

*A Centre for Infectious Diseases and Microbiology - Public Health (CIDM-PH), and  
Marie Bashir Institute for Infectious Diseases & Biosecurity (MBI) publication*

# The Broad Street Pump

## What can Australia learn from the introduction of chikungunya virus to North America?

**Dr Cameron E Webb**

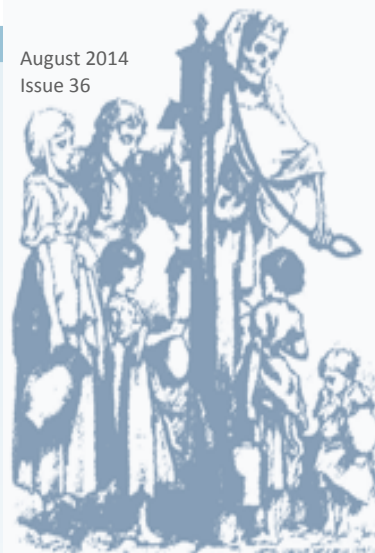
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The emergence of mosquito-borne pathogens in new geographic regions is of great concern. While debate has surrounded the role of a changing climate in the potential spread of mosquitoes and mosquito-borne pathogens<sup>1</sup>, there is little doubt that increasing globalisation, especially cheap, rapid international travel, provides an easily exploitable route for pathogens.

Chikungunya virus (CHIKV) is a mosquito-borne virus that causes potentially severe illness and has been identified as an emerging pathogen of concern<sup>2</sup>. While the burden of disease caused by CHIKV may be less substantial to that posed by dengue viruses (DENV) internationally, outbreaks have occurred in many parts of the world. Until recently, only imported cases had been reported from the Western Hemisphere but since the first reports of CHIKV detection among residents of the French side of St. Martin in the Caribbean surfaced in December 2013, there have been over 570,000 cases in Caribbean, Central America and South America.<sup>3,4</sup>

International travel, not a changing climate triggered this outbreak. There was already the mosquitoes present in the region capable of transmitting CHIKV, all that was needed for an outbreak to occur was the introduction of the virus. Infected travellers provided the spark to ignite the outbreak.

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## What can Australia learn from the introduction of chikungunya virus to North America? (continued from page 1)

With the current outbreak in the Americas, the number of infected travellers visiting or returning to North America is dramatically increasing. In the eight years to 2013, an average of 28 people per year infected with CHIKV entered the U.S. while in the first eight months of 2014, there have been over 600 imported cases.<sup>5</sup> Where the presence of suitable vectors of CHIKV are present, and high volumes of travellers from regions of endemic/epidemic CHIKV activity overlap, the risks of local outbreaks increase.<sup>6</sup>

There are only two mosquito species associated with the spread of CHIKV in North America, the container-inhabiting *Aedes aegypti* and *Aedes albopictus*. *Aedes aegypti* has been responsible for locally acquired cases of dengue in some southern regions of North America.<sup>7</sup> However, this mosquito is limited in its distribution. *Aedes albopictus*, on the other hand, has a greater distribution; being more tolerant of temperate climates. *Aedes albopictus* has been responsible for some outbreaks of chikungunya virus elsewhere in the world and has been identified as a potential driving factor in the spread of dengue activity internationally.<sup>8</sup> Could *Ae. albopictus* drive an explosive outbreak of CHIKV in North America? Fortunately, the scenario looks unlikely. Genetic studies have indicated that the current strain of CHIKV circulating in the Western Hemisphere is less prone to explosive outbreaks of disease driven by *Ae. albopictus*.<sup>9</sup> However, with these two mosquito species present in areas where infected travellers have the potential to introduce the virus, there is the potential for local cases. So far, there have been a number of locally acquired cases of CHIKV in Florida.<sup>10</sup>

### What does this mean for Australia?

We are fortunate in that only one mosquito species, *Ae. aegypti*, effective at transmitting CHIKV is present in mainland Australia and the distribution of this species is limited to Far North Queensland. However, *Ae. albopictus* has been detected in the Torres Strait and it is predicted that this species, should it be introduced into mainland Australia, could establish itself in major metropolitan regions.<sup>11,12,13</sup> The introduction, spread and establishment of *Ae. albopictus* may predispose many metropolitan regions in Australia to a risk of CHIKV. There is already evidence that Australian travellers infected with CHIKV and DENV are returning at increasing rates.<sup>14</sup> Could these travellers introduce *Ae. albopictus* to mainland Australia? Could infected travellers kick off clusters of locally acquired cases of CHIKV in Australia?

