

Vector-Borne Diseases

Arbovirus and other Vector-borne disease surveillance in NSW

NSW ANNUAL REPORT

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ACRONYMS AND ABBREVIATIONS

VBD **Vector-borne diseases**

BFV	Barmah Forest virus	MAL	Malaria
CHIKV	Chikungunya virus	MVE	Murray Valley encephalitis
DENV	Dengue virus	RRV	Ross River virus
KUNV	Kunjin virus (a West Nile virus subtype)	ZIKV	Zika virus

LHD **Local health district**

CC	Central Coast LHD	NS	Northern Sydney LHD
FW	Far West LHD	SES	South Eastern Sydney LHD
HNE	Hunter New England LHD	SNSW	Southern NSW LHD
IS	Illawarra Shoalhaven LHD	SWS	South Western Sydney LHD
M	Murrumbidgee LHD	SYD	Sydney LHD
MNC	Mid-North Coast LHD	WNSW	Western NSW LHD
NBM	Nepean Blue Mountains LHD	WS	Western Sydney LHD
NNSW	Northern NSW LHD	NSW	New South Wales

SA2 Statistical Area Level 2 ¹

¹ SA2 is the lowest level of the geographical boundary structure for which Australian Bureau of Statistics (ABS) estimated resident population (ERP) data are generally available. For more information see the [ABS SA2 description](#).

SUMMARY – VECTOR-BORNE DISEASES IN NSW

This report summarises NSW vector-borne disease (VBD)² surveillance data for notifiable arboviruses (arthropod-borne viruses) and other notifiable arthropod-borne diseases for 2016. The report notes changes in notifications over time and describes likely areas of disease acquisition for both local and exotic infections. NSW Health undertakes VBD surveillance to monitor VBD trends with the aim of implementing control measures to prevent further illness within the community from endemic local VBDs (such as Ross River virus and Barmah Forest virus), and to inform appropriate prevention messages for travellers to areas of the world with exotic vector-borne diseases (such as dengue, Zika virus and malaria).

Notified cases of local and exotic vector-borne diseases in NSW, 2016

Disease	2016		5 Year Annual Mean		% change [#]
	Count	Rate*	Count	Rate*	
Barmah Forest virus	37	0.5	315.0	4.2	-88%
Chikungunya virus	38	0.5	19.8	0.3	92%
Dengue virus	475	6.2	286.8	3.9	65%
Malaria	57	0.7	74	0.6	-22%
Ross River virus	641	8.3	798	21.1	-20%
Zika virus	32	0.4	1	0	3100%

* Rate - cases per 100,000 population, NSW (see Methods for population calculations).

Percentage change in disease case count in 2016 relative to the 5-year annual mean case count, 2011-2015.

There were no reports of human infection due to MVE virus, Kunjin virus, Japanese encephalitis virus, or yellow fever virus. All reports of infection with exotic vector-borne infections were believed to have been acquired overseas.

Key trends in 2016

- Barmah Forest virus – a marked decrease in notifications, likely reflecting both low activity in the community and stricter laboratory case definitions for surveillance.
- Chikungunya virus – 74% of cases acquired in India. Almost half of cases were residents of Western Sydney LHD.
- Dengue virus – increasing trend in notifications; 56% acquired in Indonesia, predominantly Bali.
- Ross River virus – decreased notifications overall. Notable increase in notifications in December, predominantly in western and southern NSW west of the ranges following heavy rains and flooding in inland NSW. Overall trend also influenced by stricter laboratory case definitions for surveillance.
- Malaria – 25% decrease in notifications compared to 5-year annual mean. India and Papua New Guinea were the countries where malaria was most commonly acquired.
- Zika virus – a marked increase in notifications but no cases of congenital Zika infection. The increase in cases likely reflects increased exposure of travellers in areas with Zika outbreaks, as well as increased awareness and testing.

Mosquito and sentinel chicken surveillance for arboviruses

In NSW, surveillance for the presence of arboviruses in the environment is conducted during the arbovirus season (typically November to April), and involves sentinel chicken flocks and trapping of mosquitoes at sites around the state.

Sentinel chicken surveillance monitors for the presence of local flaviviruses (Murray Valley Encephalitis and Kunjin viruses) across inland areas of NSW. Blood samples are collected from sentinel flocks each week from November to April and tested for antibodies to these flaviviruses. The mosquito trapping program serves to identify and quantify mosquito species and test them for arboviruses. For further information see the arbovirus and vector monitoring surveillance reports at: www.health.nsw.gov.au/environment/pests/vector/Pages/surveillance.aspx.

² In this report arbovirus and other notifiable arthropod-borne infections are collectively referred to as vector-borne diseases.

BARMAH FOREST VIRUS INFECTION

Barmah Forest virus (BFV) infection is a vector-borne disease which is endemic in many parts of NSW. Infection rates are generally highest in the summer and autumn months. Public health units (PHUs) usually only follow up notified cases if they are believed to have been acquired in a non-endemic area.

The major mosquito vector in inland areas is *Culex annulirostris* which breeds in freshwater habitats. BFV transmission in coastal areas is most commonly due to saltmarsh mosquitoes, including a number of *Aedes* species.

From 1 January 2016, the national surveillance case definition for BFV infection was updated so that a single IgM positive serology result would no longer meet the case definition for infection, reducing the likelihood of false positive notifications. This explains part of the decrease in BFV notifications seen in 2016 compared to previous years. In the previous 5 years (2011-15), BFV notifications based on IgM alone accounted for a mean of 9.1% of all BFV notifications.

