from each combination of host plant species and location (Table 1) were pooled together and surface sterilized before DNA extraction (Meyer and Hoy 2008, Medina et al. 2011), yielding a total of 14 samples (each containing an average of approximately 20 individuals). DNA was extracted using the DNeasy Blood and Tissue Kit (QIAGEN, Valencia, CA, USA) following the standard protocol recommended by the manufacturer. DNA concentration and quality were assessed using a NanoDrop spectrophotometer (Thermo Fisher Scientific Inc., Waltham, MA, USA). Aliquots from those same samples were also used for both taxon-specific PCR and metabarcoding.

PCR for Specific Aphid Symbionts

We used taxon-specific PCR primers to screen for nine bacterial genera found in other aphid

species. These bacterial genera included: *Arsenophonus, Cardinium, Hamiltonella, Regiella, Rickettsia, Rickettsiella, Serratia, Spiroplasma,* and *Wolbachia* (Fukatsu et al. 2001, Russell and Moran 2006, Oliver et al. 2010, Brady and White 2013). PCR reactions were run on a MyCycler Thermal Cycler (Bio-Rad, Hercules, CA, USA) in a total volume of 10 μL containing: 2.5 mM MgCl2, 10X Taq reaction buffer (NEB), 2.5 mM dNTPs (Omega Bio-Tek, Norcross, GA, USA), 5 μM of forward and reverse primers, 0.1 μL of 5U/μL *Taq* DNA Polymerase (NEB, Ipswich, MA, USA), and 2 μL of DNA template. The list of taxon-specific primers and annealing temperatures can be found in Table S1. All diagnostics included positive (i.e. symbiont-positive specimens known to host the bacteria of interest) and negative controls (i.e. nuclease-free water). PCR products were visualized on a 1% agarose gel stained with GelRed (Biotium, Fremont, CA, USA) under UV light. For samples that produced products of the expected size, we re-ran PCRs with a total volume of 25 μL and either purified the product using the GenCatch PCR Cleanup Kit (Epoch Life Sciences, Missouri City, TX, USA) or in the case of double bands appearing on a gel, the band of interest (i.e., a band matching the correct size compared to the ladder) was excised and purified using the GenCatch Gel Extraction Kit (Epoch Life Sciences, Missouri City, TX, USA). Purified products were sent to an offsite facility for Sanger sequencing (GENEWIZ, South Plainfield, NJ, USA). Resulting sequences were searched by MegaBLAST in the GenBank database default parameters, and only sequences returning 97% or greater similarity to the expected bacterial genus were considered for inclusion in bacterial presence analyses.

16S rRNA Metabarcoding

DNA samples were sent to the Molecular Research DNA Lab (MR. DNA, Shallowater, TX, USA) for metabarcoding analyses targeting the bacterial V3-V4 16S rRNA bacterial region (Herlemann

et al. 2011, Su et al. 2016). Samples were sequenced on an Illumina MiSeq platform (Illumina, San Diego, CA, USA) using the MiSeq Reagent Kit v3 300PE chemistry. Together with experimental samples, we submitted two negative controls to identify potential environmental bacterial contaminants (Salter et al. 2014). One of the negative controls consisted of a sterilized water sample run with all the chemicals and the same protocol used for the DNA extraction without any aphid DNA (Salter et al. 2014, Malacrinò et al. 2018). The second negative control consisted of a single pool of all the last wash liquids obtained from the surface sterilization of insects, which was used for the identification of bacteria likely to be potential surface contaminants.

Data Analysis

Data handling was carried out using QIIME 1.9 (Caporaso et al. 2010, Caporaso et al. 2012), quality-filtering reads (Phred ≥ 25), binning OTUs using open-reference OTU-picking through UCLUST algorithm, and discarding chimeric sequences discovered with USEARCH 6.1 (Edgar 2010). Taxonomy was assigned to each OTU through the BLAST method using Greengenes database for 16S rRNA (Caporaso et al. 2012). The OTU table was then filtered to remove all singletons, OTUs coming from amplification of chloroplast DNA and those clearly belonging to contaminants (i.e., *Gardnerella*, *Granulicatella*, *Haemophilus*, *Leptotrichia*, *Prevotella*, *Ruminococcus*, *Staphylococcus* and *Streptococcus*). The two negative controls used in this study clustered apart from the aphid samples and allowed us to further clean our dataset from contaminants. Using a statistical approach to discover potential contaminants (Davis et al. 2017), we further removed 30 OTUs from our samples. In addition, we subtracted from each sample the quantity of OTU reads found in both control types we used, under the assumption that they could be surface contaminants. Since each sample had a different sampling depth and library size, before

subtraction we normalized counts using the Variance Stabilizing Transformation algorithm from DESeq2 package (Love et al. 2014) and removed any batch effects using package limma (Ritchie et al. 2015). Negative values were then converted to zero, and we performed another round of singleton removal.

Differences in the structure of microbial communities between aphids collected from different host plants was assessed through a PERMANOVA analysis (999 permutations) using host plant as a fixed variable and sampling location as a random variable to account for geographic variability. Distances between samples were calculated through a weighted UniFrac matrix and then visualized using Non-Metric Multidimensional Scaling (NMDS). Differences in relative abundance of each bacterial genus between samples from different host plants were tested through a Generalized Linear Model (genus relative abundance ~ host plant), using False Discovery Rate (FDR) correction for multiple comparisons. All analyses were performed using R statistical software (R Core Team 2013) with the packages vegan (Dixon 2003), phyloseq (McMurdie and Holmes 2013) and picante (Kembel et al. 2018).

Results

PCR

PCR analyses did not detect bacterial symbionts commonly reported in other aphid species (i.e., *Arsenophonus*, *Hamiltonella*, *Regiella*, *Rickettsia*, *Rickettsiella*, *Spiroplasma* and *Wolbachia*) see the example for *H. defensa* (Figure S2). These bacteria were also not identified using metabarcoding, with the exception of *Rickettsiella* and *Serratia*, which were also detected in low abundances using metabarcoding.

Microbiota and Host-Association

A total of 1,081,493 reads (with a sample average of 86,565±18,914 SE paired end reads) were obtained from Illumina MiSeq, which clustered into 267 OTUs. Through a multivariate approach, we found host-associated differentiation of bacterial communities between aphids collected on sugarcane and grain sorghum ($F_{1, 12} = 4.73$; $P = 0.009$). The differentiation of the microbial community harbored by SCA clustered by host plant, which is visible in the NMDS plot (Figure 2).