While some endemic mosquito species have been shown to transmit CHIKV in the laboratory<sup>15</sup>, it is still *Ae. aegypti* and *Ae. albopictus* that pose the greatest risks. *Aedes albopictus*, given the potential establishment in some of Australia's major metropolitan regions is a major concern. While authorities are being warned to consider the risks of urban mosquito–human–mosquito or enzootic transmission cycles of CHIKV in the Western hemisphere<sup>16</sup>, should Australian authorities be planning similarly? Notwithstanding the potential role of this mosquito in CHIKV transmission, it may also play a role in the transmission of endemic mosquito-borne viruses including Ross River virus.<sup>17</sup>

It is critical that Australian authorities consider how best to undertake surveillance and control of *Ae. albopictus*. In North America, authorities already had strategies in place to address the risks posed by this mosquito. However, for the majority of Australian metropolitan regions, management of endemic and exotic container-inhabiting mosquitoes is in its infancy. While strategic plans are in place for Far North Queensland where occasional outbreaks of *Ae. aegypti* driven locally acquired dengue occur, these plans may not be easily transferrable to more heavily populated southern cities. Health authorities and local governments in SE Queensland are mindful of the risk but what about NSW, Victoria and WA? Perhaps authorities elsewhere should be mindful of the need to respond should *Ae. albopictus* “sneak in” through the back door of southern metropolitan cities.



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## An assessment of new approaches to arbovirus surveillance in NSW

**Cheryl S Toi<sup>1</sup>, John Haniotis<sup>1</sup>, Cameron E Webb<sup>1,2</sup>, John Clancy<sup>1</sup> and Stephen L Doggett<sup>1</sup>**

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Until recently, the arbovirus surveillance in NSW has relied on cell culture of homogenates from mosquitoes with definitive identification by FC-ELISA. While a reliable method, the turnaround time is relatively slow. A new approach to arbovirus surveillance has been proposed to reduce laboratory turnaround times. Rather than testing the mosquitoes, nucleic acid preservation cards (FTA), onto which trapped mosquitoes may have excreted virus, are tested using molecular assays. To complement this laboratory method has been newly developed “passive traps” that allow for longer deployment in the field than the traditional “once per week” approach using EVS traps. During the 2012-2014 surveillance period, we compared the two approaches to both mosquito collection and arbovirus detection. Preliminary investigations indicated that the use of FTA cards in EVS traps deployed for a single night per week provided as efficient approach to arbovirus detection. Ross River and Barmah Forest viruses were all detected from FTA cards. Further work is required to ensure appropriate quality assurance of molecular methods and to determine the implications of new approaches as an early warning system for the issue of public health messages.

*11th Mosquito Control Association of Australia Conference, Mandurah, Western Australia, 7-10 September 2014*



