Risk factors for infection during a dengue-1 outbreak in Maui, Hawaii, 2001

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1. Introduction

Dengue is a mosquito-borne, acute viral disease caused by any one of four flaviviruses (DEN-1, -2, -3 and -4), transmitted by Aedes mosquitoes. All four serotypes can cause dengue fever syndrome, with fever, headache, body pains and rash; the severe form of the illness, dengue hemorrhagic fever (DHF), which is characterized by plasma leakage, low platelets and hemorrhage; and shock (dengue shock syndrome) (Rigau-Pérez et al., 1998). Although dengue has a worldwide distribution in tropical and many subtropical areas, local transmission of dengue in the state of Hawaii was last detected in 1945, and at that time the mosquito vector was A. aegypti (Wilbar, 1947). The last statewide mosquito survey, conducted in 1968, found widespread A. albopictus and limited A. aegypti foci (Wells et al., 1968).

In September 2001, the Hawaii Department of Health (HDOH) received reports of suspected dengue in eastern Maui residents who had not traveled internationally and resided in an area of high rainfall with dense tropical vegetation and high A. albopictus density. Laboratory testing in Hawaii and by the Dengue Branch of the U.S. CDC confirmed that dengue was being transmitted in this area. DEN-1 was identified as the infecting serotype and A. albopictus as the vector. In the entomologic surveys conducted during the outbreak, A. albopictus was present in all communities surveyed on O‘ahu, Maui, Molokai and Kauai, but no A. aegypti were found at any site (Effler et al., 2005). The HDOH eventually reported a total of 122 cases of locally transmitted dengue fever from May 2001 to February 2002. Of these, 80 occurred in the eastern Maui area (with less than 0.3% of the state’s population) where the outbreak was first detected. All virus isolations during the epidemic were DEN-1, and genetic analysis identified the virus strain as the Tahiti genotype (Effler et al., 2005). This article presents results of a seroprevalence survey undertaken by the HDOH and the CDC, with the objectives of estimating the incidence of dengue in an affected community, assessing the presence of the vector, and identifying personal and residential risk factors for infection.

Summary

Autogenous dengue virus transmission, last identified in the state of Hawaii in 1945, was detected again in 2001. A seroepidemiological survey in a high-incidence community (Nahiku) and a nearby low-incidence community (Hana Subdivision) was implemented. The two communities studied differed in median household size (two vs. four persons), median lot size (2.8 vs. 0.8 acres), proportion of households with mosquito larvae (81 vs. 28%) and incidence of recent infection (19% [28/147] vs. 1% [1/131]). The average number of reported anti-mosquito actions by residents at both locations remained low, and approximately 50% (42/80) of the inspected houses had larvae, evidencing the need for more effective community mosquito control. Logistic regression analysis of risk factors for infection in Nahiku identified residing in properties with birds in the house or yard as significantly associated with infection (odds ratio 7.0, 95% CI 1.7—28.5), probably as an indicator of unspecified environmental characteristics that were attractive to the vector. We documented that nearly 40% of Nahiku residents had acquired dengue locally in 2001 and that undetected dengue outbreaks had occurred in Hawaii. Our data suggest that ecological characteristics may help Hawaii health officials identify communities at increased risk of dengue infection.

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To test for clustering of recent infections within households, the $\chi^2$-type statistic ($\chi^2 = \sum (O_i - E_i)^2 / E_i$) was used, where significance was determined using a Monte Carlo approximation to the randomization distribution of $\chi^2$.

Values for the expected number of recent positive individuals in a household, $E_i$, were computed under the null hypothesis of no within-household clustering, based on the number of household members providing blood samples and using the observed rate of recent infections (39%, see Results). The $P$-value of the test was computed based on 9999 realizations of $\chi^2$ under the null hypothesis.

### 2.2. Household surveys

Environmental inspectors evaluated household premises for characteristics such as house construction material, number of floors, window screening, air conditioning, lot size, proximity to neighbors, amount of vegetative coverage, tree and bush size, shade and presence and types of containers (both artificial and natural) with mosquito larvae (any type), while health educators or public health students administered questionnaires and physicians or nurses obtained blood samples. In each household, health educators asked one adult about mosquito control actions, sources of potable water, presence of animals, behaviors associated with mosquito exposure, recent visitors from foreign countries, and each resident's age, sex, occupation, gardening activity, lifetime and recent history of travel to tropical/subtropical areas, anti-flavivirus vaccination history, and illness and symptom history since 1 April 2001. All residents were asked to provide venous or fingerprick blood samples unless they had been previously identified by the HDOH surveillance system as having had a recent dengue infection in 2001. For fingerprick samples, two filter paper disks (1.27 cm diameter) were saturated with blood, air-dried and refrigerated until tested.