Summary 2016

- Case count: 37
- Notification rate per 100,000: 0.5

Overall trend:

- 89% decrease in the 2016 notification rate compared to 5 year annual mean (4.2 per 100,000)

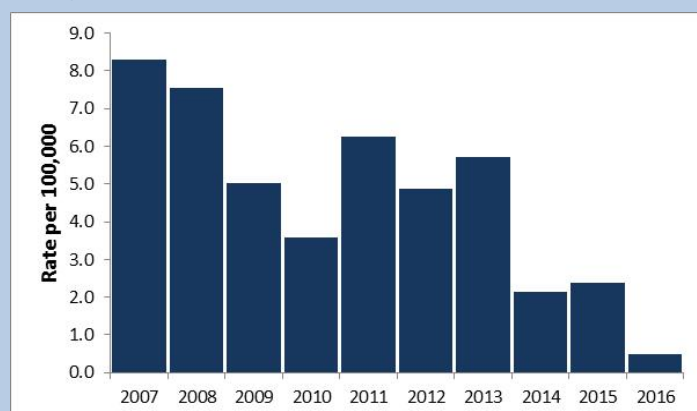
Groups with the highest notification rates in 2016

- Age: 40-49 and 50-59 years (24% of cases, each – 0.9 per 100,000, each)
- Sex: Female (51% of cases – 0.5 per 100,000)
- LHD: Northern NSW (54% of NSW cases - 5.7 per 100,000)

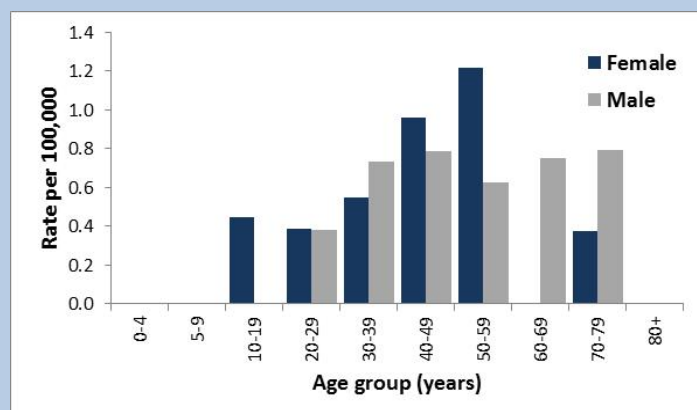
Seasonality

- Notifications were highest in May (8 cases) and December (7 cases)

Notification rate per 100,000 population by year, 2007 – 2016, NSW



Notification rate per 100,000 population by age category and sex, 2016, NSW



Number of cases and rates (per 100,000) by Local Health District, 2016, NSW

LHD	Count		Rate	
	2016	5 Year Annual Mean	2016	5 Year Annual Mean
CC	1	9.4	0.3	2.9
FW	0	4.6	0.0	14.8
HNE	4	56.2	0.4	6.3
IS	0	11.2	0.0	2.9
M	4	16.0	1.4	5.5
MNC	6	62.4	2.8	29.6
NBM	0	4.4	0.0	1.2
NNSW	17	120.4	5.7	41.2
NS	0	3.0	0.0	0.3
SES	0	1.6	0.0	0.2
SNSW	1	10.2	0.5	5.1
SWS	0	1.8	0.0	0.2
SYD	1	0.6	0.2	0.1
WNSW	3	11.8	1.1	4.3
WS	0	1.4	0.0	0.2
NSW	37	0.5	315.0	4.2

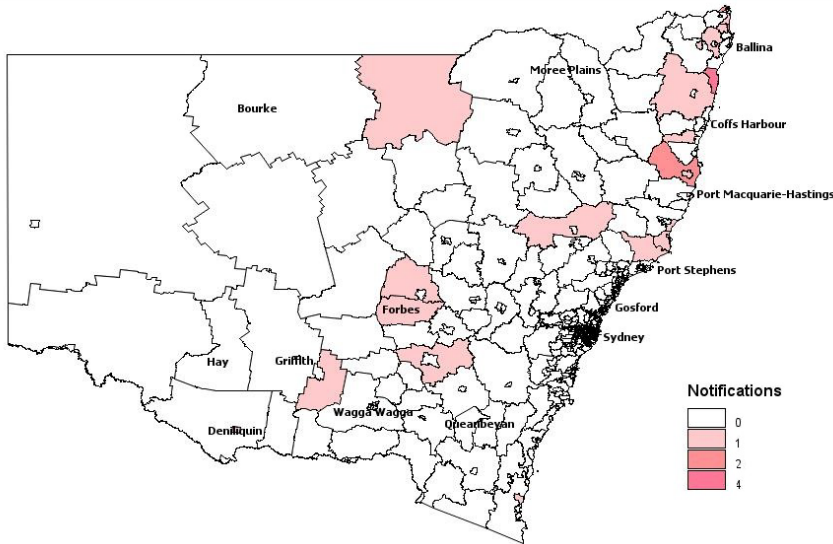
Barmah Forest virus infection – continued

Place of acquisition

Place of residence is used as a surrogate for place of acquisition for BFV infection. The highest numbers of BFV notifications were in the Northern NSW LHD, particularly in the Brunswick Heads/Ocean Shores and Maclean/Yamba/Iluka regions.

Barmah Forest virus notifications by Statistical Area-2 (SA2) region, 2016, NSW.

Map of BFV notifications by SA2 region, 2016, NSW



Number of cases and rates (per 100,000) by SA2 region, 2016, NSW *

Region (SA2)	Count	Rate/100,000
Brunswick Heads - Ocean Shores	4	47.0
Maclean - Yamba - Iluka	4	24.3
Kempsey Region	2	21.5
Tweed Heads	2	10.4

* Data presented for the 4 districts with more than one BFV notification in 2016.

CHIKUNGUNYA VIRUS INFECTION

Chikungunya virus (CHIKV) is an alphavirus, the same genus as Ross River virus (RRV), Barmah Forest virus (BFV) and Sindbis virus. CHIKV infections occur in many parts of Africa and Asia, including many areas where dengue is also common.

CHIKV is transmitted by the bite of an infected *Aedes* spp. mosquito, predominantly *Ae. aegypti* and *Ae. albopictus*. While there have been no reports of chikungunya virus acquired in Australia, transmission remains a risk in parts of north Queensland where transmission-competent mosquitoes circulate.

The increasing trend in annual notifications of CHIKV infection likely reflects increasing clinician awareness of and testing for this disease, as well as discovery during testing for other arbovirus infections such as dengue and Zika virus.

Summary 2016

- Case count: 38
- Notification rate per 100,000: 0.5
- Major source country: India (74%)

Overall trend:

- 87% increase in 2016 notification rate compared to 5 year annual mean (0.3 per 100,000)
- Similar to 2015 (36 cases, 0.5 per 100,000).