## Medical Entomology in Australia, 1964—2014

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Australia has had a rich history in the field of Medical Entomology, in both practical and applied research, particularly over the last 50 years, which has placed the nation on the world stage. Innovations in taxonomy has seen the change from the classical taxonomists, including Marks, Dobrotworsky and Lee (mosquitoes), Kettle, Dyce and Debenham (Ceratopogonidae) and ticks (Roberts), to the development of proteomics (including Bryan, Sweeney and Foley on mosquitoes), to modern molecular based taxonomy (Beebe again on mosquitoes). The emphasis of research over the last 50 years in Medical Entomology has focused on mosquitoes due to their nuisance biting and propensity to transmit infectious agents. This includes the mapping of malaria vectors (Sweeney and colleagues), mosquito biology (notably Russell & Kay), investigations into mosquito borne disease, surveillance and vector competence (most notably Marshal, Mackenzie & colleagues, Cloonan, Russell & colleagues, and van den Hurk), saltmarsh mosquito management (Dale and Easton in runnelling, Whelan and Muller in practical control), constructed wetlands design to minimise vectors (Russell and Webb), repellents (Frances), and to modelling (Williams). In more recent years, many of the research initiatives relating to Dengue and the control of its main vector, *Aedes aegypti*, have been led by Ritchie and colleagues, with the development of such innovations as lethal and biodegradable ovitraps, and new surveillance technology. More recently, Gates Foundation money has been provided to Scott and colleagues to investigate the use of the intracellular bacteria, *Wolbachia*, to minimise Dengue transmission. Outside of mosquitoes, researchers such as Tovey have investigated dust mites, while various workers have examined ticks in their impact upon human morbidity (Graves on rickettsia, Russell *et al.* on Lyme disease, van Nunen on mammalian meat allergies). Geary has led the way in providing a world class pathology service and was the first to employ disinfected maggots for wound debridement. Finally, I have proudly worked with a team who were the first in the world to develop an industry standard to combat the global bed bug resurgence. This presentation will focus on the Medical Entomology researchers, their research and achievements, during the 50 year history of the Australian Entomological Society.

*Annual Conference of the Australian Entomological Society, Canberra, ACT, 28 September – 1 October 2014*



*Stephen Doggett (Medical Entomology, Pathology West – ICPMR Westmead) and Prof Chow-Yang Lee (Urban Entomology Laboratory, Universiti Sains Malaysia) discuss new strategies for the management of bed bugs at the 8th International Conference on Urban Pests, Zurich, Switzerland.*



Dr James Logan (The London School of Hygiene & Tropical Medicine), David Lilly (University of Sydney) and Frances McKim (Pest Magazine) inside the converted WWII bunkers housing the School's mosquito colonies.

## Implications of insecticide resistance in *Cimex lectularius* (Hemiptera: Cimicidae), in Australia

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Insecticide resistance in bed bugs (*Cimex lectularius* L. and *C. hemipterus* F.) has been nominated as a major factor in the pest's resurgence. Various studies across Europe, Asia and North America have demonstrated resistance to the pyrethroids, carbamates and, to a lesser extent, the organophosphates. Resistance has been suspected in Australia, with anecdotal reports of poor product performance. Laboratory studies applying insecticides via topical application have demonstrated insecticide resistance in a previously suspected-resistant field strain of bed bugs, with substantial differences in LD<sub>50</sub> values when compared to a susceptible strain. The resistance factors for each compound were: permethrin = 1.4 million, deltamethrin = 430,000, bendiocarb = 240, pirimiphos-methyl = 2.8, imidacloprid = 2.7. Thus resistance was confirmed in the field-collected strain with the pyrethroids and carbamates, but not the organophosphates or neonicotinoids (the small number being unrelated to resistance). With demonstrated resistance in bed bugs, professional pest management operations require the development of new strategies to combat the pest. Regulatory authorities must similarly consider the implications of resistance to multiple insecticide groups when registering new products utilizing either existing or new modes of action. One of the gaps in our current knowledge is an investigation of the drivers of this resistance and further research is required to elucidate the breadth, magnitude and mechanisms of the resistance observed.

8th International Conference on Urban Pests, Zurich, Switzerland, 20 - 23 July 2014