### 2.3. Laboratory methods

All serum samples were tested at the CDC Dengue Branch, in San Juan, Puerto Rico, for anti-dengue IgM antibody with an antibody-capture ELISA (MAC-ELISA) (Burke et al., 1982). In addition, all samples were tested for anti-dengue IgG antibody with an IgG-ELISA to determine whether the infection was primary or secondary (Kuno et al., 1991; Miagostovich et al., 1999). Virus strains used for both antigen production and for neutralization tests were the standard laboratory strains of the four dengue serotypes: dengue 1 HAW (Hawaii 1944), dengue 2 NGC (New Guinea 1944), dengue 3 H87 (Philippines 1956) and dengue 4 H241 (Tahiti 1985). Because the measurement of IgM antibody may fail to diagnose about 5% of secondary dengue infections, testing by IgG-ELISA was also used to detect anamnestic IgG anti-dengue antibody responses indicative of recent secondary infections (Ruechusatsawat et al., 1994). Some community residents had been tested before the serosurvey as part of the HDOH's response to the outbreak; these diagnostic samples were sent to the CDC Dengue Branch for MAC-ELISA testing, or if appropriate, for dengue virus isolation. Serum specimens collected less than 6 days after the onset of illness were either processed for virus isolation in C6/36 mosquito cell cultures or inoculated into Toxorhynchites amboinensis mosquitoes. Dengue viruses were detected by the use of a direct fluorescence antibody test using pooled human serum and subsequently identified to serotype using specific monoclonal antibodies in an indirect fluorescence antibody test on virus-infected cell cultures (Gubler et al., 1984; Rosen and Gubler, 1974). Blood samples which had sufficient blood remaining after IgM and IgG testing and were negative for IgM antibody and dengue virus isolation but gave low IgG titer readings were tested by the plaque reduction neutralization test in an attempt to determine the serotype that had caused the previous dengue infection (Russell et al., 1967).

The neutralization test was a serum dilution-constant virus test using two-fold serum dilutions starting at 1:40. Seventy percent plaque reduction end points are reported. Titers of 1:40 or greater were considered significant. All serologic tests, on samples obtained during the serosurvey and before the serosurvey, were tested in duplicate; if results were discrepant, the testing was repeated.

### 2.4. Case definitions

People with a confirmed recent infection were identified by the presence of dengue virus, anti-dengue IgM antibody or a high IgG antibody titer ($\geq 163840$) in those who had not traveled abroad since April 2001 (Kuno et al., 1991; Miagostovich et al., 1999; Rosen and Gubler, 1974; Ruechusatsawat et al., 1994). People with probable recent infection were identified by the presence of low anti-dengue IgG antibodies in the absence of dengue virus or anti-dengue IgM antibody, and a monospecific neutralization reaction to DEN-1. A probable recent infection was also identified by epidemiologic nexus, through the presence of low anti-dengue IgG antibodies in the absence of dengue virus or anti-dengue IgM antibody, but if no neutralization tests were performed, in people who had not traveled abroad or had antiflavivirus immunization and who shared a household with a person with a confirmed recent infection. Confirmed and probable recent infections were considered together as recent infections (RI). Persons with previous dengue infections were identified by the presence of IgG anti-dengue antibodies. Dengue-negative individuals showed neither IgM nor IgG anti-dengue antibodies. A case of dengue-like illness (DLI) was based on a person reporting having had, since 1 April 1 2001, fever plus two or more of the following symptoms: headache; retro-orbital pain; bone or joint pains; chills; nausea, vomiting or diarrhea; rash; hemorrhagic manifestations; cough; or nasal congestion. Primary infections were defined by the absence of IgG antibody in the presence of IgM antibody or virus isolation. Secondary infections were identified by the presence of IgG anti-dengue antibody titers in the presence of IgM antibody or virus isolation, or a high IgG antibody titer in the absence of IgM antibody or virus isolation.

The incidence of DLI was defined as the proportion of survey participants who fulfilled the DLI case definition during the study period. The incidence of RI was defined as the proportion of survey participants who fulfilled the RI case definition during the study period among the people who provided an adequate sample for testing. IgG antibody prevalence was defined as the proportion of people with a positive result for anti-dengue IgG among the persons who provided an adequate sample for testing.
The study plan was reviewed by HDOH officials and the Human Subjects Coordinator at the National Center for Infectious Diseases, CDC, and determined to be a public health response that did not require further human subject review. Before administering the questionnaire, interviewers informed participants about the purpose of the investigation, what participation entailed and that participation was voluntary, and ensured that each resident had given written consent to participate.

