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Peer reviewed

## Forum

# Highlights of Veterinary Entomology, 2022

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The field of veterinary entomology is dominated by research concerning insects and arthropods that negatively impact the health of domestic animals. A curated selection of peer-reviewed research which was highlighted at the 2022 Joint Meeting between the Entomological Society of America, the Entomological Society of Canada, and the Entomological Society of British Columbia, which prioritized exploring entomology through the lens of art, science, and culture are summarized. Articles are categorized into (i) biting and non-biting flies, (ii) ectoparasites, and (iii) review articles, with the overall goal of showcasing innovative methodologies, addressing overlooked questions in veterinary entomology, and highlighting comprehensive reviews. While not exhaustive, the selected studies represent a myriad of arthropods, methodologies, and perspectives, to inspire future scientists with diverse research avenues and emphasize the continual evolution and importance of entomological studies in today's world.

**Key words:** integrated pest management, methods, ectoparasites, filth flies

Peer-reviewed articles from leading entomology journals between December 2021 and October 2022 were selected, summarized, and presented. This special collection presents research categorized into 3 groups: (i) biting and non-biting flies, (ii) ectoparasites, and (iii) review articles. The papers highlighted are not intended to offer a comprehensive picture of all veterinary entomology research published in 2022. Instead, they highlight novel methods that examine a wide range of veterinary entomology questions as well as review articles that support the 2022 Entomological Society of America, Entomological Society of Canada, and Entomological Society of British Columbia Joint Meetings theme of “entomology as inspiration: insects through art, science and culture.” The goal is to showcase a diverse group of arthropods, research groups, and perspectives on science to inspire the next generation of scientists to conduct innovative and exciting research in years to come.

## Biting and Non-biting Flies

Biting and non-biting flies are of significant concern to animal production due to their adverse effects on livestock health and productivity. These insects can transmit pathogens, cause direct injury to animals through painful bites, and reduce livestock productivity. Moreover, parasitic flies, such as the primary screwworm, can infest open wounds, which can lead to secondary bacterial infections

and death. A thorough understanding of the biology and ecology of pestiferous flies allows for the development of successful management programs and enables scientists to harness the potential of flies for beneficial purposes such as xenosurveillance, which in turn may transform flies from pests into valuable monitoring tools for emerging pathogens.

## Morphological and Molecular Identification of *Culicoides*

*Culicoides* Latreille are small blood-feeding flies belonging to the family Ceratopogonidae and are commonly called biting midges. Known for their irritating bites to both humans and animals, these midges also act as vectors for important animal pathogens, including epizootic hemorrhagic disease virus (EHDV) and bluetongue virus (BTV). A major challenge with studying *Culicoides* is that subtle morphological differences exist between some species making it difficult to distinguish between vector and nonvector species. In addition, a limited number of gene sequences for species have been published to identify them molecularly.

Zhang et al. (2022a) sought to collect and identify *Culicoides* species present in the Southern California Desert, using both morphological and molecular methods. *Culicoides* were captured using CDC suction traps baited with either CO<sub>2</sub> or UV light from May 2018 through July 2020 at the Phillip L. Boyd Deep Canyon Desert

Research Center (Deep Canyon). Following collection, a novel approach to process *Culicoides* was completed. First, *Culicoides* were morphologically identified by 2 authors (X. Z. and R. P.). Following agreement on their identification, specimens were molecularly identified using either COI or 28S rDNA genes. A total of 19 distinct species (or species aggregates) were identified, including 6 new species records for the Deep Canyon area. This study added COI and 28S gene sequences to the GenBank database for 16 North American *Culicoides* species. Thus, this article identified a combined morphological and molecular approach to identifying *Culicoides* that will facilitate future studies on these midges, particularly for researchers who are not well-versed in taxonomy.