## Detection of knockdown resistance (*kdr*) in *Cimex lectularius* and *Cimex hemipterus* (Hemiptera: Cimicidae)

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Worldwide, there are many reports of pyrethroid resistance in bed bugs (*Cimex* spp.). Previous studies on the Common bed bug, *Cimex lectularius* L., have identified two mutations (V419L and L925I) in the voltage-gated sodium channel (VGSC) gene responsible for knockdown resistance (*kdr*). However, nothing is known on possible *kdr* mutations in Australian strains of *C. lectularius* or on the Tropical bed bug, *C. hemipterus* F. This study aimed to identify the status of *kdr* mutations in Australian *C. lectularius* strains, and *C. hemipterus* in Australia and international strains. Samples of *C. lectularius* were obtained from 24 sites across Australia, while the *C. hemipterus* were sourced from Australia, as well as Africa, India, Malaysia and Thailand. DNA was extracted, purified and examined for the *kdr*-related genes by PCR and Sanger sequencing. In *C. lectularius* field populations, the haplotypes A (neither V419L nor L925I), B (L925I only), and C (V419L and L925I) were found, with most (88%) of the field populations being haplotype B. A novel mutation, I936F, was identified in an 'Adelaide' strain (initially identified as haplotype A), which may be linked with *kdr*-type resistance. In *C. hemipterus*, the V419L and L925I mutations were not detected, however, three novel mutations, M918I (Methionine to Isoleucine), D953G (Aspartic acid to Glycine) and L1014F (Leucine to Phenylalanine), were identified. Samples from Thailand have the three mutations, while samples from Australia and India have both M918I and L1014F mutations. Only the L1014F mutation was evident in the samples from Malaysia and Africa. The M918I and L1014F were assumed to be *kdr* mutations and contribute to the high pyrethroid resistance in *C. hemipterus*. Further studies are in process to determine the non-*kdr* type resistance mechanisms.

8th International Conference on Urban Pests, Zurich, Switzerland, 20 - 23 July 2014



Kai Dang (Nankai University and Medical Entomology, Pathology West – ICPMR Westmead), David Lilly (University of Sydney) and Stephen Doggett (Medical Entomology, Pathology West – ICPMR Westmead) outside the London School of Hygiene & Tropical Medicine where all three presented the findings of bed bug research as part of the School's 'Bugging you' seminars for the Public Health and Entomology Groups. Funding support from CIDM-PH enabled Kai to present the findings of his collaborative research with Medical Entomology/University of Sydney at the 8th International Conference on Urban Pests, Zurich, Switzerland.

## Managing mosquitoes in urban wetlands: Strategic control and social communications

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Mosquito management programs in urban wetlands need to find a balance between reducing nuisance-biting and mosquito-borne disease risk with wetland conservation and rehabilitation. Community engagement is critical. The mosquito management program at Sydney Olympic Park has been in place since 1998. The region contains extensive estuarine wetlands that provide ideal habitats for the saltmarsh mosquito, *Aedes vigilax*. The region also has a growing residential and working population as well as attracting millions of visitors each year. A coordinated treatment program associated with a carefully designed surveillance program, including timely notifications to the public and stakeholders, ensures that mosquito treatment is undertaken with minimal or no interruption to the community. Operational efficiencies have ensured that both peaks in mosquito abundance and frequency of wetland treatments have been minimised. Community engagement is a priority, not only with regard to mosquito awareness but broader wetland conservation within the region. With increasing accessibility of online resources via smartphones, local authorities must develop strategies to effectively use social media for communications. In particular, the ability to easily engage with traditional media outlets through a network of social media platforms further increases exposure beyond online communities. Examples from this region will be discussed with implications for state and national community engagement strategies.

11th Mosquito Control Association of Australia Conference, Mandurah, Western Australia, 7-10 September 2014