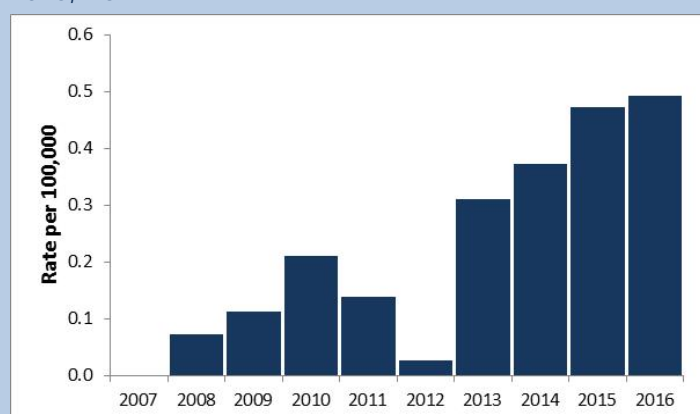
Groups with highest notification rate in 2016

- Age: 50-59 years (32% of cases - 1.2 per 100,000)
- Sex: Female (63% of cases – 0.6 per 100,000)
- LHD: Western Sydney (47% of NSW cases – 1.9 per 100,000)

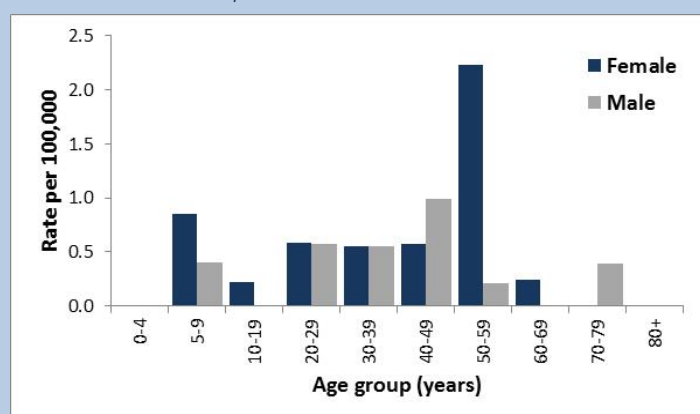
Place of acquisition in 2016

- India (74%)
- Indonesia (11%)
- Philippines (8%)

Notification rate per 100,000 population, by year, 2007 – 2016, NSW



Notification rate per 100,000 population by age category and sex from 2016, NSW



Number of cases and rate (per 100,000) by Local Health District, 2016, NSW

LHD	Count		Rate	
	2016	5 Year Annual Mean	2016	5 Year Annual Mean
CC	0	0.6	0.0	0.2
FW	0	0.0	0.0	0.0
HNE	2	1.2	0.2	0.1
IS	2	1.6	0.5	0.4
M	0	0.0	0.0	0.0
MNC	0	0.4	0.0	0.2
NBM	1	0.8	0.3	0.2
NNSW	2	0.6	0.7	0.2
NS	4	2.0	0.4	0.2
SES	4	3.8	0.4	0.4
SNSW	0	1.2	0.0	0.6
SWS	1	2.0	0.1	0.2
SYD	3	2.8	0.5	0.5
WNSW	1	0.2	0.4	0.1
WS	18	2.6	1.9	0.3
NSW	38	19.8	0.5	0.3

Chikungunya virus infection – continued

Place of acquisition

India was the most common source of chikungunya infection amongst notified cases in 2016, with 28 cases (74%) notified, compared to just 3 notified cases in 2015 linked to travel to India. A total of 15 (54%) of the 28 cases acquired in India were residents of Western Sydney LHD.

There were no NSW cases of CHIKV acquired in Australia in 2016.

Number of cases of chikungunya by country of acquisition, 2016, NSW.

Country of acquisition	Total	% Total
Fiji	2	5%
India	28	74%
Indonesia	4	11%
Philippines	3	8%
Sri Lanka	1	3%
Total	38	100%

DENGUE

Dengue virus (DENV) is a flavivirus. Four serotypes of dengue viruses have been described - dengue 1, 2, 3 and 4. Each of the 4 serotypes is capable of causing the full spectrum of clinical manifestations following DENV infection. Humans and non-human primates are reservoirs for the virus and maintain it in limited forest settings of Asia, Africa, and the Americas. Periodic DENV outbreaks in Pacific Island nations and territories also put NSW travellers at risk.

Transmission is via the bite of an infective female mosquito, principally *Aedes aegypti*. This is a highly domesticated urban mosquito found in countries of the tropics and subtropics. In Australia, this mosquito is currently confined to parts of northern Queensland. *Ae. aegypti* is a day-biting species, with increased biting activity in the few hours after sunrise and before sunset. Humans are the preferred source of blood. *Ae. albopictus* can also transmit DENV.

The increase in DENV notifications in 2016 likely reflects increasing clinician awareness of and testing for this disease, as well as discovery during increased testing for other arbovirus infections, particularly Zika virus infection.

Summary 2016

- Case count: 475
- Notification rate per 100,000: 6.2
- Most common country acquired: Indonesia

Overall trend:

- 65% increase in cases compared to 5 year annual mean.
- DENV-2 most common serotype (53%), where serotype available (18%)

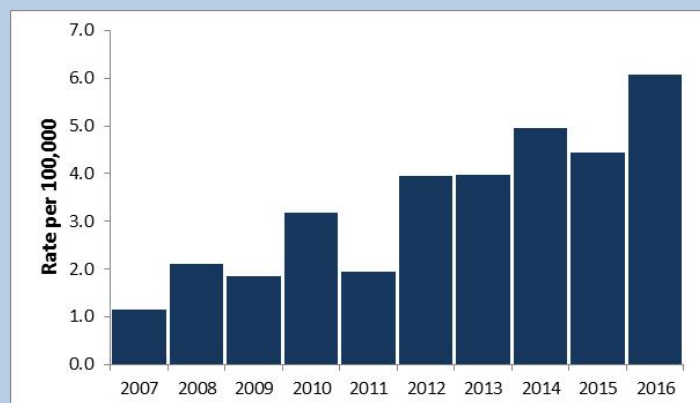
Groups with highest notification rate in 2016