3. Results

Survey participation rates in Nahiku and the Hana Subdivision differed in the proportion of households completing the survey’s epidemiological questionnaire (66% [39/59] vs. 90% [44/49]) and households allowing an environmental survey (63% [37/59] vs. 88% [43/49]). The proportion of residents agreeing to phlebotomy was similar in the two communities: 53% (72/135) in Nahiku and 57% (131/229) in the Hana Subdivision. Comparisons of community environmental characteristics are presented in Table 1.

### 3.1. Individual characteristics

The median age of residents surveyed in Nahiku was 42 years (range 1–76 years) vs. 28 years (range 2 months to 94 years) in the Hana Subdivision. The male to female ratio was 1.14:1 in Nahiku vs. 0.85:1 in the Hana Subdivision, and in both

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Nahiku</th>
<th>Hana</th>
</tr>
</thead>
<tbody>
<tr>
<td>Median household size (no. people)a</td>
<td>2 (range 1–5)</td>
<td>4 (range 1–11)</td>
</tr>
<tr>
<td>Household with continuous water supply – municipal systemb</td>
<td>6% (27/39)</td>
<td>93% (41/44)</td>
</tr>
<tr>
<td>Household with animals in the house or on the premisesc</td>
<td>90% (35/39)</td>
<td>77% (35/44)</td>
</tr>
<tr>
<td>Household that ate meals in unscreened outdoors ≥ 1 per week</td>
<td>28% (11/39)</td>
<td>30% (13/44)</td>
</tr>
<tr>
<td>Household with international visitors since 1 April 2001</td>
<td>10% (4/39)</td>
<td>5% (2/44)</td>
</tr>
<tr>
<td>Houses constructed in woodd</td>
<td>97% (36/37)</td>
<td>80% (35/44)</td>
</tr>
<tr>
<td>Single level houses</td>
<td>81% (30/37)</td>
<td>91% (39/43)</td>
</tr>
<tr>
<td>Houses with screens on all windows</td>
<td>61% (22/36)</td>
<td>51% (21/41)</td>
</tr>
<tr>
<td>Houses with screens on all doorsd</td>
<td>42% (15/36)</td>
<td>35% (14/40)</td>
</tr>
<tr>
<td>Completely screened housesd</td>
<td>39% (14/36)</td>
<td>27% (11/41)</td>
</tr>
<tr>
<td>Houses with air-conditioninge,f</td>
<td>8% (3/36)</td>
<td>26% (11/42)</td>
</tr>
<tr>
<td>Median estimated lot sizeg</td>
<td>2.8 acres (range 0.5–38 acres)</td>
<td>0.8 acres (range 0.5–1.6 acres)</td>
</tr>
<tr>
<td>Houses from which it was possible to see neighbor’s homeh</td>
<td>39% (12/31)</td>
<td>98% (41/42)</td>
</tr>
<tr>
<td>Area covered by thick vegetation in a 30-ft perimeter around homei</td>
<td>50% (range 3–100%)</td>
<td>25% (range 4–75%)</td>
</tr>
<tr>
<td>Median tree height in a 30-ft perimeter around homei</td>
<td>25 ft (range 6–50 ft)</td>
<td>12 ft (range 3–25 ft)</td>
</tr>
<tr>
<td>Household with containers infested with mosquito larvae</td>
<td>81% (30/37)</td>
<td>28% (12/43)</td>
</tr>
<tr>
<td>Median number of mosquito-infested containers per householdj</td>
<td>2 (range 0–17)</td>
<td>0 (range 0–3)</td>
</tr>
<tr>
<td>Median number of actions against mosquitoes taken per household before 1 September 2001k</td>
<td>1 (range 0–5)</td>
<td>0 (range 0–5)</td>
</tr>
<tr>
<td>Median number of actions against mosquitoes taken per household after 1 September 2001k</td>
<td>2 (range 0–6 actions)</td>
<td>2 (range 0–7)</td>
</tr>
</tbody>
</table>

a Significant difference at P < 0.05.

b 23% (9/39) of Nahiku homes collected rainwater.

c Animals such as chickens, other birds, pigs, dogs, cats, horses or cows.

d Only houses with screens in good condition.

e Only window unit air-conditioning, no houses observed with central air-conditioning.

f 135 containers with mosquito larvae found in Nahiku, 18 containers in Hana.