## High phylogenetic diversity of the cat flea (*Ctenocephalides felis*) at two mitochondrial DNA markers

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The cat flea, *Ctenocephalides felis* (Siphonaptera: Pulicidae) (Bouché), is the most common flea species found on cats and dogs worldwide. We investigated the genetic identity of the cosmopolitan subspecies *C. felis felis* and evaluated diversity of cat fleas from Australia, Fiji, Thailand and Seychelles using mtDNA sequences from cytochrome c oxidase subunit I (cox1) and II (cox2) genes. Both cox1 and cox2 confirmed the high phylogenetic diversity and paraphyletic origin of *C. felis felis*. The African subspecies *C. felis strongylus* (Jordan) is nested within the paraphyletic *C. felis felis*. The south East Asian subspecies *C. felis orientis* (Jordan) is monophyletic and is supported by morphology. We confirm that Australian cat fleas belong to *C. felis felis* and show that in Australia they form two distinct phylogenetic clades, one common with fleas from Fiji. Using a barcoding approach, we recognize two putative species within *C. felis* (*C. felis* and *C. orientis*). Nucleotide diversity was higher in cox1 but COX2 outperformed COX1 in amino acid diversity. COX2 amino acid sequences resolve all phylogenetic clades and provide an additional phylogenetic signal. Both cox1 and cox2 resolved identical phylogeny and are suitable for population structure studies of *Ctenocephalides* species.

The Australian Society for Parasitology Annual Conference, Canberra, ACT, 30 June – 3 July 2014

## Solving the common mystery of the cat flea and their role in public health risks

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Fleas infest our pets and our homes. We treat them with a variety of substances and yet they persist and occasionally bite people, causing annoyance and sometimes severe skin reactions. Although they're considered pests<sup>1</sup>, they're often overlooked in terms of their significance to animal health, their competence as disease vectors and the impacts they make on our everyday lives. However, studies have demonstrated that companion cats and dogs can be commonly infested with fleas carrying bacterial pathogens of significance to human and animal health<sup>2</sup>. There is much more to these irritating insects than meets the eye.

The most common flea encountered in Australia is the cat flea, *Ctenocephalides felis*. Despite their common name, these fleas are found on both cats and dogs. It is often assumed that if a dog has fleas, it must be due to dog fleas (*Ctenocephalides canis*). This is a common misconception. In fact, it appears as if the dog flea is something of a mythical creature in Australia. Despite historical records and anecdotal reports of dog flea infestations, there is no recent literature confirming their presence. Despite historical records and anecdotal reports of dog flea infestations, there is no recent literature confirming their presence. A recent study<sup>3</sup> of over 2,500 pets failed to find a dog flea.

Notwithstanding the economic impact of flea control treatments on domestic animals, the cat flea also carries zoonotic pathogens such as *Bartonella*<sup>4</sup> and *Rickettsia*<sup>5</sup>. There may be many cases of underdiagnosed febrile illnesses caused by flea-borne pathogens that fly under the radar due to the presentation of generic fever and flu-like symptoms that rarely warrant further pathological investigation. Of course, the most famous and historically significant pathogen spread by fleas is the plague bacteria, *Yersinia pestis*. Plague is certainly not a thing of the past with recent outbreaks in Madagascar and up to 17 cases reported from North America each year. Although cat fleas aren't considered a primary vector of *Y. pestis*, recent studies in Uganda have suggested that these fleas may play a role in local transmission risk<sup>6</sup>. Considering

the highly ubiquitous nature of fleas in human environments, and tendency of many species to be host generalists, particularly the cat flea, shouldn't we be more concerned or at least more aware of the risk factors?

Given the impact these little parasites have on our lives, it is baffling how little we know about them. The genetic profile of the cat flea is highly understudied and yet within the genetic code lies hidden implications for the evolution of insecticide resistance, disease transmission and the passage of fleas across continents and the global sphere. A study<sup>2</sup> across 5 states of Australia cat fleas collected from veterinary practices were 100% genetically identical at the mitochondrial DNA. This was a very unusual result as populations of other flea species are generally very diverse. The result was comforting news at the time for the regulation of veterinary pharmaceuticals as the efficacy of flea control products were able to be compared against flea populations across the entire country.

If fleas from Australia are genetically similar but what about elsewhere? When fleas from Australia are compared to those collected from Thailand, Fiji and Seychelles, the results showed that from a global perspective, cat fleas are genetically diverse<sup>7</sup>. The 2013 study yielded a novel second Australian haplotype found in north-east Australia which contradicts the unanimous results from the previous study in 2011. This haplotype was shared with most fleas tested from Fiji, suggesting some recent flea transfer between the two countries. With the rapid emergence of this second haplotype since the previous study, it sparks the question of whether there may be a division of fitness between the two haplotypes. Could this division be resulting in a steady 'invasion' of Australia by the second haplotype?