As anticipated, the majority of the bacterial reads belonged to the obligate aphid bacterial symbiont *Buchnera.* The raw unweighted percentages for *Buchnera* averaged between 90 to 99%, which overpowers the signal of less prominent bacteria if uncorrected. Consequently, all values are reported in weighted relative abundances. *Buchnera* composed a greater proportion of the bacterial community in aphids feeding on sorghum than those collected on sugarcane ($F_{2,12} = 10.58$; $P = 0.006$; 41.4 ± 6.9% and 29.7 ± 6.1%, respectively). In addition, metabarcoding detected bacteria (with abundances >1%) belonging to nineteen different genera in twelve orders (Table S2). A significantly greater proportion of *Arcobacter* sequences were detected in SCA associated with sugarcane than in SCA associated with sorghum ($F_{2,12} = 12.73$; $P < 0.01$; Figure 3, Table S2). In contrast, a greater proportion of *Citrobacter* sequences were detected in SCA associated with sorghum than in SCA associated with sugarcane ($F_{2,12} = 7.03$; $P = 0.02$; Figure 3, Table S2). Some aphid-associated bacteria occurred at a low abundance of reads and included *Acidovorax*, *Lactobacillus*, *Ralstonia*, *Rickettsiella*, and *Serratia* (Table S2). The sample from Louisiana sugarcane collected during 2007-2009 lacked *Citrobacter* and *Serratia*, while hosting *Rickettsiella* (Table S3).

Discussion

Advances in technology have allowed us to go from the identification of bacteria through classical microbiology techniques (Escobar-Zepeda et al. 2015) to the use of PCR to screen for specific bacterial taxa (Haynes et al. 2003, Vorburger et al. 2009, Ferrari et al. 2011, Brady et al. 2014) and now to the ability to screen for entire microbiomes using high throughput sequencing without any prior knowledge of their composition. Our approach using taxon-specific PCR and metabarcoding allowed us to screen for bacteria previously reported in aphids, while enabling us to identify other potential bacteria that SCA harbors.

The use of PCR confirmed that sugarcane aphids harbor few commonly known aphid bacterial symbionts, with the exception of the obligate symbiont *Buchnera aphidicola* and facultative symbionts *Rickettsiella* and *Serratia* (identified in low abundances <1% with metabarcoding). Using metabarcoding we identified novel bacteria not previously reported in aphids (*Arcobacter*, *Bifidobacterium*, *Citrobacter*). In addition, metabarcoding allowed us to identify significantly higher abundances of bacteria in aphids from sugarcane (i.e., Arcobacter) when compared to aphids in grain sorghum (i.e., *Buchnera* and *Citrobacter*). A reduction in the abundance of the obligate symbiont *Buchnera aphidicola* in the presence of other bacteria is anticipated and was observed in pea aphids that had reduced *Buchnera* abundances in the presence of the secondary symbiont *Rickettsia* (Sakurai et al. 2005).

Bacterial symbionts can facilitate nitrogen use, sugar breakdown or pesticide degradation in their insect hosts (Anderson et al. 2013, Ben-Yosef et al. 2014, Cheng et al. 2017). We identified *Bifidobacterium* in SCA collected from grain sorghum and sugarcane, a bacterium that it is known to break down carbohydrates in both insects and humans (Killer et al. 2009, O'Callaghan and van

Sinderen 2016, Alberonia et al. 2018) and in SCA may play a role in processing phloem. In addition two bacteria associated with detoxification in other insects were found. For example, *Citrobacter* is associated with increased insecticide resistance in the tephritid fruit fly *Bactrocera dorsalis* (Hendel) (Cheng et al. 2017). Similarly, bacteria in the genus *Pseudomonas* are known to detoxify caffeine in coffee berry beetles *Hypothemus hampei* (Ceja-Navarro et al. 2015) and may have a similar detoxifying potential in SCA.

Some bacteria may be biologically relevant even when found in low abundances (Stouthamer et al. 2018). While a relative abundance lower than 1% may reflect some sequencing error, our use of stringent quality control filtering helped increase the reliability of low abundance reads (Bokulich et al. 2013). Both *Rickettsiella* spp. and *Serratia* spp. are reported to have biologically relevant functions at low abundances in other aphids (Enders and Miller 2016). Interestingly, *Rickettsiella*, which is known to alter body color in pea aphids (Tsuchida et al. 2010), was found in SCA and if similar in function, might influence the attractiveness of SCA to natural enemies (i.e. predators and parasitoids). SCA also harbored *Serratia*, which has been reported to provide heat tolerance in other aphids (Russell and Moran 2006, Oliver et al. 2010).

In addition to the potential symbionts mentioned above, we detected *Acidovorax* spp., *Corynebacterium* spp. and *Ralstonia* spp. *Acidovorax* spp. has been reported to cause tissue browning in some plants (Xie et al. 2011) and red stripe disease in infected sugarcane plants (Girard et al. 2014, Santa Brigida et al. 2016, Yonzone and Devi 2018). Similarly, *Corynebacterium* spp. is known as an animal and plant pathogen (Christie et al. 1991, Barba et al. 2015, Hu 2019), with green peach aphid reported as capable of transmitting this bacterium to potatoes resulting in ring rot (Christie et al. 1991) while *Ralstonia* spp. is known to cause plant

wilting and death in numerous agricultural crops (Álvarez et al. 2010, Meng 2013). Further investigation is required to determine whether the strains of these bacteria found in SCA are plant pathogens and if SCA is capable of their transmission.

While the bacteria reported above have been identified in other insects and some have known functions , other bacteria that we identified that have been reported from other insects require further investigation (i.e., *Acinetobacter*, *Arcobacter, Bacillus*, *Burkholderia*, *Cloacibacterium, Delftia, Flavobacterium*, *Propionibacterium, Sphingomonas*) (Srivastava and Rouatt 1963, Kikuchi et al. 2005, Konig 2006, Xiang et al. 2006, Killer et al. 2009, Leroy et al. 2011, Malhotra et al. 2012, Morales-Jiménez et al. 2012, Cakici et al. 2014, Montagna; et al. 2014, Ceja-Navarro et al. 2015, Meirelles et al. 2016, Meriweather et al. 2016, Segata et al. 2016, Cheng et al. 2017, Duguma et al. 2017, Luna et al. 2018). For example, *Flavobacterium* has been reported from pea aphids (Srivastava and Rouatt 1963) and while members of the family Flavobacteriaceae are reported to provision their insect hosts with nutrients (Wu et al. 2006, Bennett et al. 2014, Rosas-Pérez et al. 2014) it is unknown whether this bacteria would have a similar role in SCA. Similarly, *Micrococcus* in the European Corn Borer has potential contributions to gut enzymatic activity (Vilanova et al. 2012), however its potential function in SCA is not known.

Interestingly, we did not detect bacterial symbionts that are well-known from previous aphid studies with either PCR or metabarcoding. For example, we did not detect any reads associated with *Hamiltonella defensa,* which was previously reported for SCA (Harris-Shultz et al. 2017). We conclude that the presence of these other symbionts may be rare or completely absent in SCA populations in the US.