- Age: 30-39 years (25% of cases – 10.9 per 100,000)
- Sex: Female (50% of cases – 6.2 per 100,000)
- LHD: South East Sydney (22% of NSW cases – 11.2 per 100,000), Northern NSW (9.7% of NSW cases – 15.0 per 100,000)

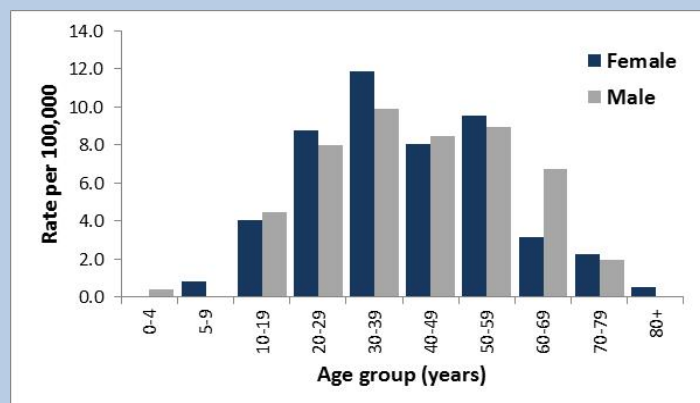
Place of acquisition in 2016

- Indonesia (56.0%) - mainly Bali (86%)
- India (8.0%), Thailand (4.8%)

Notification rate per 100,000 population by year, 2007 – 2016, NSW



Notification rate per 100,000 population by age category and sex, 2016, NSW



Number of cases and rates (per 100,000) by Local Health District, 2016, NSW

LHD	Count		Rate	
	2016	5 Year Annual Mean	2016	5 Year Annual Mean
CC	36	16.4	10.6	5.0
FW	0	0.0	0.0	0.0
HNE	34	27.4	3.6	3.1
IS	20	23.4	5.0	6.0
M	5	5.0	1.7	1.7
MNC	11	6.0	5.1	2.8
NBM	10	7.2	2.7	2.0
NNSW	46	24.8	15.0	8.5
NS	96	39.8	10.5	4.5
SES	102	54.4	11.2	6.2
SNSW	11	5.4	5.3	2.7
SWS	17	19.0	1.6	2.1
SYD	36	20.2	5.7	3.4
WNSW	7	3.4	2.5	1.2
WS	44	34.4	4.6	3.9
NSW	475	6.2	286.8	3.9

Dengue – continued

Place of acquisition

Indonesia remained the most common source of dengue infection amongst notified cases in 2016, accounting for 56% of all cases. Of the 266 cases believed to have been acquired in Indonesia, 229 reported travel to the island of Bali (86.1% of Indonesia cases, 48% overall).

There were no locally-acquired cases of DENV in 2016, and no cases imported from other parts of Australia.

Dengue serotypes

Dengue serotype information was available for 18% of cases notified. Of these, dengue serotype 2 (DENV-2) was the most common serotype reported, accounting for 9.4% of cases overall, and 53% of the cases where serotype was available.

Number of cases of dengue virus infection by country of acquisition and serotype (DENV 1 to 4), 2016, NSW.

County of acquisition	DENV-1	DENV-2	DENV-3	DENV-4	UNK#	Total	% Total
Argentina	0	0	0	0	2	2	0.4%
Bangladesh	0	1	0	1	3	5	1.1%
Brazil	0	0	0	0	4	4	0.8%
Cambodia	0	0	0	0	5	5	1.1%
Fiji	0	2	0	0	3	5	1.1%
French Polynesia	0	0	0	0	4	4	0.8%
India	1	1	1	1	34	38	8.0%
Indonesia	8	21	8	9	220	266	56.0%
Laos	0	0	0	0	2	2	0.4%
Malaysia	0	0	0	0	12	12	2.5%
Nepal	0	0	0	0	3	3	0.6%
Nicaragua	0	0	0	0	3	3	0.6%
Papua New Guinea	0	1	0	0	6	7	1.5%
Philippines	0	2	0	0	18	20	4.2%
Samoa	0	0	0	0	7	7	1.5%
Singapore	0	1	0	0	1	2	0.4%
Solomon Islands	1	2	0	0	14	17	3.6%
South-East Asia (NEC)	0	1	0	0	4	5	1.1%
Sri Lanka	0	3	0	0	10	13	2.7%
Taiwan	0	0	0	0	2	2	0.4%
Thailand	1	4	1	0	17	23	4.8%
Timor-Leste	0	3	0	0	1	4	0.8%
Vietnam	2	0	0	0	4	6	1.3%
Unknown	0	0	1	0	2	3	0.6%
Total **	15	45	13	12	390	475	100%

UNK – unknown

* NEC – not elsewhere coded

** Totals include cases from countries or regions where only one case of dengue virus infection was notified but which are not shown in the Table. These were Costa Rica, El Salvador, Guatemala, Kenya, Maldives, Melanesia (NEC), Mexico, Pakistan, Peru, Polynesia (NEC), Somalia, South America (NEC), South Sudan, Southern Asia (NEC), Sudan, and Tonga.

MALARIA

Malaria is an infection of the liver and red blood cells caused by microscopic protozoan parasites of the *Plasmodium* type. There are five species of parasites that cause malaria: *P. falciparum*, *P. ovale*, *P. malariae*, *P. vivax* and, rarely, *P. knowlesi*. Malaria due to *P. falciparum* is associated with more severe symptoms and most fatal cases.

Malaria parasites are spread through the bite of infective *Anopheles* mosquitoes. There are no competent vectors of malaria known to occur in NSW.

Mainland Australia is free of malaria but it is occasionally detected in the Torres Strait. Travellers are at risk of contracting malaria when travelling without appropriate protection in malaria-endemic parts of tropical and subtropical areas of Asia, Africa, Central and South America, the Pacific Islands and parts of the Middle East.