### Species Delimitation and Mitonuclear Discordance Within the *Culicoides variipennis* Species Complex

The *Culicoides variipennis* species complex currently consists of 3 distinct species: *Culicoides occidentalis* Wirth and Jones, *Culicoides sonorensis* Coquillett, and *C. variipennis* Coquillett; with 2 additional species, *Culicoides albertensis* Wirth and Jones and *Culicoides australis* Wirth and Jones, considered synonyms of *C. sonorensis*. In North America, this species complex is considered one of the most important groupings of *Culicoides*, as *C. sonorensis* is one of the major BTV and EHDV vectors. One notable challenge with this group lies in the difficulty of distinguishing between them due to subtle morphological differences and genetic similarities. This further complicates vector surveillance as misidentifications may lead to lowered seroprevalence rates through artificially inflated vector population sizes in collections. Shults et al. (2022) conducted a single nucleotide polymorphism (SNP) analysis, using ddRADseq to analyze 206 *Culicoides* midges in the *C. variipennis* complex, collected from 17 sites across North America to evaluate the genetic structure and test the hypothesis of 3 distinct species. Following a population structure analysis, the authors determined that 5 groupings or populations allowed for the most unambiguously assigned groupings, indicating that in addition to the initial 3 distinct species, there are 2 additional cryptic species within this group: *C. albertensis* and an unidentified San Diego population. Interestingly, 8 of 17 sites had more than 1 species in sympatry, and at 4 sites, a total of 7 individuals were hybrids.

Shultz and colleagues also sequenced a 546 bp region of the COI gene from 285 individuals across 27 states as well as British Columbia and Ontario, Canada, to compare SNP species identification to COI gene identification. Past attempts to separate these species using barcoding genes have been inconclusive. Four distinct haplotypes were identified from the haplotype network. *Culicoides occidentalis* formed 2 haplotypes, the San Diego population formed another, and interestingly *C. sonorensis*, *C. albertensis*, and *C. variipennis* formed one haplotype, which could not be differentiated from one another. This result confirms that using the COI gene to differentiate 3 of the 5 species within this complex is unreliable. Overall, the study highlighted the difficulties in species identification within the *C. variipennis* complex. This stresses the need for appropriate molecular tools to separate species and further conduct proper vector surveillance to accurately calculate infection rates among vector species.

### The Redescription of an Abundant and Widespread North American Horse Fly

North American horse flies are robust (10–30 mm), blood-feeding flies known for their painful bites and persistent attacks on livestock, wildlife, and humans. Commonly recognized by large, brilliant eyes,

robust bodies, and diurnal biting habits. Their bites not only cause discomfort but can also mechanically transmit numerous livestock pathogens, including surra, anaplasmosis, and equine infectious anemia, making them a significant livestock pest. *Tabanus sulcifrons* Macquart is an abundant and serious livestock pest across much of eastern North America, spanning from north Florida to New York, west across Illinois and southern Iowa, and south through Kansas and east Texas. *Tabanus sulcifrons* is known to have a high degree of morphological variation across its range. In fact, 2 forms of the fly exist in some regions of the country, like eastern Tennessee (*T. sulcifrons* and the Carolina/late-flying form). Each form exhibits a unique seasonal flight pattern (June through August and August until October, respectively). Due to the phenotypic and ecological variation between the 2 forms, it has been hypothesized that they may be different species. Mullens et al. (2022) used traditional morphology, ecological evidence, quantitative morphological analysis, and molecular techniques to examine if the 2 forms could be separated into distinct species. It was determined that the 2 forms are, in fact, different species (*T. sulcifrons* and *Tabanus variegatus* Fabricius). Molecular evidence places the suspected species in separate clades and morphometric analyses indicate the wing vein arrangement and palp shapes are significantly different between the 2 species. In addition, *T. variegatus* females were shown to have more microsetae present. Following this determination, a redescription of *T. variegatus* was completed, and an approximate geographic distribution map was determined using museum collections. *Tabanus variegatus* was found to occupy most of the southeastern range of *T. sulcifrons*, including northern Florida through Delaware and across southern Pennsylvania, Ohio, and Illinois, and as far southwest as eastern Oklahoma and Texas. Future work is needed to fully resolve the geographic and seasonal occurrence of *T. variegatus* vs. *T. sulcifrons*.

### A Novel Method to Measure Effects of Horn Fly Infestation on Behavior, Water, Feed Intake, and Digestion in Beef Cattle