To investigate the haplotype diversity in this study we developed a novel genetic marker capable of clearly delineating different flea species, subspecies and haplotypes. Previously, genetic studies primarily used a mitochondrial DNA marker called *cox2*. However, there is an emerging global standard of genetic taxonomy called DNA barcoding, which uses a similar gene called *cox1*. This method involves storing massive amount of short DNA sequences in an electronic database, accessible to anyone with internet access. Currently the database called Barcode of Life Database or BOLD holds 3 million 'barcodes', 2 million of which are arthropod barcodes. It is surprising given the global significance fleas that the marker has not been optimised before. The 'barcodes' collected from this study are now available on BOLD and can be searched allowing greater dissemination of and accessibility to flea genetic data.



## Solving the common mystery of the cat flea and their role in public health risks

(continued from page 8)

A change in the genetic makeup of Australia's flea population as discovered recently has implications for the pharmaceutical companies who can no longer apply a blanket approach to flea control efficacy testing. It is hoped that this research may yield greater understanding of the cat flea genetic puzzle that will lead to finding the key to effective control of these tenacious blood-sucking creatures and the diseases they carry.

With recent insights into genetic differences amongst cat fleas internationally, it is critical for the development of surveillance systems to prevent flea-borne disease outbreaks, as well as flea control strategies, that the relationships between fleas, pathogens, companion animals and wildlife are understood<sup>8</sup>. Future studies are also underway to determine the role fleas play in public health risks in Australia. The development of rapid diagnostic tests for flea-borne pathogens will allow investigations into the role *Ct. felis* may play as a vector of zoonotic pathogens.

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- <sup>4</sup>Barrs, V., Beatty, J., Wilson, B., Evans, N., Gowan, R., Baral, R., Lingard, A., Perkovic, G., Hawley, J. and Lappin, M. (2010), Prevalence of *Bartonella* species, *Rickettsia felis*, haemoplasmas and the *Ehrlichia* group in the blood of cats and fleas in eastern Australia. *Australian Veterinary Journal*, 88: 160-165.
- <sup>5</sup>Williams M, Izzard L, Graves SR, Stenos J, Kelly JJ. (2011) First probable Australian cases of human infection with *Rickettsia felis* (cat-flea typhus). *Medical Journal of Australia*, 194: 41-43.
- <sup>6</sup>Eisen RJ, Borchert JN, Holmes JL, Amatre G, Van Wyk K, Ensore RE, Babi N, Atiku LA, Wilder AP, Vetter SM, Bearden SW, Monteneri JA and Gage KL. (2008) Early-phase transmission of *Yersinia pestis* by cat fleas (*Ctenocephalides felis*) and their potential role as vectors in a plague-endemic region of Uganda. *American Journal of Tropical Medicine and Hygiene*, 78: 949-956
- <sup>7</sup>Lawrence AL, Brown GK, Peters B, Spielman DS, Morin-Adeline V and Šlapeta J. (2014), High phylogenetic diversity of the cat flea (*Ctenocephalides felis*) at two mitochondrial DNA markers. *Medical and Veterinary Entomology* [early view] doi: 10.1111/mve.12051
- <sup>8</sup>McElroy KM, Blagburn BL, Breitschwerdt EB, Mead PS and McQuiston JH (2010) Flea-associated zoonotic diseases of cats in the USA: bartonellosis, flea-borne rickettsioses, and plague, *Trends in Parasitology*, 26: 197-204.