We originally predicted that a change in the SCA microbiome composition might be responsible for SCA switching from sugarcane to grain sorghum resulting in the pest outbreak in 2013. While our results show host-associated bacterial differentiation in SCA collected from sugarcane and sorghum, these differences seem to correspond to the characterization of two genetically distinct aphid Multilocus Lineages or MLLs (Nibouche et al. 2018). These genetically distinct MLLs differ in host plant use: MLL-D prefers to feed on sugarcane and has likely been present in the US since the 1970s while MLL-F prefers to feed on sorghum and was only recently detected in the US (Nibouche et al. 2015, Nibouche et al. 2018). Therefore, the sudden SCA outbreak was likely caused by the introduction of a sorghum adapted strain of SCA, which also has host-associated bacterial differences, and not by the sudden acquisition or loss of a specific bacterial symbiont. Analysis of sugarcane aphids from Louisiana grain sorghum and sugarcane before and after the pest outbreak show an increase in the sorghum adapted MLL-F in sugarcane (Nibouche et al. 2018). In SCA, sugarcane populations had greater abundances of *Arcobacter* and a lower abundance of *Citrobacter* when compared to samples collected on sorghum. In addition, bacteria such as *Citrobacter* and *Serratia* (lacking in samples collected before SCA invasion on US sorghum) were detected in aphids from both grain sorghum and sugarcane after 2013, suggesting that the sorghum adapted MLL-F aphids are spilling over into sugarcane. Alate aphids can be transported by wind to new locations and host plants (Wiktelius 1984, Irwin et al. 1988, Loxdale et al. 1993, Mann et al. 1995), which may explain why some SCA samples collected from sugarcane after 2013 (in Alabama, Florida, and Louisiana) have microbial compositions that cluster closer to SCA collected on grain sorghum. Our findings suggest a spillover of SCA from sorghum to sugarcane likely due to dispersal. Although changes in the microbiota composition

between SCA before and after 2013 are unlikely to have caused the SCA outbreak in sorghum, the bacteria that we identified may play important roles in SCA.

Overall, we found that populations of SCA in the continental US contain few of the well-studied facultative symbionts reported in aphids. However, SCA do contain a diversity of novel bacteria some of which have known functions in other insects. In addition, we found evidence of host-associated differentiation in SCA microbiota. This study provides a foundation for understanding the bacterial composition of SCA, which can be used to better inform Integrated Pest Management (IPM) of this pest in grain sorghum by providing novel targets for control.

Acknowledgements

This work was supported by the National Institute of Food and Agriculture, U.S. Department of Agriculture Hatch Program (TEX09185 to RFM and 0224651 to JAW) and by a grant from the Texas Grain Sorghum Board (to RFM). We thank the Texas A&M Office of Graduate and Professional Studies (OGAPS) for funding JRH through the Diversity Excellence Fellowship and the Texas A&M College of Agriculture for the Lechner Excellence Fellowship. Thank you to our collaborators M. Brewer, R. Chappa, C. Crumley, M. Donahoe, T. Felderhoff, Flanders, W. Golden, K. Gravois, D. Kerns, D. Sekula, M. Spearman, R. Villanueva, M. Warren, S. Williams, B. White, MO Way, S. Youngblood for contributing samples and to Kerry Oliver for providing positive controls for the PCR work.

Figure legends

Figure 1. Collection locations for sugarcane aphid (SCA). Specimens were collected in a total of 21 different sampling locations from sugarcane and grain sorghum. Collection sites included multiple locations in Texas, Louisiana, Alabama, Florida and South Africa. Grain sorghum specimens are represented by blue circles. Sugarcane specimens are represented by the orange diamonds.

Figure 2. NMDS (Non-Metric Multidimensional Scaling) analysis showing host-associated clustering in bacterial composition (PERMANOVA: $F_{1, 12} = 4.73$, $P = 0.009$). Samples collected in 2007-2009, before the pest outbreak, are marked with an asterisk. The grain sorghum samples are surrounded by a solid ellipse while the sugarcane samples are surrounded by a dashed ellipse. Host plants: GS (grain sorghum) and SC (sugarcane). Locations: AL (Alabama), C (lab colony collected from Texas), FL (Florida), LA (Louisiana), SA (South Africa) and TX (Texas).

Figure 3. Relative abundance of bacterial taxa in SCA collected from grain sorghum and sugarcane. Three bacterial genera (i.e., *Arcobacter*, *Buchnera*, and *Citrobacter*) showed significantly different abundances between aphids on different host plants. ns = $P > 0.05$; *$P = 0.02$; **$P < 0.01$