Summary 2016

- Case count: 57
- Notification rate per 100,000: 0.7

Overall trend:

- 25% decrease in 2016 notification rate compared to 5 year annual mean (1.0 per 100,000)

Malaria species

- 61% *P. falciparum*, 32% *P. vivax*

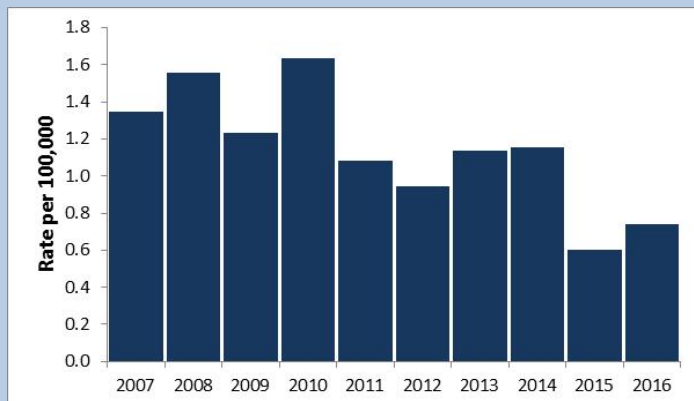
Groups with highest notification rate in 2016

- Age: 30-39 years (25% of cases - 1.3 per 100,000), 40-49 years (21% of cases - 1.2 per 100,000)
- Sex: Male (67% of cases – 1.0 per 100,000)
- LHD: Western Sydney (33% of NSW cases), Mid North Coast (notification rate 2.8 per 100,000)

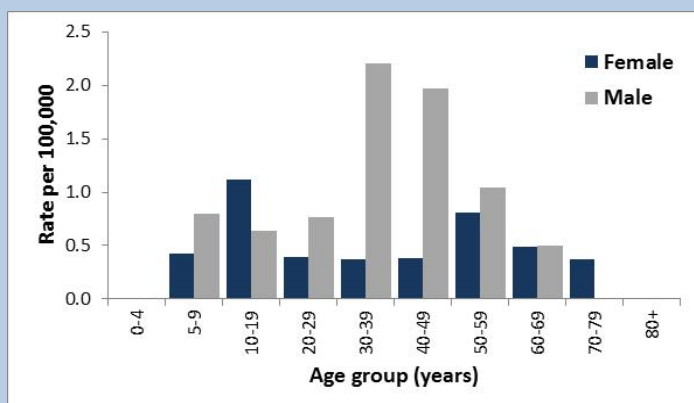
Place of acquisition in 2016

- India and Papua New Guinea (8 cases each, 14%)
- 88% *P. falciparum* cases acquired in African countries

Notification rate per 100,000 population by year, 2007 – 2016, NSW



Notification rate per 100,000 population by age category and sex, 2016, NSW



Number of cases and rates (per 100,000) by Local Health District, 2016, NSW

LHD	Count		Rate	
	2016	5 Year Annual Mean	2016	5 Year Annual Mean
CC	1	1.0	0.3	0.3
FW	0	0.2	0.0	0.6
HNE	2	7.4	0.2	0.8
IS	2	5.0	0.5	1.3
M	2	2.6	0.7	0.9
MNC	6	2.4	2.8	1.1
NBM	2	3.4	0.5	1.0
NNSW	1	2.2	0.3	0.8
NS	1	3.6	0.1	0.4
SES	8	6.6	0.9	0.8
SNSW	4	1.4	1.9	0.7
SWS	3	4.6	0.3	0.5
SYD	4	9.8	0.6	1.6
WNSW	2	1.8	0.7	0.7
WS	19	20.8	2.0	2.3
NSW	57	0.7	72.8	1.0

Malaria – continued

Place of acquisition

India and Papua New Guinea were the most common source countries for malaria cases notified in 2016, accounting for 14% of cases each, followed by Sudan.

There were no NSW cases of malaria acquired in Australia in 2016.

Malaria species

P. falciparum was the most common species identified, accounting for 34 (61%) of the 56 cases where species information was available, followed by *P. vivax* (32%). Most (88%) of the *P. falciparum* cases were acquired in countries in Africa while most (66%) of the *P. vivax* cases were associated with travel to India or Papua New Guinea.

Number of cases of malaria by country of acquisition and species, 2016, NSW.

County of acquisition	Malaria species					Total	% Total
	<i>P. falciparum</i>	<i>P. malariae</i>	<i>P. ovale</i>	<i>P. vivax</i>	UK [#]		
Angola	1	0	0	0	0	1	1.8%
Central and West Africa - NEC*	1	0	0	0	0	1	1.8%
DR of Congo	1	0	0	0	0	1	1.8%
Ghana	3	0	0	0	0	3	5.3%
Guinea	0	0	0	1	0	1	1.8%
India	1	0	0	6	1	8	14.0%
Indonesia	1	0	0	3	0	4	7.0%
Kenya	1	0	1	0	0	2	3.5%
Madagascar	1	0	0	0	0	1	1.8%
Malawi	4	0	0	0	0	4	7.0%
Mali	0	1	0	0	0	1	1.8%
Nigeria	1	0	1	0	0	2	3.5%
Papua New Guinea	2	0	0	6	0	8	14.0%
Rwanda	1	0	0	0	0	1	1.8%
Sierra Leone	4	0	0	0	0	4	7.0%
Solomon Islands	0	0	0	1	0	1	1.8%
South Africa	0	1	0	0	0	1	1.8%
South Sudan	2	0	0	0	0	2	3.5%
Southern and East Africa - NEC*	1	0	0	0	0	1	1.8%
Sudan	5	0	0	0	0	5	8.8%
Tanzania	1	0	0	0	0	1	1.8%
Uganda	2	0	0	1	0	3	5.3%
Zambia	1	0	0	0	0	1	1.8%
Total	34	2	2	18	1	57	100%

UK – unknown

* NEC – not elsewhere coded. Multiple possible exposure countries reported.

ROSS RIVER VIRUS INFECTION

Ross River virus (BFV) infection is a vector-borne disease which is endemic in many parts of NSW. Infection rates are generally highest in the summer and autumn months. Cases are usually only followed up if they are believed to have been acquired in a non-endemic area.

As with BFV infection, the major mosquito vector for RRV in inland areas is *Culex annulirostris* which breeds in freshwater habitats. RRV transmission in coastal areas is most commonly due to saltmarsh mosquitoes, including a number of *Aedes* species. Some marsupials are a natural reservoir for RRV and are likely to be important in the circulation of RRV that includes sporadic transmission to humans.