Examples: use of insect repellent applied to the body or clothing, candles/plants/oils, larvicde, aerosol insecticide; wearing long sleeves/long pants; staying inside during peak mosquito biting times; eliminating larval breeding sites/items that can collect water/emptying standing water.
Risk factors for dengue, Maui, Hawaii

communities people older than 18 years had an average of 12 or more years of education. For persons older than 18 years, Nahiku had more residents who worked outdoors than did the Hana Subdivision (64 [33/52] vs. 41% [57/140]). In both communities less than half the residents reported working in the garden for at least 30 min per day (94 [49/48] vs. 44% [87/200]). More Nahiku residents reported having lived in or traveled to South Asia or Southeast Asia, the Philippines, the Pacific Islands (not Hawaii), the Caribbean, Mexico and Central or South America than did Hana Subdivision residents (40 [35/88] vs. 14% [28/201]). In both communities most residents reported having never been vaccinated for yellow fever or Japanese encephalitis (91 [80/88] vs. 98% [199/202]). More Nahiku residents reported traveling outside of Hawaii, the continental United States, Canada or Europe since 1 April 2001, than did Hana Subdivision residents (3 [3/88] vs. 1% [1/202]); the Nahiku travelers had visited Samoa and Fiji, South America and Tahiti.

A higher proportion of Nahiku residents reported having had at least one symptom of a DLI since 1 April 1 2001 than Hana Subdivision residents (37 [42/113] vs. 12% [26/212]). The symptom reported most often by Nahiku residents was fever (86% [36]), followed in frequency by headache (74%, 31), chills (69%, 29), pain in the joints or muscles (60%, 23), pain behind the eyes, cough, nasal congestion equally (33%, 14 each), rash (31%, 13), and nausea, vomiting, or diarrhea and bleeding equally (17%, 7 each). In comparison, although the Hana Subdivision residents also reported fever most frequently (92%, 24), the frequency of the other symptoms was different: chills (62%, 16), headache (58%, 15), nasal congestion (46%, 12), cough (42%, 11), pain in the joints or muscles (35%, 9), nausea, vomiting, or diarrhea (31%, 8), pain behind the eyes (15%, 4), rash (12%, 3) and bleeding (4%, 1).

The estimate of the incidence of DLI was 37% (33/90, 95% CI 26–48) in Nahiku and 8% (16/207, 95% CI 4–12) in the Hana Subdivision, with no significant age or gender difference in either location.

For the 72 Nahiku residents who provided blood samples (53% [72/135] of the population), the median age was 42 years (range 1–76 years), and 56% (40) were males. For the 131 Hana Subdivision residents who provided blood samples (57% [131/229] of the population), the median age was 30 years (range 1–94 years), and 40% (53) were males. In both communities, children aged 0–9 years were less likely to provide samples than persons older than 9 years (Nahiku: 62% [8/13], 95% CI 32–86 vs. 83% [63/76], 95% CI 73–91; Hana Subdivision: 39% [16/41], 95% CI 24–56 vs. 69% [113/164], 95% CI 61–76). In both locations, about 90% of the households that completed the epidemiological questionnaire had at least one person who gave a blood sample (Nahiku, 90% [35/39]; Hana Subdivision, 91% [40/44]).

3.2. Laboratory-positive dengue

We identified 28 cases of RI in Nahiku, for an estimated incidence of 3% (28/72, 95% CI 2–51) and one in the Hana Subdivision, for an estimated incidence of 1% (1/131, 95% CI 0–4). The single Hana Subdivision RI case reported a history of potential exposure in an area bordering Nahiku and was diagnosed by both IgM positivity and virus isolation (DEN-1). Of the 28 RIs in Nahiku (age range 1–65 years, median 36 years), one was diagnosed by IgM positivity, virus isolation (DEN-1) and secondary IgG response; two by both IgM positivity and virus isolation (DEN-1); two by virus isolation (DEN-1) only; two by both IgM positivity and secondary IgG response; 19 by IgM positivity; and two in accordance with the probable RI definition (epidemiologic nexus). Sixty-six percent (19) of the 29 RIs had low IgG titers, 24% (7) were negative for IgG and 10% (3) had high IgG titers, which indicates that 90% (26) of the RIs were probably primary flavivirus infections. The incidence of RI was highest in males but without statistical significance — for both communities combined the incidence in males was 19.4% (18/93) and in females 10.5% (11/110); for Nahiku alone the incidence in males was 42.5% (17/40) and for females 34.4% (11/32). The incidence of RI in Nahiku was highest (although without statistical significance) in the age group 20–29 years (75%, 3/4) with lower rates in people 10–19 years (43%, 6/14) and 30–39 years old (38%, 3/8). Among participating Nahiku households, 46% (16/35) included at least one person with a recent dengue infection. Twenty percent (7/35) of households had more than one person with a recent infection, indicating the presence of clustering within households (P < 0.001).