Figures

Figure 1

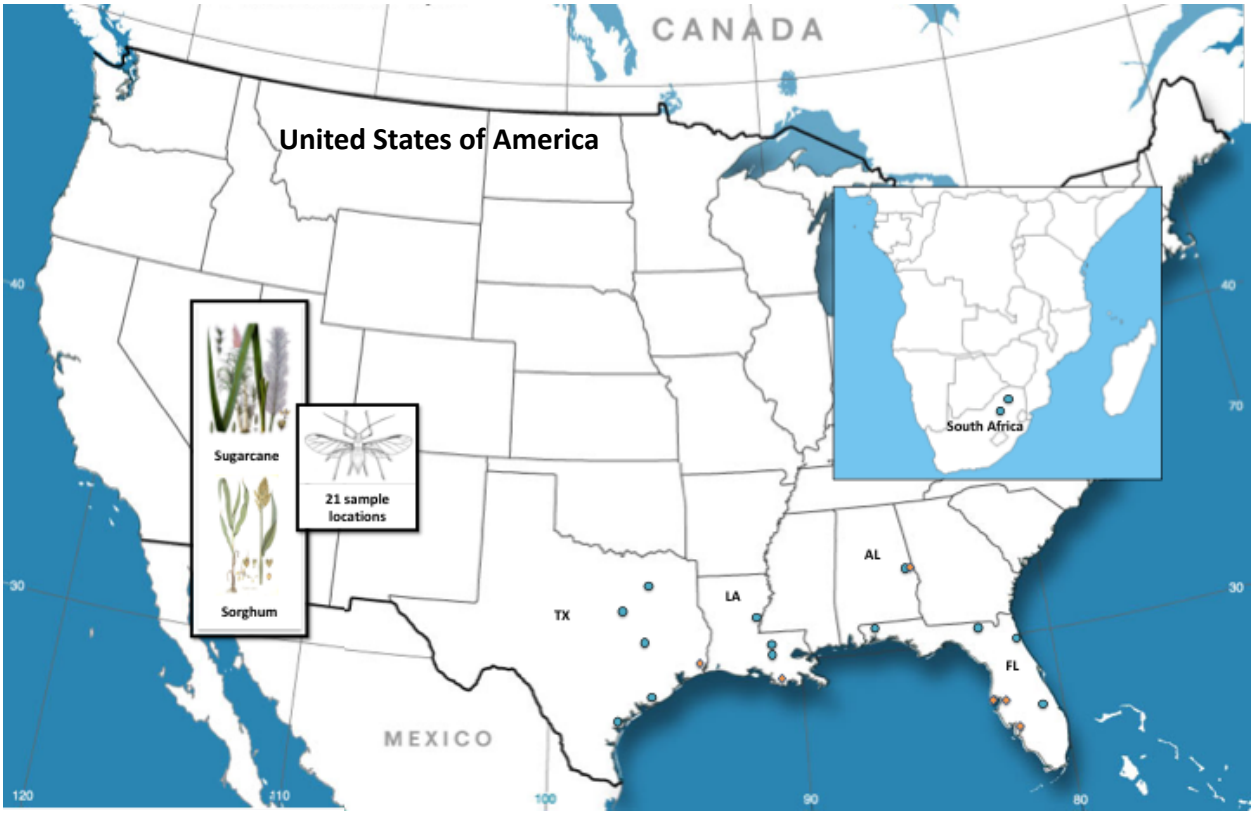


Figure 2

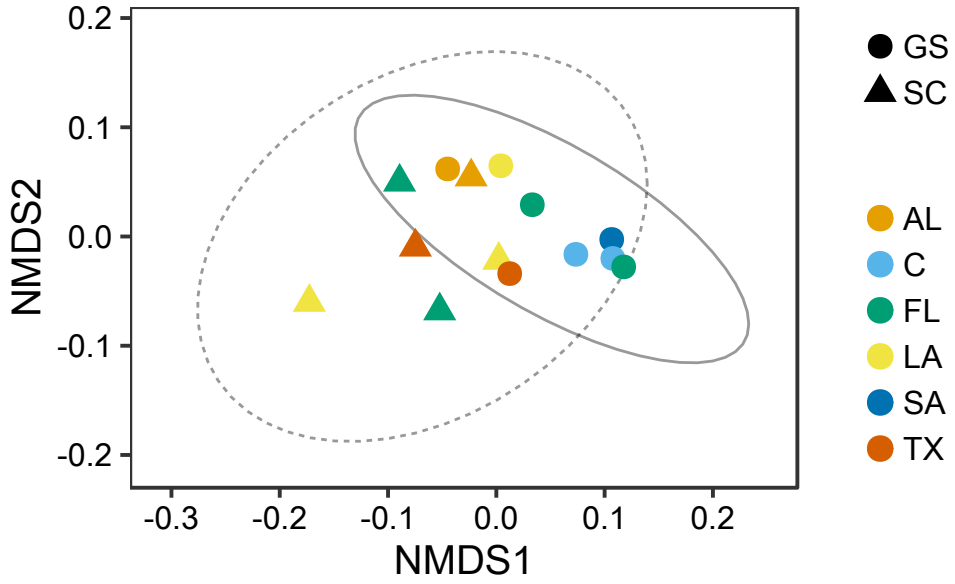
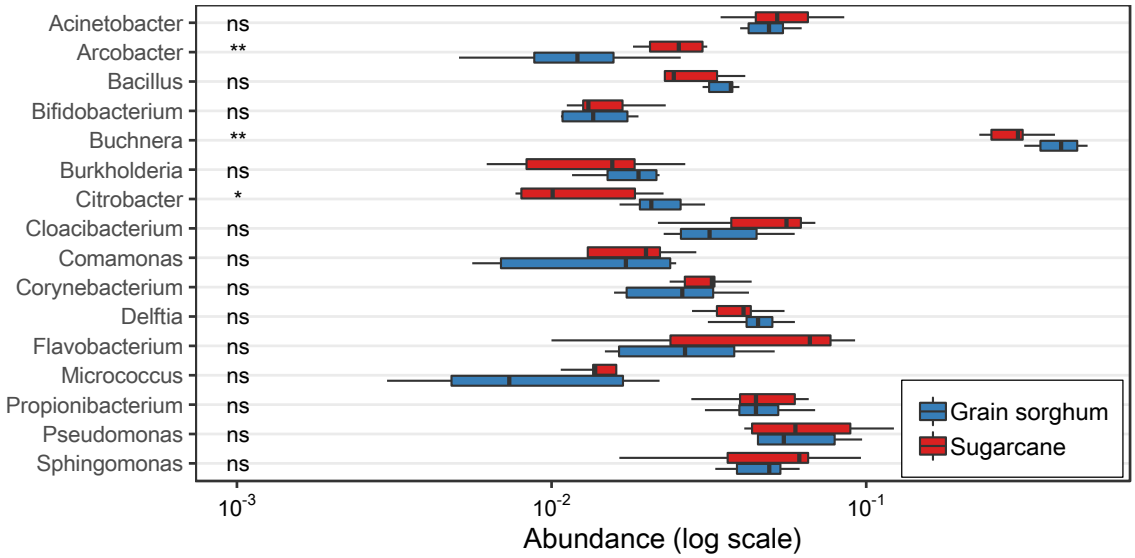


Figure 3


Acinetobacter
Arcobacter
Bacillus
Bifidobacterium
Buchnera
Burkholderia
Citrobacter
Cloacibacterium
Comamonas
Corynebacterium
Delftia
Flavobacterium
Micrococcus
Propionibacterium
Pseudomonas
Sphingomonas
ns
**
ns
ns
**
ns
*
ns
ns
ns
ns
ns
ns
ns
ns
10^{-3}
10^{-2}
10^{-1}
Abundance (log scale)
Grain sorghum
Sugarcane

Tables

Table 1. Number of sugarcane aphids for each host plant and state combination used in microbial analyses. Within each county each aphid was collected at least 1 km away from each other (except for lab colony aphids).

Location & Year	Grain Sorghum	Sugarcane
Alabama 2014	18	9
Lab Colony 2015 – 2017	25	0
Lab Colony (non-surface sterilized) 2015	30	0
Florida 2014	24	21
Florida 2015	30	0
Louisiana 2007-2009	0	7
Louisiana post 2013	17	20
South Africa 2013	19	0
Texas 2013-2015	21	20

References

Abdelfattah, A., A. Malacrino, M. Wisniewski, S. O. Cacciola, and L. Schena. 2018. Metabarcoding: A powerful tool to investigate microbial communities and shape future plant protection strategies. Biol. Control 120: 1-10.

Adams, A. S., F. O. Aylward, S. M. Adams, N. Erbilgin, B. H. Aukema, C. R. Currie, G. Suen, and K. F. Raffa. 2013. Mountain pine beetles colonizing historical and naïve host trees are associated with a bacterial community highly enriched in genes contributing to terpene metabolism. Appl. Environ. Microbiol. 79(11): 3468-3475.

Alberonia, D., F. Gaggìaa, L. Baffonia, M. M. Modestoa, B. Biavatib, and D. D. Gioia. 2018. *Bifidobacterium xylocopae* sp. nov. and *Bifidobacterium aemilianum* sp. nov., from the carpenter bee (*Xylocopa violacea*) digestive tract. Syst. Appl. Microbiol. in press.

Álvarez, B., E. G. Biosca, and M. M. López. 2010. On the life of *Ralstonia solanacearum*, a destructive bacterial plant pathogen. Current Research, Technology and Education Topics in Applied Microbiology and Microbial Biotechnology: 267-279.

Anderson, K. E., A. Johansson, T. H. Sheehan, B. M. Mott, V. Corby-Harris, L. Johnstone, R. Sprissler, and W. Fitz. 2013. Draft genome sequences of two *Bifidobacterium* sp. from the honey bee (*Apis mellifera*). Gut Pathog. 5: 42.

Armstrong, J. S., W. L. Rooney, G. C. Peterson, R. T. Villenueva, M. J. Brewer, and D. Sekula-Ortiz. 2015. Sugarcane aphid (Hemiptera: Aphididae): host range and sorghum resistance including cross-resistance from greenbug sources. J. Econ. Entomol. 108(2): 576-582.