## UPCOMING EVENTS...

### **Chasing the tiger and the pursuit of innovative solutions to mosquito borne disease threats**

**Friday, 12 September 2014**

**Westmead Millenium Institute, Level 2, Conference Room C2.20, 176 Hawkesbury Road, Westmead, Sydney**

**Registration:** [sydney.edu.au/mbi](http://sydney.edu.au/mbi)

### **Whole Genome Sequencing in Clinical and Public Health Microbiology Symposium**

**Friday, 10 October 2014**

**Loewenthal Auditorium, Westmead Education & Conference Centre, Westmead Hospital, Sydney**

**Registration:** [sydney.edu.au/mbi](http://sydney.edu.au/mbi)

### **MBI Colloquium**

**Tuesday, 25 November 2014**

**Auditorium, Charles Perkins Centre, University of Sydney**

**Registration:** [sydney.edu.au/mbi](http://sydney.edu.au/mbi)

### **CRE In Critical Infection Colloquium**

**Tuesday 18 - Friday 21 November 2014**

**New Law School, Main Campus, University of Sydney**

**Registration:** [sydney.edu.au/medicine/criticalinfection](http://sydney.edu.au/medicine/criticalinfection)

### **CIDM-PH Colloquium**

**Friday, 5 December 2014**

**Lecture Theatre 2, Westmead Education & Conference Centre, Westmead Hospital, Sydney**

**Registration:** [WSLHD-CIDM-PH@health.nsw.gov.au](mailto:WSLHD-CIDM-PH@health.nsw.gov.au)

## Staff Profile

**Name:** Kai Dang

**Position:** PhD Student, Department of Medical Entomology, CIDM-PH, Pathology West – ICPMR Westmead

**Phone:** (612) 9845 7265

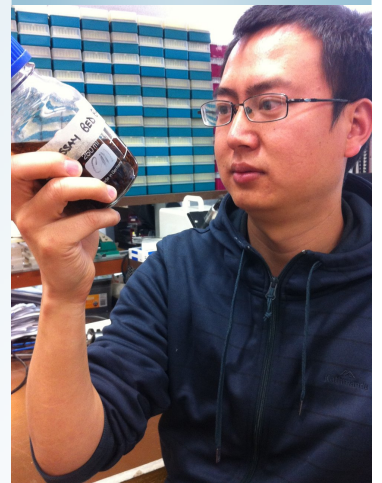
**Email:** [kaidangyu@gmail.com](mailto:kaidangyu@gmail.com)

Kai Dang is a PhD student currently working with the Department of Medical Entomology (CIDM-PH) as part of an internationally collaborative research project with the Institute of Entomology, Nankai University, Tianjin, China. Kai is currently undertaking molecular research into the genetic drivers of insecticide resistance in bed bugs, a major concern for local authorities in managing the impacts of these nuisance-biting insects. Previous studies on the Common bed bug, *Cimex lectularius* L., have identified two mutations (V419L and L925I) in the voltage-gated sodium channel (VGSC) gene responsible for knockdown resistance (*kdr*). However, possible *kdr* mutations in Australian strains of *C. lectularius* or on the Tropical bed bug, *C. hemipterus* F have not been documented.

Kai, in collaboration with Stephen Doggett and Dr Cheryl Toi (Pathology West – ICPMR Westmead) and David Lilly (University of Sydney) aim to identify the status of *kdr* mutations in Australian *C. lectularius* strains as well as local and international strains of *C. hemipterus*. Current research findings have shown that *kdr* mutations may be driving resistance to commonly used insecticides in local bed bug populations.

Kai grew up in south-west China. After undergraduate studies focused on plant protection science, Kai primarily studied the agricultural pest lace bugs (Family: Tingidae) for his MSc at Nankai University before turning his attention to bed bugs. His project has opened his eyes to the importance of bed bugs as urban pests and hopes to continue working on them in the future, perhaps as part of post-doctoral research. He hopes to take back what he has learned on Australia to help authorities in China raise awareness of bed bugs as a problem and develop better strategies to control these pests.

Kai has enjoyed his time at Westmead and grown to love the people, culture and environment of Australia. While many may complain of air pollution in Sydney, Kai is happy to report he much prefers it to China! Medical Entomology has enjoyed having Kai as part of its team and we wish him all the best for future endeavours after he leaves us later in the year.



## CONTACT US

For more information on any articles or CIDM-PH & SEIB events, or to join the e-lists and receive regular updates, please contact us at:

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