The horn fly (*Haematobia irritans* L.) is a significant and economically important external parasite of cattle worldwide. Horn flies cause direct damage through numerous blood-feeding bouts per day. In large numbers, horn flies will cause reduced weight gain, feed efficiency, and milk production in cattle. While these negative impacts are thoroughly documented, variation in horn fly-infested cattle responses indicates additional physiological and nutritional factors may be contributing to the observed outcomes. Sanchez-Sandoval et al. (2022) utilized cannulated cattle to examine the effects of such infestations on horn fly-induced defensive behaviors, water and feed intake, and to investigate the nutrient digestion patterns of infested and noninfested beef cows. Using a cross-over study design, cattle were assigned to be infested with horn flies or serve as uninfested controls. Following a 14-day experimental period, control and treatment groups were switched. Cattle were held in individual, temperature-controlled, screen-walled rooms where defensive behaviors, forage, and water consumption were recorded daily. Nutrient digestion was measured through the collection of intestinal chyme, rumen fluid, and fecal matter. Host defensive behaviors were observed to be significantly increased in infested vs. uninfested animals, aligning with previous studies such as Mullens et al. (2006). All other measured metrics, including water and nutrient intake, volatile fatty acid and true ruminal digestion, flow of nutrients to the duodenum, fecal excretion, total tract digestion, as well as plasma urea nitrogen and amino acid concentrations, did not significantly

differ between treatment groups. The authors hypothesized the confined nature of the pens used in their study likely limited the feeding-specific energy requirements that would be observed in a field setting. While no significant differences in nutrient digestion were detected between infested and uninfested animals in the study, the use of cannulated animals to examine the impacts of host-parasite interactions shows promise and should be used by researchers in the future.

### Attempting to Use Flies and Cockroaches as a Xenosurveillance Tool for SARS-CoV-2

SARS-CoV-2, the causative agent of the global COVID-19 pandemic, has prompted extensive research into its transmission dynamics and reservoirs. Insects have been investigated as potential biological and mechanical vectors of the virus. While insects likely do not play a significant role in transmission, they have been shown to be able to acquire SARS-CoV-2 they have not been shown to transmit infectious viruses. Only noninfectious viral RNA was able to be transferred by flies to virus-free surfaces (Balaraman et al. 2021a, b). In this context, flies have emerged as potential tools for xenosurveillance, offering a novel approach to detect and monitor the virus' presence in diverse environments. Roundy et al. (2022) attempted to examine if SARS-CoV-2 could be detected from insects collected from households with at least 1 confirmed human COVID-19 case. Homes received between 1 and 3 traps (sticky or liquid), which were placed either indoors or outside depending on the preference of the resident. Following trap collection, insects were identified, grouped by taxa, and screened via RT-qPCR for 2 SARS-CoV-2 genes, RNA-dependent RNA polymerase (RDRP), and envelope (E). In total, 245 traps were deployed at 81 homes. In total, 133 insect traps containing 1,345 insects from 11 Dipteran families and Blattodea were examined. No positive pools or samples tested positive for SARS-CoV-2 RNA. One potential explanation for the lack of positive insect pools may be that traps were deployed an average of 8.2 days following the human diagnosis of COVID-19, indicating the home's residents may have progressed through the disease and were no longer positive or shedding viral RNA. Future studies and responses to pandemics should consider conducting similar investigations, as understanding the interactions between pathogens and the insect world may provide crucial insights into transmission dynamics and potential avenues for early detection and surveillance.

### Examination of Sex-Specific Feeding Preference in Adult House Flies

The house fly, *Musca domestica* L. is a synanthropic pest fly species commonly associated with confined animal and urban waste facilities. Large amounts of microbe-rich materials are produced in these facilities, which is ideal for larval house-fly development. House flies are considered significant nuisance pests and have been implicated in the harborage/transmission of over 200 pathogens (reviewed by Nayduch and Burrus 2017). The production of large numbers of adult flies in animal facilities can result in litigation against animal producers causing significant economic losses (Thomas and Skoda 1993). While adult house flies are often considered indiscriminate feeders, it is known that the nutritional composition of food is critical for fly reproduction and longevity. Neupane et al. (2023) investigated if house-fly mating status or sex affected their preference for foods with varying macronutrient profiles. Male (mated/unmated) and female (mated/unmated) flies were exposed to a 4-choice feeding preference assay, offering 10% solutions of (i) nonfat dry milk (35% protein, 52% carbohydrate,

and 0% lipid), (ii) egg yolk (25% protein, 50% lipid, and 0% carbohydrate), (iii) powdered sugar (100% carbohydrate as sugar and cornstarch, 0% protein, and 0% lipid), and (iv) water (deionized, no macronutrient). Each solution was dyed a different color using nontoxic food dye to differentiate ingested food types in the digestive tract. Flies were allowed to forage freely on the solutions for a 4-h feeding window and were then dissected to examine feeding preference. Results indicated female flies significantly preferred to feed on milk, with mated females exhibiting the greatest preference for milk (protein and carbohydrate-rich). Males preferred to feed on sugar (carbohydrate-rich) food sources. Females were also significantly more likely to feed on multiple food sources, which has potential implications for the acquisition and dissemination of pathogens in the environment. This research indicates that when developing bait-based control strategies to manage house flies, sex-specific food preferences should be considered if attempting to target male and female flies effectively.