From 1 January 2016, the national surveillance case definition for RRV infection was updated so that a single IgM positive serology result would no longer meet the case definition for infection, reducing the likelihood of false positive notifications. This is likely to have improved the validity of RRV infection notifications but makes comparisons with incidence rates in previous years more difficult. In the previous 5 years (2011-15), RRV notifications based on IgM alone accounted for a mean of 20.4% of all RRV notifications.

Summary 2016

- Case count: 641
- Notification rate per 100,000: 8.3

Overall trend:

- 23% decrease in 2016 notification rate compared to 5 year annual mean (10.5 per 100,000)

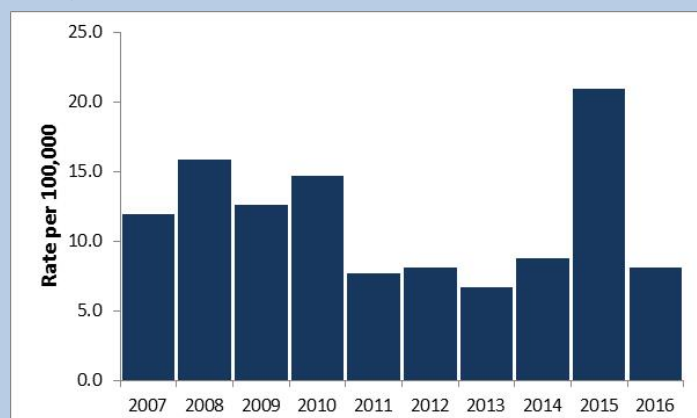
Groups with highest notification rate in 2016

- Age: 50-59 years (22% of cases – 14.6 per 100,000)
- Sex: Female (51% of cases – 8.1 per 100,000)
- LHD: Murrumbidgee (34% of NSW cases – 73.7 per 100,000)

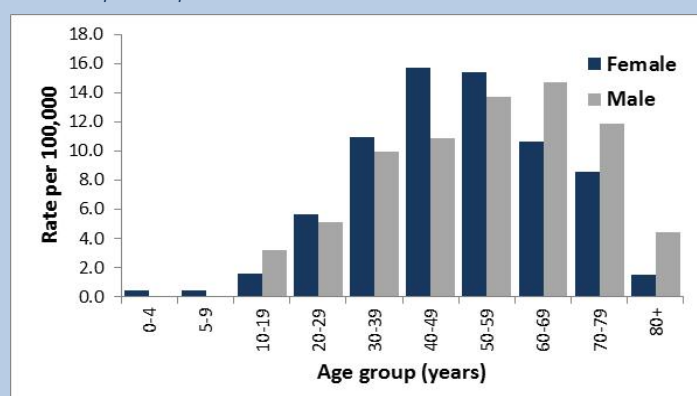
Seasonality

- Typical autumn peak but with notable early season increase in December.

Notification rate per 100,000 population by year, 2007 – 2016, NSW



Notification rate per 100,000 population by age category and sex, 2016, NSW



Number of cases and rates (per 100,000) by Local Health District (LHD), 2016, NSW

LHD	Count		Rate	
	2016	5 Year Annual Mean	2016	5 Year Annual Mean
CC	12	31.2	3.5	9.5
FW	23	20.0	68.9	64.5
HNE	114	198.4	12.4	22.2
IS	10	12.8	2.5	3.3
M	217	82.2	73.7	28.4
MNC	36	103.2	16.6	49.0
NBM	8	23.4	2.1	6.6
NNSW	52	176.2	17.3	60.4
NS	9	17.6	1.0	2.0
SES	12	11.0	1.3	1.3
SNSW	8	16.8	3.8	8.4
SWS	3	6.8	0.3	0.7
SYD	3	6.2	0.5	1.0
WNSW	126	66.6	42.5	24.2
WS	8	8.8	0.8	1.0
NSW	641	8.3	781.2	10.5

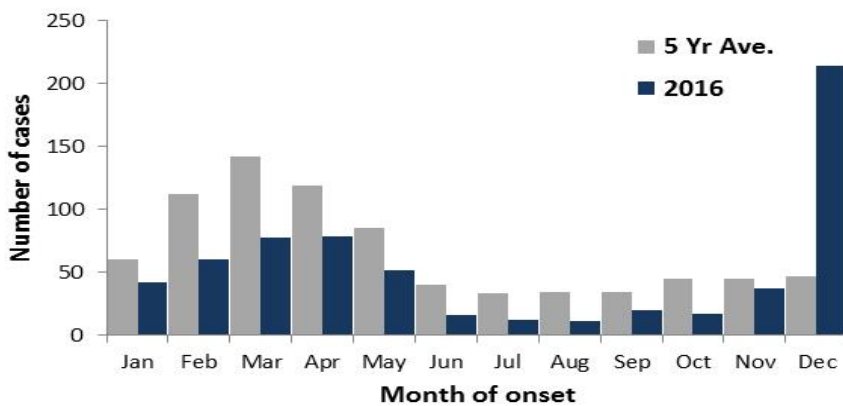
Ross River virus infection – continued

Month of acquisition

There was a typical increasing trend in notifications in the 2015-16 arbovirus season from January to a peak in April. There was also a marked early rise in RRV activity at the end of the year, rising to 214 notifications in December, which heralded an early start to the 2016-17 arbovirus season and a new RRV outbreak. Notifications in December primarily affected residents of inland regions of NSW, in contrast to the 2014-15 outbreak when NSW coastal areas were most affected, particularly along the north coast.

The rise in RRV notifications in December followed the wettest September ever recorded for large parts of inland NSW especially in the State's western half. Major flooding was recorded in the Bogan, Macquarie and Lachlan Rivers, resulting in large bodies of standing water throughout the region. This led to ideal conditions for mosquito breeding in the following months.

Number of RRV cases by month of onset, 2016 compared to 5-year annual mean, 2011-2015, NSW.