Bansal, R., M. A. R. Mian, and A. P. Michel. 2014. Microbiome diversity of *Aphis glycines* with extensive superinfection in native and invasive populations. Environ. Microbiol. Rep. 6(1): 57-69.

Barba, M., A. J. Stewart, T. Passler, A. A. Wooldridge, E. van Santen, M. F. Chamorro, R. C. Cattley, T. Hathcock, J. A. Hogsette, and X. P. Hu. 2015. Experimental transmission of *Corynebacterium pseudotuberculosis* Biovar *equi* in horses by house flies. J. Vet. Intern. Med. 29(2): 636-643.

Ben-Yosef, M., Z. Pasternak, E. Jurkevitch, and B. Yuval. 2014. Symbiotic bacteria enable olive flies (*Bactrocera oleae*) to exploit intractable sources of nitrogen. J. Evol. Biol. 27(12): 2695-2705.

Bennett, G. M., J. P. McCutcheon, B. R. MacDonald, D. Romanovicz, and N. A. Moran. 2014. Differential genome evolution between companion symbionts in an insect-bacterial symbiosis. mBio 5: e01697-01614.

Bokulich, N. A., S. Subramanian, J. J. Faith, D. Gevers, J. I. Gordon, R. Knight, D. A. Mills, and J. G. Caporaso. 2013. Quality-filtering vastly improves diversity estimates from Illumina amplicon sequencing. Nat. Methods 10: 57-59.

Bowling, R. D., M. J. Brewer, D. L. Kerns, J. Gordy, N. Seiter, N. E. Elliott, G. D. Buntin, M. O. Way, T. A. Royer, S. Biles, and E. Maxson. 2016. Sugarcane aphid (Hemiptera: Aphididae): a new pest on sorghum in North America. J. Integr. Pest. Manag. 7(1): 12.

Brady, C. M., and J. A. White. 2013. Cowpea aphid (*Aphis craccivora*) associated with different host plants has different facultative endosymbionts. Ecol. Entomol. 38(4): 433-437.

Brady, C. M., M. K. Asplen, N. Desneux, G. E. Heimpel, K. R. Hopper, C. R. Linnen, K. M. Oliver, J. A. Wulff, and J. A. White. 2014. Worldwide populations of the aphid *Aphis craccivora* are infected with diverse facultative bacterial symbionts. Microb. Ecol. 67(1): 195-204.

Brown, A. M. V., L. Y. Huynh, C. M. Bolender, K. G. Nelson, and J. P. McCutcheon. 2014. Population genomics of a symbiont in the early stages of a pest invasion. Mol. Ecol. 23(6): 1516-1530.

Cakici, F. O., A. Sevim, Z. Demirbag, and I. Demir. 2014. Investigating internal bacteria of *Spodoptera littoralis* (Boisd.) (Lepidoptera: Noctuidae) larvae and some *Bacillus* strains as biocontrol agents. Turkish J. Agric. For. 38: 99-110.

Caporaso, J. G., C. L. Lauber, W. A. Walters, D. Berg-Lyons, J. Huntley, N. Fierer, S. M. Owens, J. Betley, L. Fraser, M. Bauer, N. Gormley, J. A. Gilbert, G. Smith, and R. Knight. 2012. Ultra-high-throughput microbial community analysis on the Illumina HiSeq and MiSeq platforms. ISME J. 6: 1621-1624.

Caporaso, J. G., J. Kuczynski, J. Stombaugh, K. Bittinger, F. D. Bushman, E. K. Costello, N. Fierer, A. G. Peña, J. K. Goodrich, J. I. Gordon, G. A. Huttley, S. T. Kelley, D. Knights, J. E. Koenig, R. E. Ley, C. A. Lozupone, D. McDonald, B. D. Muegge, M. Pirrung, J. Reeder, J. R. Sevinsky, P. J. Turnbaugh, W. A. Walters, J. Widmann, T. Yatsunenko, J. Zaneveld, and R. Knight. 2010. QIIME allows analysis of high-throughput community sequencing data. Nat. Methods 7: 335-336.

Ceja-Navarro, J. A., F. E. Vega, U. Karaoz, Z. Hao, S. Jenkins, H. C. Lim, P. Kosina, F. Infante, T. R. Northen, and E. L. Brodie. 2015. Gut microbiota mediate caffeine detoxification in the primary insect pest of coffee. Nat. Commun. 6: 7618.

Chen, D. Q., B. C. Campbell, and A. H. Purcell. 1996. A new *Rickettsia* from a herbivorous insect, the pea aphid *Acyrthosiphon pisum* (Harris). Curr. Microbiol. 33(2): 123-128.

Cheng, D., Z. Guo, M. Riegler, Z. Xi, G. Liang, and Y. Xu. 2017. Gut symbiont enhances insecticide resistance in a significant pest, the oriental fruit fly *Bactrocera dorsalis* (Hendel). Microbiome 5: 13.

Christie, R. D., A. C. Sumalde, J. T. Schulz, and N. C. Gudmestad. 1991. Insect transmission of the bacterial ring rot pathogen. Am. Potato J. 68(6): 363-372.

Darby, A. C., L. M. Birkle, S. L. Turner, and A. E. Douglas. 2001. An aphid-borne bacterium allied to the secondary symbionts of whitefly. FEMS Microbiol. Ecol. 36(1): 43-50.

Davis, N. M., D. Proctor, S. P. Holmes, D. A. Relman, and B. J. Callahan. 2018. Simple statistical identification and removal of contaminant sequences in marker-gene and metagenomics data. Microbiome 6: 266.

Denmark, H. A. 1988. Sugarcane aphids in Florida (Homoptera: Aphididae). Fla. Dept. Agric. & Consumer Serv., Div. Plant Industry. Entomol. Circ. 302: 2.

Dixon, P. 2003. VEGAN, a package of R functions for community ecology. J. Veg. Sci. 14(6): 927-930.

Duguma, D., M. W. Hall, C. T. Smartt, and J. D. Neufeld. 2017. Effects of organic amendments on microbiota associated with the *Culex nigripalpus* mosquito vector of the Saint Louis Encephalitis and West Nile viruses. mSphere 2: e00387-00316.

Edgar, R. C. 2010. Search and clustering orders of magnitude faster than BLAST. Bioinformatics 26(19): 2460-2461.

Enders, L. S., and N. J. Miller. 2016. Stress-induced changes in abundance differ among obligate and facultative endosymbionts of the soybean aphid. Ecol. Evol. 6(3): 818-829.

Escobar-Zepeda, A., A. Vera-Ponce de León, and A. Sanchez-Flores. 2015. The road to metagenomics: from microbiology to DNA sequencing technologies and bioinformatics. Front. Genet. 6: 348.

Fakhour, S., J. Ambroise, F. Renoz, V. Foray, J.-L. Gala, and T. Hance. 2018. A large-scale field study of bacterial communities in cereal aphid populations across Morocco. FEMS Microbiol. Ecol. 94(3): fiy003.