### Characterizing House Fly Bacterial Communities Collected Across Time in Different Habitats

Building on the understanding of sex-specific house-fly feeding preferences and the potential implications it has on the acquisition of bacteria in the environment, Neupane and Nayduch (2022) examined the effects of habitat and sampling time on the bacterial composition and diversity in the gut of the female house fly. As these flies interact with various habitats, the associated bacterial communities undergo dynamic changes influenced by both their surroundings and feeding patterns. Female house flies were collected from 3 habitats (agriculture, urban, and mixed), during 3 months (May, June, and July) in 2019. Individual flies were dissected to remove their digestive tracts. Characterization of the bacterial communities associated with fly digestive tracts was completed using amplicon sequencing of the V3-V4 region of the 16s rRNA gene. Flies collected from the agricultural habitat exhibited the greatest diversity, species richness, and were the most evenly distributed when compared to flies in urban or mixed environments. The most abundant bacterial taxa were prevalent in the digestive tracts of flies from all 3 habitats. This may indicate house flies have a core microbiome. The bacterial communities found in the digestive tract of female house flies displayed significant diversity which may be influenced by their habitat and, to a lesser degree, by the time of sampling. This research not only elucidates the complexities of the house flies microbiome but also highlights that flies may be used as tools to monitor current and emerging microbial pathogens.

### The Microbiome of Wild and Mass-Reared Primary Screwworm

The primary screwworm, *Cochliomyia hominivorax* Coquerel, is a devastating, obligate parasite of mammalian hosts. Its larvae infest and feed on living tissue, causing significant wounds. In the United States, prior to its initial eradication in 1959, primary screwworm resulted in severe livestock losses. Eradication efforts were primarily successful through the release of sterile males (as screwworm flies only mate once), which eliminated *C. hominivorax* from most of North America, though the fly remains a concern in parts of Central America and throughout South America. Primary screwworm is currently managed by the Panama-USA Commission for the Eradication & Control of Screwworm (COPEG), which continuously rears and releases millions of sterile insects each week along the Panama-Columbia border. The microbiome of mass-reared primary screwworms is likely to differ from those of wild flies because

they are raised in controlled environments with regimented diets and consistent environmental conditions though little has been published on the microbiome of *C. hominivorax*. [Arp et al. \(2022\)](#) conducted the first culture-independent microbial survey of *C. hominivorax* from different life stages and development sites in lab strains (third instar larvae, adult flies, and the larval diet), and field-collected flies (larvae obtained from cows experiencing active cases of myiasis and adults captured by sweep net). Bacterial communities were examined using amplicon sequencing of the V4 region of the 16S rRNA gene. Unsurprisingly, wild-collected samples had a significantly greater diversity of bacterial communities when compared to those of flies from the mass-rearing facility. However, several bacterial taxa were identified across all sample types from both lab and field-collected samples. This may indicate a potential core microbiome of *C. hominivorax*. The results of this study have the potential to improve the success of the primary screwworm mass-rearing system, as it will allow for future research to explore the effect bacterial communities have on screwworm fitness and reproduction.

## Ectoparasites

Ectoparasites of veterinary importance, including mites, lice, and ticks pose significant threats to animal health and productivity. These parasites not only cause direct harm through infestation, leading to skin irritations, anemia, and weight loss but also act as vectors transmitting a variety of pathogens. An improved understanding and the effective control of ectoparasites are crucial for the well-being of livestock to mitigate economic losses in veterinary and agricultural sectors.