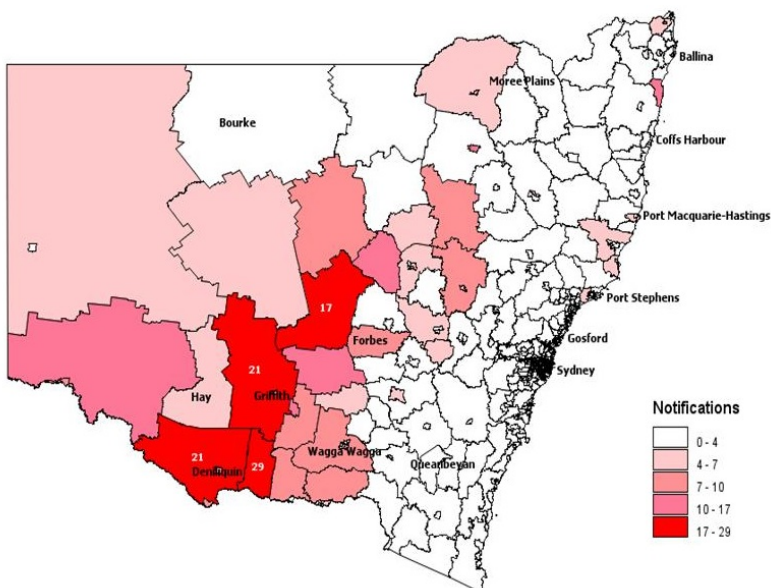


Place of acquisition

Place of residence is used as a surrogate for place of acquisition for Ross River virus infection. The highest numbers of RRV notifications were in the Murrumbidgee and Western NSW LHDs, particularly in the Tocumwal-Finley-Jerilderie, Deniliquin and Griffith regions.

Ross River notifications by Statistical Area-2 (SA2) region, 2016, NSW.

Map of RRV notifications by SA2 region, 2016, NSW



Number of cases and rates (per 100,000) by SA2 region, 2016, NSW *

Region (SA2)*	Count	Rate/100,000
Tocumwal - Finley - Jerilderie	29	301.2
Deniliquin	21	305.1
Griffith	21	159.2
Condobolin	17	236.2
Leeton	14	134.5
Narrabri	12	163.7
Maclean - Yamba - Iluka	12	72.9
Griffith (NSW)	12	63.0
Narromine	11	158.1
Wentworth-Balranald	10	268.3

* Data presented for the 10 districts with the highest number of notifications.

ZIKA VIRUS INFECTION

Zika virus (ZIKV) is a flavivirus, closely related to dengue virus. It was first isolated in 1947 in Uganda's Zika forest. There are two distinct ZIKV lineages: the African lineage and the Asian lineage, the latter of which has emerged more recently in the Pacific and the Americas. The first outbreak of ZIKV infection identified outside of Africa and Asia, occurred on Yap Island, Federated States of Micronesia in 2007. In 2015, ZIKV emerged in South America with widespread outbreaks reported initially in Brazil and Columbia, with subsequent spread to many countries in South and Central America and the Caribbean.

Like dengue, transmission is principally via the bite of an infective *Aedes aegypti* mosquito. Maternal-fetal transmission of ZIKV has also been well documented with potentially serious consequences for the unborn child, including congenital abnormalities such as microcephaly. Sexual transmission of ZIKV is rare but well documented.

The increase in ZIKV notifications in 2016 likely reflects increasing clinician awareness of and testing for this disease, particularly in relation to the risk of congenital Zika virus infection for pregnant women or couples planning pregnancy.

Summary 2016

- Case count: 32 (no congenital cases)
- Notification rate per 100,000: 0.4

Overall trend:

- A dramatic increase in notifications following outbreaks in the Americas and in the Pacific

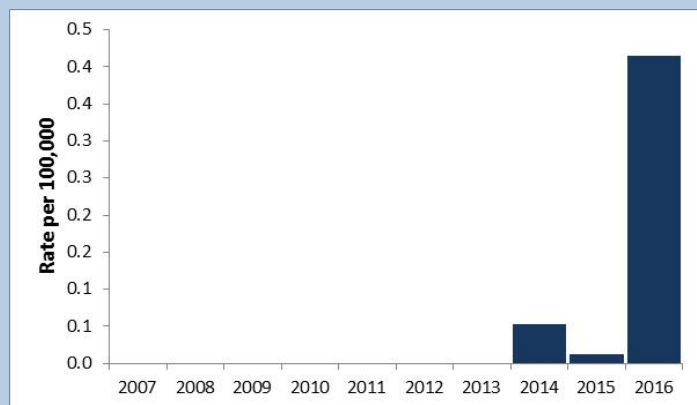
Groups with highest notification rate in 2016

- Age: 30-39 and 40-49 years (34% of cases, each – 1.0 and 1.1 per 100,000, respectively)
- Sex: Female (66% of cases - 0.5 per 100,000)
- LHD: South East Sydney (22% of NSW cases – 0.8 per 100,000)

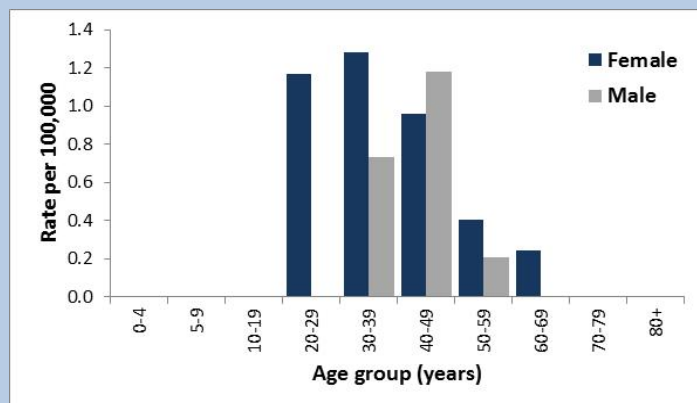
Place of acquisition in 2016

- Brazil (12.5%), Mexico (12.5%), Tonga (12.5%)

Notification rate per 100,000 population by year, 2007 – 2016, NSW



Notification rate per 100,000 population by age category and sex, 2016, NSW



Number of cases and rates (per 100,000) by Local Health District, 2016, NSW

LHD	Count		Rate	
	2016	5 Year Annual Mean	2016	5 Year Annual Mean
CC	1	0.0	0.3	0.0
FW	0	0.0	0.0	0.0
HNE	0	0.0	0.0	0.0
IS	5	0.0	1.2	0.0
M	2	0.2	0.7	0.1
MNC	1	0.0	0.5	0.0
NBM	0	0.2	0.0	0.1
NNSW	0	0.2	0.0	0.1
NS	6	0.4	0.7	0.0
SES	7	0.0	0.8	0.0
SNSW	0	0.0	0.0	0.0
SWS	2	0.0	0.2	0.0
SYD	5	0.0	0.8	0.0
WNSW	1	0.0	0.4	0.0
WS	2	0.0	0.2	0.0
NSW	32	0.4	1.0	0.0

Zika virus infection – continued

Place of acquisition

The most common countries associated with ZIKV infection were Brazil, Mexico and Tonga (4 cases each, 12.5%).