Ferrari, J., J. A. West, S. Via, and H. C. J. Godfray. 2011. Population genetic structure and secondary symbionts in host-associated populations of the pea aphid complex. Evolution 66(2): 375-390.

Findley, K., D. R. Williams, E. A. Grice, and V. L. Bonham. 2016. Health disparities and the microbiome. Trends Microbiol. 24(11): 847-850.

Fukatsu, T., T. Tsuchida, N. Nikoh, and R. Koga. 2001. *Spiroplasma* symbiont of the pea aphid, *Acyrthosiphon pisum* (Insecta: Homoptera). Appl. Environ. Microbiol. 67(3): 1284-1291.

Gauthier, J.-P., Y. Outreman, L. Mieuzet, and J.-C. Simon. 2015. Bacterial communities associated with host-adapted populations of pea aphids revealed by deep sequencing of 16S Ribosomal DNA. PLoS One 10: e0120664.

Girard, J.-C., J. Noëll, F. Larbre, P. Roumagnac, and P. Rott. 2014. First report of *Acidovorax avenae* subsp. avenae causing Sugarcane Red Stripe in Gabon. Plant Dis. 98(5): 684.

Guyomar, C., F. Legeai, E. Jousselin, C. Mougel, C. Lemaitre, and J.-C. Simon. 2018. Multi-scale characterization of symbiont diversity in the pea aphid complex through metagenomic approaches. Microbiome 6: 181.

Hall, D. G. 1987. The sugarcane aphid, *Melanaphis sacchari* (Zehntner), in Florida. J. ASSCT 7: 26-29.

Hammer, T. J., and M. D. Bowers. 2015. Gut microbes may facilitate insect herbivory of chemically defended plants. Oecologia 179(1): 1-14.

Harris-Shultz, K., X. Ni, P. A. Wadl, X. Wang, H. Wang, F. Huang, K. Flanders, N. Seiter, D. Kerns, R. Meagher, Q. Xue, D. Reisig, D. Buntin, H. E. Cuevas, M. J. Brewer, and X. Yang. 2017. Microsatellite markers reveal a predominant sugarcane aphid (Homoptera: Aphididae) clone is found on sorghum in seven states and one territory of the USA. Crop Sci. 57: 2064–2072.

Hartstra, A. V., K. E. Bouter, F. Backhed, and M. Nieuwdorp. 2015. Insights into the role of the microbiome in obesity and type 2 diabetes. Diabetes Care 38(1): 159-165.

Haynes, S., A. C. Darby, T. J. Daniell, G. Webster, F. J. F. van Veen, H. C. J. Godfray, J. I. Prosser, and A. E. Douglas. 2003. Diversity of bacteria associated with natural aphid populations. Appl. Environ. Microbiol. 69(12): 7216-7223.

Herlemann, D. P., M. Labrenz, K. Jürgens, S. Bertilsson, J. J. Waniek, and A. F. Andersson. 2011. Transitions in bacterial communities along the 2000 km salinity gradient of the Baltic Sea. ISME J. 5: 1571-1579.

Hosokawa, T., Y. Kikuchi, M. Shimada, and T. Fukatsu. 2007. Obligate symbiont involved in pest status of host insect. Proc. Biol. Sci. 274(1621): 1979–1984.

Irwin, M. E., J. M. Thresh, and B. D. Harrison. 1988. Long-range aerial dispersal of cereal aphids as virus vectors in North America. Philos. Trans. Royal Soc. B 321(1207): 421-446.

Jousselin, E., A. L. Clamens, M. Galan, M. Bernard, S. Maman, B. Gschloessl, G. Duport, A. S. Meseguer, F. Calevro, and A. Coeur d'acier. 2016. Assessment of a 16S rRNA amplicon Illumina sequencing procedure for studying the microbiome of a symbiont-rich aphid genus. Mol. Ecol. Resour. 16(3): 628-640.

Kembel, S. W., P. D. Cowan, M. R. Helmus, W. K. Cornwell, H. Morlon, D. D. Ackerly, S. P. Blomberg, and C. O. Webb. 2018. Picante: R tools for integrating phylogenies and ecology. Bioinformatics 26(11): 1463-1464.

Kerns, D. Year. Published. Sugarcane aphid: A new pest of sorghum in the U.S. *In*, Eighteenth Annual National Conservation Systems Cotton & Rice Conference, 2015, Baton Rouge, LA.

Kikuchi, Y., X. Y. Meng, and T. Fukatsu. 2005. Gut symbiotic bacteria of the genus *Burkholderia* in the broad-headed bugs *Riptortus clavatus* and *Leptocorisa chinensis* (Heteroptera: Alydidae). Appl. Environ. Microbiol. 71(7): 4035-4043.

Killer, J., J. Kopečný, J. Mrázek, V. Rada, O. Benada, I. Koppová, J. Havlík, and J. Straka. 2009. *Bifidobacterium bombi* sp. nov., from the bumblebee digestive tract. J. Syst. Evol. Microbiol. 59(8): 2020-2024

Konig, H. 2006. *Bacillus* species in the intestine of termites and other soil invertebrates. J. Appl. Microbiol. 101(3): 620-627.

Leonardo, T. E., and G. T. Muiru. 2003. Facultative symbionts are associated with host plant specialization in pea aphid populations. Proc. R. Soc. Lond. B. 270: S209–S212.

Leroy, P. D., A. Sabri, S. Heuskin, P. Thonart, G. Lognay, F. J. Verheggen, F. Francis, Y. Brostaux, G. W. Felton, and E. Haubruge. 2011. Microorganisms from aphid honeydew attract and enhance the efficacy of natural enemies. Nat. Commun. 2: 348.

Love, M. I., W. Huber, and S. Anders. 2014. Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. Genome Biol. 15: 550.

Loxdale, H. D., J. Hardie, S. Halbert, R. Foottit, N. A. C. Kidd, and C. I. Carter. 1993. The relative importance of short-range and long-range movement of flying aphids. Biol. Rev. 68(2): 291-311.

Lukasik, P., H. Guo, M. van Asch, J. Ferrari, and H. C. Godfray. 2013. Protection against a fungal pathogen conferred by the aphid facultative endosymbionts *Rickettsia* and *Spiroplasma* is expressed in multiple host genotypes and species and is not influenced by co-infection with another symbiont. J. Evol. Biol. 26(12): 2654-2661.

Luna, E., L. v. Eck, T. Campillo, M. Weinroth, J. Metcalf, A. L. Perez-Quintero, A.-M. Botha, T. W. Thannhauser, D. Pappin, N. A. Tisserat, N. L. V. Lapitan, C. T. Argueso, P. J. Ode, M. L. Heck, and J. E. Leach. 2018. Bacteria associated with Russian wheat aphid (*Diuraphis noxia*) enhance aphid virulence to wheat. Phytobiomes 2(3): 151-164.

Malacrinò, A. 2018. Meta-Omics Tools in the World of Insect-Microorganism Interactions. Biology 7(4): 50.