### Diversity and Prevalence of Ectoparasites on Poultry From Open Environment Farms in the Western United States

The landscape of domestic poultry production has been undergoing significant transformations in recent years, driven by technological advancements, consumer demand for more sustainable and ethical practices, and evolving market dynamics. There has been a noticeable shift in the United States toward cage-free, free-range, and open-environment farming methods that allow poultry flocks to forage outdoors ([Cornell et al. 2022](#)). While the transition to these production management practices has accelerated in recent years due to consumer pressure in the United States, little is known about the impacts ectoparasites may pose on poultry productivity and health in these settings. [Chambless et al. \(2022\)](#) sought to assess ectoparasites found in open environment farming systems across 17 farms in the western United States across Washington, Idaho, Oregon, and California. For this study, 18–25 chickens were randomly selected on each farm and inspected for ectoparasites. Each bird was scored for an abundance of ectoparasites, followed by physically removing them from infested birds with tweezers and by removal of infested feathers. Overall, 61% of birds inspected were infested with at least 1 ectoparasite. Of the ectoparasites collected, 97% were poultry lice and 3% mites. In this study, 8 species of ectoparasites (6 louse and 2 parasitic mites) were collected from birds: *Dermanyssus gallinae* De Geer, *Goniocotes gallinae* De Geer, *Goniodes gigas* Taschenberg, *Lipeurus caponis* Linnaeus, *Menacanthus cornutus* Schömmmer, *M. stramineus* Nitzsch, *Menopon gallinae* Linnaeus, and *Ornithonyssus sylviarum* Canestrini & Fanzago. The wide variety and prevalence of ectoparasites found on poultry in these open-environment farms underscores the need for continued research on the impacts that ectoparasites may pose on poultry productivity and health in these evolving housing environments.

### First Detection of the Invasive Asian Longhorned Ticks on Passerines in the Americas

The Asian longhorned tick (*Haemaphysalis longicornis* Neuman) is a parthenogenetic, 3-host tick species native to Central and Eastern Asia and was recently introduced into the United States. *Haemaphysalis longicornis* was first detected in the United States when it was collected from sheep in New Jersey in 2017 ([Rainey et al. 2018](#)). Following the initial discovery, *H. longicornis* has now been found in 19 states (Arkansas, Connecticut, Delaware, Georgia, Indiana, Kentucky, Maryland, Massachusetts, Missouri, New Jersey, New York, North Carolina, Ohio, Pennsylvania, Rhode Island, South Carolina, Tennessee, Virginia, and West Virginia). In the native habitat of *H. longicornis*, migratory birds have been shown to disperse this tick over vast distances ([Zhang et al. 2022b](#)). [Pandey et al. \(2022\)](#) aimed to determine if *H. longicornis* is found on passerine and near passerine birds in the United States, given the significant implications this may have on strategies used to prevent the spread of this tick. Over the 3-year study (2018–2021), 1,168 birds representing 67 species of passerines, near passerines, and 1 raptor were examined for ticks. *Haemaphysalis longicornis* larvae were found on 3 migratory bird species and 2 nonmigratory bird species in August and September of 2021. This represents the first discovery of the tick on migratory passerines in the United States. Due to the parthenogenetic nature of *H. longicornis*, even a single female tick dispersing on a migratory bird may lead to a rapid range expansion of this tick across the United States.

### Examining State Animal Import Requirements to Controlling Invasive Ticks and Tick-Borne Disease

Invasive tick species and the pathogens they transmit pose significant threats to wildlife, livestock, and human populations. As the speed and frequency of global movement become more prevalent, the risk of introducing non-native tick species to new regions has surged. While the factors influencing tick dispersal from state to state are multifaceted, the movement of livestock has often played a significant part, though little infrastructure exists to control the movement of animals. In a concerning survey of veterinarians in Ohio who conduct veterinary inspections of livestock, 24.3% believed it was appropriate to allow animals to be sold or transported with ticks on them (Pesapane, unpublished data), indicating a lack of knowledge or concern over tick dispersal or the diseases that these ticks vector. [Swisher and Pesapane \(2022\)](#) evaluated state animal import requirements for the United States to examine if regulations existed pertaining to ticks or tick-borne diseases. Overall, 35 out of 50 states not only failed to mention ticks in their importation requirements but also had no mention of parasites whatsoever. Only 6 out of 50 states specifically mentioned ticks in their regulations, and regulations were generally only applied to particular animal species. More concerningly, importation requirements not only did not mention ticks, but 40 states did not mention *any* requirements for testing of any tick-borne disease before importation. In order to prevent the future range expansion of ticks and tick-borne diseases across the country, it is imperative that state importation and movement regulations are updated to include clear guidelines on visual inspection for ticks and screening for common tick-borne pathogens.

## Review Articles

The COVID-19 pandemic forced many research laboratories to temporarily close their doors, leading to a pause in experimental work. As a result, many researchers pivoted to writing review articles, synthesizing existing knowledge, and providing insights into the field



of veterinary entomology. This shift not only allowed scientists to stay engaged with their research areas but also enriched academic literature by offering comprehensive overviews and new perspectives.