There have only been five cases of ZIKV infection reported previously in NSW; one in 2015 (acquired in Solomon Islands) and four in 2014 (all acquired in Cook Islands).

There were no NSW cases of ZIKV acquired in Australia in 2016.

Number of cases of Zika virus infection by country of acquisition, 2016, NSW.

Country of acquisition	Total	% Total
Belize	1	3.1%
Brazil	4	12.5%
Costa Rica	1	3.1%
Curacao	1	3.1%
Fiji	1	3.1%
Guatemala	3	9.4%
Haiti	2	6.3%
Indonesia	2	6.3%
Jamaica	1	3.1%
Mexico	4	12.5%
Nicaragua	1	3.1%
Panama	1	3.1%
Samoa	2	6.3%
South America - NEC*	3	9.4%
Tonga	4	12.5%
Unknown	1	3.1%
Total	32	100%

* NEC – not elsewhere coded. Cases reported travel to two or more potential exposure countries.

OTHER VECTOR-BORNE DISEASES

There were two reports of 'Flavivirus – unspecified' where the testing laboratories could not conclusively distinguish the specific flavivirus involved. Both of the cases were in people who had travelled overseas just prior to their illness onset – one person had travelled to Indonesia (Bali) while the other had travelled to Sri Lanka.

There were no cases of human infection with Japanese encephalitis virus, yellow fever virus, Kunjin virus, Murray Valley encephalitis virus, Sindbis virus or other arboviruses reported in 2016. There were also no cases of plague, tularaemia or epidemic typhus reported in 2016.

Number of cases of other vector-borne diseases, 2007-2016, NSW.

Condition	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016
Flavivirus - unspecified	2	0	0	1	0	0	0	1	0	2
Japanese encephalitis	0	1	0	0	0	0	0	0	1*	0
Kunjin	4	0	0	0	1	0	0	0	1#	0
Murray Valley encephalitis	3	1	0	0	3	0	0	0	0	0
Sindbis	1	0	0	0	0	0	0	0	0	0

* Case acquired in Indonesia

Case acquired in USA (West Nile virus)

METHODS

The data in this report are derived from disease surveillance and outbreak investigation activities undertaken by staff from NSW public health units and Communicable Diseases Branch. The management of human vector-borne disease surveillance in NSW is the shared responsibility of NSW public health units, and both Communicable Diseases Branch and Environmental Health Branch³ of Health Protection NSW.

Notifiable vector-borne diseases in NSW

Under the Public Health Act 2010 (NSW), all arboviral infections are notifiable in NSW, including Yellow fever and other arboviral haemorrhagic fevers. Other notifiable vector-borne diseases include malaria, plague, tularaemia and epidemic typhus. Arthropods have been suggested as possible transmission vectors for some other notifiable diseases (such as tick-borne Q fever) but these are likely to be rare events.

NSW laboratories report cases to NSW public health units. Notifiable disease data are routinely entered by public health unit staff into the NSW Notifiable Conditions Information Management System (NCIMS).⁴

Data sources for this report

Data in this report has been extracted from NCIMS held by Health Protection NSW.

Analysis

We analysed data for all notifiable vector-borne diseases with onset in 2016. In June 2017, 2016 data was extracted from NCIMS using Secure Analytics for Population Health Research and Intelligence (SAPHaRI) using the date of onset of disease. The counts of each notifiable vector-borne disease for 2016 were compared to the annual mean for the years 2011 to 2015. The NSW estimated resident population for 30 June of each year from 2007-2016 was used to calculate crude annual notification rates for each disease.⁵

The analyses excluded cases in persons whose age or sex was unknown, or who were not NSW residents at the time of diagnosis.

Notification maps of BFV and RRV infection by ABS statistical area level 2 (SA2) of residence for 2016 are shown. Place of residence is used as a surrogate for place of acquisition for cases of these infections but the infection may have been acquired elsewhere.

Further information

Notifiable vector-borne disease data is available for further analysis on the NSW Health website.

See the [Infectious Diseases Data](http://www.health.nsw.gov.au/infectious/pages/data.aspx) page (www.health.nsw.gov.au/infectious/pages/data.aspx) and select the condition of interest. Various data filters are available, including date range, age-group, gender and LHD.

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3. Environmental Health Branch auspices the NSW mosquito and sentinel chicken surveillance for vector-borne arboviruses which is coordinated by the Medical Entomology Department, CIDMLS, ICPMR, Pathology West. For surveillance reports see: www.health.nsw.gov.au/environment/pests/vector/Pages/surveillance.aspx.
 4. NSW Health Notifiable Conditions Information Management System (NCIMS), Communicable Diseases Branch and Centre for Epidemiology and Evidence, NSW Ministry of Health
 5. Notifications per 100,000 estimated resident population based on ABS 2006 and 2011 Census counts. Population projections by the Centre for Epidemiology and Evidence, NSW Ministry of Health, based on data from the NSW Department of Planning and Environment.

ACKNOWLEDGEMENTS

The NSW Vector-Borne Diseases Annual Report 2016 was possible due to the collaborative work of many people who contribute in varying capacities to the management of communicable diseases in NSW, including the following:

- NSW public health unit staff for surveillance, reporting and investigation of unusual disease cases and outbreaks
- Public and private laboratories, supported by the NSW Arbovirus Reference Laboratory, Clinical Virology, CIDMLS, ICPMR, Pathology West
- Communicable Diseases Branch, Health Protection NSW, NSW Health.
- Clinicians across NSW who assist in the diagnosis and follow up vector-borne diseases.