Malacrinò, A., O. Campolo, R. F. Medina, and V. Palmeri. 2018. Instar- and host-associated differentiation of bacterial communities in the Mediterranean fruit fly *Ceratitis capitata*. PLoS One 13: e0194131.

Malhotra, J., A. Dua, A. Saxena, N. Sangwan, U. Mukherjee, N. Pandey, R. Rajagopal, P. Khurana, J. P. Khurana, and R. Lal. 2012. Genome sequence of *Acinetobacter* sp. strain HA, isolated from the gut of the polyphagous insect pest *Helicoverpa armigera*. J. Bacteriol. 194(18): 5156.

Mann, J. A., G. M. Tatchell, M. J. Dupuch, R. Harrington, S. J. Clark, and H. A. McCartney. 1995. Movement of apterous *Sitobion avenae* (Homoptera: Aphididae) in response to leaf disturbances caused by wind and rain. Ann. Appl. Biol. 126(3): 417-427.

Marchesi, J. R., D. H. Adams, F. Fava, G. D. A. Hermes, G. M. Hirschfield, G. Hold, M. N. Quraishi, J. Kinross, H. Smidt, K. M. Tuohy, L. V. Thomas, E. G. Zoetendal, and A. Hart. 2016. The gut microbiota and host health: a new clinical frontier. Gut 65(2): 330-339.

Mardis, E. R. 2008. The impact of next-generation sequencing technology on genetics. Trends Genet. 24(3): 133-141.

McMurdie, P. J., and S. Holmes. 2013. phyloseq: An R package for reproducible interactive analysis and graphics of microbiome census data. PLoS ONE 8: e61217.

Mead, F. W. 1978. Sugarcane aphid, *Melanaphis sacchari* (Zehntner) - Florida - new continental United States record. Cooperative Plant Pest Report 3: 475.

Medina, R. F., P. Nachappa, and C. Tamborindeguy. 2011. Differences in bacterial diversity of host-associated populations of *Phylloxera notabilis* Pergande (Hemiptera: Phylloxeridae) in pecan and water hickory. J. Evol. Biol. 24(4): 761-771.

Medina, R. F., S. J. Armstrong, and K. Harrison. 2017. Genetic population structure of sugarcane aphid *Melanaphis sacchari*, in sorghum, sugarcane, and Johnsongrass in the continental USA. Entomol. Exp. Appl. 162: 358-365.

Meirelles, L. A., Q. S. McFrederick, A. Rodrigues, J. D. Mantovani, C. de Melo Rodovalho, H. Ferreira, M. Bacci, Jr., and U. G. Mueller. 2016. Bacterial microbiomes from vertically transmitted fungal inocula of the leaf-cutting ant *Atta texana*. Environ. Microbiol. Rep. 8(5): 630-640.

Meng, F. 2013. *Ralstonia Solanacearum* species complex and bacterial wilt disease. J. Bacteriol. Parasitol. 4:2.

Meriweather, M., S. Matthews, R. Rio, and R. S. Baucom. 2016. A 454 survey reveals the community composition and core microbiome of the common bed bug (*Cimex lectularius*) across an urban landscape. PLoS One 8: e61465.

Meyer, J. M., and M. A. Hoy. 2008. Molecular survey of endosymbionts in Florida populations of *Diaphorina citri* (Hemiptera: Psyllidae) and its parasitoids *Tamarixia radiata* (Hymenoptera: Eulophidae) and *Diaphorencyrtus aligarhensis* (Hymenoptera: Encyrtidae). Fla. Entomol. 91(2): 294-305.

Montagna, M., J. Gómez-Zurita, A. Giorgi, S. Epis, G. Lozzia, and C. Bandi. 2014. Metamicrobiomics in herbivore beetles of the genus *Cryptocephalus* (Chrysomelidae): toward the understanding of ecological determinants in insect symbiosis. J. Insect Sci. 22(3): 340-352.

Morales-Jiménez, J., G. Zúñiga, H. C. Ramírez-Saad, and C. Hernández-Rodríguez. 2012. Gut-associated bacteria throughout the life cycle of the bark beetle *Dendroctonus rhizophagus* Thomas and Bright (Curculionidae: Scolytinae) and their cellulolytic activities. Microb. Ecol. 64(1): 268–278.

Munson, M. A., P. Baumann, and M. G. Kinsey. 1991. *Buchnera* gen-nov and *Buchnera aphidicola* sp.-nov. a taxon consisting of the mycetocyte-associated, primary endosymbionts of aphids. Int. J. Syst. Bacteriol. 41(4): 566-568.

Nibouche, S., B. Fartek, S. Mississipi, H. Delatte, B. Reynaud, and L. Costet. 2014. Low genetic diversity in *Melanaphis sacchari* aphid populations at the worldwide scale. PLoS ONE 9: e106067.

Nibouche, S., S. Mississipi;, B. Farlek;, H. Delate;, B. Reynaud;, and L. Costet;. 2015. Host plant specialization in the sugarcane aphid *Melanaphis sacchari*. PLoS One 10: e0143704.

Nibouche, S., L. Costet, J. R. Holt, A. Jacobson;, A. Pekarcik, J. Sadeyen, J. S. Armstrong, G. C. Peterson, N. McLaren;, and R. F. Medina. 2018. Invasion of sorghum in the Americas by a new sugarcane aphid (*Melanaphis sacchari*) superclone. PLoS ONE 13: e0196124.

O'Callaghan, A., and D. van Sinderen. 2016. *Bifidobacteria* and their role as members of the human gut microbiota. Front. Microbiol. 7: 925.

Oliver, K. M., N. A. Moran, and M. S. Hunter. 2006. Costs and benefits of a superinfection of facultative symbionts in aphids. Proc. Biol. Sci. 273(1591): 1273-1280.

Oliver, K. M., J. A. Russell, N. A. Moran, and M. S. Hunter. 2003. Facultative bacterial symbionts in aphids confer resistance to parasitic wasps. PNAS 100(4): 1803-1807.

Oliver, K. M., P. H. Degnan, G. R. Burke, and N. A. Moran. 2010. Facultative symbionts in aphids and the horizontal transfer of ecologically important traits. Annu. Rev. Entomol. 55: 247-266.

Ritchie, M. E., B. Phipson, D. Wu, Y. Hu, C. W. Law, W. Shi, and G. K. Smyth. 2015. limma powers differential expression analyses for RNA-sequencing and microarray studies. Nucleic Acids Res. 43: e47.

Rosas-Pérez, T., M. Rosenblueth, R. Rincón-Rosales, J. Mora, and E. Martínez-Romero. 2014. Genome sequence of "*Candidatus* Walczuchella monophlebidarum" the Flavobacterial endosymbiont of *Llaveia axin axin* (Hemiptera: Coccoidea: Monophlebidae). Genome Biol. Evol. 6(3): 714-726.

Russell, J. A., and N. A. Moran. 2006. Costs and benefits of symbiont infection in aphids: variation among symbionts and across temperatures. Proc. Royal Soc. B. 273(1586): 603-610.