### A Review of the Vector Status of North American *Culicoides* for Arboviruses of Concern

While species such as *C. sonorensis* and *C. insignis* Lutz have their vector status well-established by meeting the 4 criteria for vector incrimination as defined by the World Health Organization, the vector status of many midge species remains unknown. McGregor et al. (2022) reviewed the current knowledge on confirmed and putative *Culicoides* arbovirus vectors in North America. They discussed the habitat preferences and blood-feeding behavior of *Culicoides* as well as their associations with livestock and wildlife pathogens. In addition, the authors highlighted the challenges in determining the vector status of most *Culicoides* species within the United States. Challenges include the fact that most *Culicoides* species cannot be established as laboratory colonies, meaning producing laboratory viral transmission experiments is tedious at best and impossible at worst. In addition, the authors discuss the challenges of differentiating between vector and nonvector species within the *C. varipennis* species complex. This includes *C. sonorensis*, which has likely led to an artificial range expansion for the species. The authors called for an all-hands-on-deck approach to better understand the interactions between United States *Culicoides*, the viruses they vector, and the transmission dynamics with wildlife and livestock.

### Eye Gnat Biology, Ecology, and Management

In 1979, the United States Department of Agriculture (USDA) organized a meeting to identify the need to improve pest management in livestock production. Veterinary entomologists from the United States and Canada were tasked with evaluating integrated pest management (IPM) programs for filth flies and suggesting future research and extension priorities (Anonymous 1979). A similar report based on a workshop was produced in 1994 and then further revised in 2001 (Geden and Hogsette 1994, 2001). In 2021, a special collection of articles was compiled by members of the S-1076: Multistate research project on fly management in animal agriculture systems and impacts on animal health and food safety, where individual filth fly species of veterinary importance were reviewed (Brewer et al. 2021, Geden et al. 2021, Murillo et al. 2021, Rochon et al. 2021, Trout Fryxell et al. 2021). While not included in the initial special collection, Klepzig et al. (2022) reviewed what is currently known about the biology, vector status, ecology, and management of eye gnats (*Liohippelates*). While much research has been conducted on eye gnats dating back to the 1930s, Klepzig et al. (2022) highlighted the need for future research into the ecology of the eye gnat, as there is little information on the position of eye gnats' within the trophic food web. In addition, the authors stressed the need for future development of traps, repellents, and IPM approaches to control and possibly eliminate eye gnat populations.

### A Call for the Development of a Sustainable Pest Management Program for Pest Flies of Livestock

As animal production and fly management practices have changed over the last 40 years, the IPM approaches used to control these pests should also be evolving. To wrap up the collection of papers highlighting filth fly species of veterinary importance compiled by members of the S1076 multistate group, Smith et al. (2022) reviewed the literature on the economic effects of horn flies, stable flies, and face flies, emphasizing the need for the formation of a

transdisciplinary IPM approach that incorporates the economics of fly control in animal production. Adjusted for inflation, estimated annual losses in the United States caused by face, stable, and horn flies are \$127 million, \$1.45 billion, and \$1.95 billion, respectively. Current IPM practices to control these flies vary widely depending on management practices (cow-calf and stocker vs. feedlot). To appropriately monitor for and manage these flies, farm activity evaluations are needed, as animal and crop production on farms likely influences fly populations. Realistic models for evaluating fly populations should be developed to allow producers to make real-time decisions incorporating economic data (losses and expenses) incurred from each fly species present. In addition, using SMART (sensors, monitoring, analysis, and reporting technologies), such as on-animal sensors to investigate animal welfare and behavior in response to flies, should be implemented for more effective and accurate fly surveillance and real-time assessments of control tactics. Ultimately, the authors suggested developing a multifaceted IPM program for fly control to provide actionable information that will drive economic decisions while improving animal welfare and health.

### Summary

The Highlights of Veterinary Entomology for 2022 summarized innovative methodologies, delved into previously unaddressed questions within veterinary entomology, and showcased thorough reviews contributed by researchers spanning various career stages. This compilation, enriched by the diverse backgrounds and perspectives of its contributors, is designed not only to shed light on the current state of veterinary entomology but also to motivate and inspire current and future scientists to embark on paths of innovative and impactful scientific exploration in the field of veterinary entomology.

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### Author Contributions

Caleb Hubbard (Conceptualization [lead], Formal analysis [lead], Methodology [lead], Writing—original draft [lead], Writing—review & editing [lead])

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