Russell, J. A., A. Latorre, B. Sabater-Munoz, A. Moya, and N. A. Moran. 2003. Side-stepping secondary symbionts: widespread horizontal transfer across and beyond the Aphidoidea. Mol. Ecol. 12(4): 1061-1075.

Russell, J. A., S. Weldon, A. H. Smith, K. L. Kim, Y. Hu, P. Łukasik, S. Doll, I. Anastopoulos, M. Novin, and K. M. Oliver. 2013. Uncovering symbiont-driven genetic diversity across North American pea aphids. Mol. Ecol. 22(7): 2045-2059.

Sakurai, M., R. Koga, T. Tsuchida, X.-Y. Meng, and T. Fukatsu. 2005. *Rickettsia* symbiont in the pea aphid *Acyrthosiphon pisum*: novel cellular tropism, effect on host fitness, and interaction with the essential symbiont *Buchnera*. Appl. Environ. Microbiol. 71(7): 4069-4075.

Salter, S. J., M. J. Cox, E. M. Turek, S. T. Calus, W. O. Cookson, M. F. Moffatt, P. Turner, J. Parkhill, N. J. Loman, and A. W. Walker. 2014. Reagent and laboratory contamination can critically impact sequence-based microbiome analyses. BMC Biology 12: 87.

Sandstrom, J. P., J. A. Russell, J. P. White, and N. A. Moran. 2001. Independent origins and horizontal transfer of bacterial symbionts of aphids. Mol. Ecol. 10(1): 217-228.

Santa Brigida, A. B., C. A. Rojas, C. Grativol, E. M. de Armas, J. O. Entenza, F. Thiebaut, M. F. Lima, L. Farrinelli, A. S. Hemerly, S. Lifschitz, and P. C. Ferreira. 2016. Sugarcane transcriptome analysis in response to infection caused by *Acidovorax avenae* subsp. *avenae*. PLoS One 11: e0166473.

Segata, N., F. Baldini, J. Pompon, W. S. Garrett, D. T. Truong, R. K. Dabiré, A. Diabaté, E. A. Levashina, and F. Catteruccia. 2016. The reproductive tracts of two malaria vectors are populated by a core microbiome and by gender- and swarm-enriched microbial biomarkers. Sci. Rep. 6: 24207.

Simon, J.-C., S. Carré, M. Boutin, N. Prunier–Leterme, B. Sabater–Muñoz, A. Latorre, and R. Bournoville. 2003. Host–based divergence in populations of the pea aphid: insights from nuclear markers and the prevalence of facultative symbionts. Proc. Biol. Sci. 270(1525): 1703-1712.

Singh, B. U., P. G. Padmaja, and N. Seetharama. 2004. Biology and management of the sugarcane aphid, *Melanaphis sacchari* (Zehntner) (Homoptera: Aphididae), in sorghum: a review. Crop Protection 23(9): 739-755.

Srivastava, P. N., and J. W. Rouatt. 1963. Bacteria from the alimentary canal of the pea aphid, *Acyrthosiphon pisum* (Harr.) (Homoptera, Aphididae). J. Insect Physiol. 9(4): 435-438.

Stouthamer, C. M., S. Kelly, and M. S. Hunter. 2018. Enrichment of low-density symbiont DNA from minute insects. J. Microbiol. Meth. 151: 16-19.

Su, M.-M., L. Guo, Y.-L. Tao, Y.-J. Zhang, F.-H. Wan, and D. Chu. 2016. Effects of host plant factors on the bacterial communities associated with two whitefly sibling species. PLoS ONE 11: e0152183.

Tsuchida, T., R. Koga, and T. Fukatsu. 2004. Host plant specialization governed by facultative symbiont. Science 303(5666): 1989-1989.

Tsuchida, T., R. Koga, M. Horikawa, T. Tsunoda, T. Maoka, S. Matsumoto, J.-C. Simon, and T. Fukatsu. 2010. Symbiotic bacterium modifies aphid body color. Science 330(6007): 1102-1104.

Vilanova, C., G. Marcoa, L. Domínguez-Escribà, S. Genovés, V. Sentandreu, E. Bataller, D. Ramón, and M. Porcar. 2012. Bacteria from acidic to strongly alkaline insect midguts: Potential sources of extreme cellulolytic enzymes. Biomass and Bioenergy 45: 288-294.

Villanueva, R. T., M. Brewer, M. O. Way, S. Biles, D. Sekula, E. Bynum, J. Swart, C. Crumley, A. Knutson, P. Porter, R. Parker, G. Odvody, C. Allen, D. Ragsdale, W. Rooney, G. Peterson, D. Kerns, T. Royer, and S. Armstrong. 2014. Sugarcane aphid: a new pest of sorghum, pp. 4, Texas AgriLife Extension.

Vorburger, C., L. Gehrer, and P. Rodriguez. 2009. A strain of the bacterial symbiont *Regiella insecticola* protects aphids against parasitoids. Biol. Lett. 6(1): 109-111.

Wagner, S. M., A. J. Martinez, Y. M. Ruan, K. L. Kim, P. A. Lenhart, A. C. Dehnel, K. M. Oliver, and J. A. White. 2015. Facultative endosymbionts mediate dietary breadth in a polyphagous herbivore. Funct. Ecol. 29(11): 1402-1410.

White, W. H., T. E. Reagan, and D. G. Hall. 2001. *Melanaphis sacchari* (Homoptera: Aphididae), a sugarcane pest new to Louisiana. Fla. Entomol. 84(3): 435-436.

Wiktelius, S. 1984. Long range migration of aphids into Sweden. Int. J. Biometeorol. 28(3): 185-200.

Wu, D., S. C. Daugherty, S. E. Van Aken, G. H. Pai, K. L. Watkins, H. Khouri, L. J. Tallon, J. M. Zaborsky, H. E. Dunbar, P. L. Tran, N. A. Moran, and J. A. Eisen. 2006. Metabolic complementarity and genomics of the dual bacterial symbiosis of sharpshooters. PLoS Biol 4: e188.

Xiang, H., G.-F. Wei, S. Jia, J. Huang, X.-X. Miao, Z. Zhou, L.-P. Zhao, and Y.-P. Huang. 2006. Microbial communities in the larval midgut of laboratory and field populations of cotton bollworm (*Helicoverpa armigera*). Can. J. Microbiol. 52(11): 1085-1092.

Xie, G. L., G. Q. Zhang, H. Liu, M. M. Lou, W. X. Tian, B. Li, X. P. Zhou, B. Zhu, and G. L. Jin. 2011. Genome sequence of the rice-pathogenic bacterium *Acidovorax avenae* subsp. *avenae* RS-1. J. Bacteriol. 193(18): 5013-5014.

Yonzone, R., and M. S. Devi. 2018. Red Stripe/ Top Rot Disease of Sugarcane: A Review. IJCMAS 7(1): 1469-1478.

Zapata, S. D., R. Villanueva, D. Sekula, G. Esparza-Diaz, K. Duke, and M. Mutaleb. 2016. The economic impact of the sugarcane aphid on sorghum production, pp. 1-21, Southern Agricultural Economics Association San Antonio, Texas (No. 229992).