The estimated proportion of Nahiku residents positive for IgG antibodies was 32% (23/72, 95% CI 21–44), whereas for the Hana Subdivision it was 9% (12/131, 95% CI 5–16). For the 23 Nahiku residents identified with IgG antibodies, 91% (21/23) were Ri. Of these 21, three (14%) had high IgG titers indicative of secondary infections. All three met the DLI case definition, and two had a history of living or traveling in dengue-endemic areas. For the two remaining Nahiku residents with IgG antibodies but who were not Ri, both had a history of living or traveling in dengue-endemic areas. Therefore, in Nahiku, all positive IgG results could be explained by previous travel or RI.

All 12 IgG-positive Hana Subdivision residents had low IgG titers, and one was a case of RI. Only three (27%) of the other 11 IgG positive residents reported a history of living or traveling in dengue endemic areas. Of the other eight, two met the DLI case definition. One of these also reported a DLI in 1999, and neither reported hosting visitors recently returned from dengue-endemic areas. Plaque reduction neutralization test on sera from the 11 IgG-positive Hana Subdivision residents without RI were attempted, but there was insufficient quantity of serum from the residents and a history of living or traveling abroad. We found nonspecific DEN-2 specific responses in 9 of the 10 participants, one of whom had a history of living or traveling abroad in dengue-endemic areas. Their median age was 53 years (range 9–67 years), 78% (7/9) were female and 71% (5/7) provided a history of outdoor work exposure. Therefore, by contrast to Nahiku, eight Hana Subdivision residents without any reported history of traveling or living in dengue endemic areas had serologic results indicative of exposure to DEN-2 in the past, and two of these were 9 and 10 years of age.

Of the 30 Nahiku residents who met the DLI case definition and agreed to phlebotomy, 67% (20/30, 95% CI 57–83) had an RI. Of the 13 Hana Subdivision residents who met the DLI case definition and agreed to phlebotomy, 8% (1/13, 95% CI 0–36) had an RI. Within the group of 72 Nahiku residents who agreed to phlebotomy, DLI was found to have a significant association with RI (OR 8.5, 95% CI 2.5–29.8). For the Hana Subdivision the OR could not be calculated, because there was only one RI in the community. Within the
group of 38 Nahiku residents who reported that they had had a fever or flu-like symptoms since 1 April 2001 and agreed to phlebotomy, the only symptoms with significant associations with RI were rash (OR 16.7, 95% CI 3.4—411.5) and joint or muscle pain (OR 5.7, 95% CI 1.1—31.4). Of the 29 RI cases, 28% (8/29, 95% CI 13—47) did not meet the DLI case definition.

3.3. Factors associated with recent infection in Nahiku

Because our sample of Hana Subdivision had a single RI, only Nahiku serosurvey results were used to identify risk factors for RI. In a preliminary screening, potential risk factors statistically (P < 0.2) associated with recent infection were considered for inclusion in a multiple logistic regression model that compared the characteristics of respondents with RI and those without RI. These characteristics are summarized in Tables 2 and 3. Multiple logistic regression using more than four of these variables simultaneously was not possible due to the relatively small number of people in the study. Models with various combinations of variables were therefore considered, and a backward selection procedure was used to select the best model. Following this approach, residence in properties with birds in the house or yard (including presence of wild birds, caged exotic birds or free-ranging domestic fowl) remained statistically significant (OR 7.0, 95% CI 1.7—28.5).

### Table 2
Factors statistically associated (P < 0.2) with recent dengue infection considered for inclusion in a multiple logistic regression, Nahiku, Maui, Hawaii, 2001; dichotomous variables (odds ratios)

<table>
<thead>
<tr>
<th>Factor</th>
<th>RI cases with risk factor/total RI cases (%)</th>
<th>Non-cases with risk factor/total non-cases (%)</th>
<th>Odds ratio</th>
<th>95% CI</th>
<th>P-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>No actions against mosquitoes by household before September 2001a</td>
<td>16/28 (57)</td>
<td>13/44 (30)</td>
<td>3.18</td>
<td>0.8–12.6</td>
<td>0.10</td>
</tr>
<tr>
<td>Received mail at community mailboxa</td>
<td>5/28 (18)</td>
<td>17/44 (39)</td>
<td>0.35</td>
<td>0.09–1.3</td>
<td>0.12</td>
</tr>
<tr>
<td>Lived in single-story homeb</td>
<td>14/26 (54)</td>
<td>37/44 (84)</td>
<td>0.22</td>
<td>0.05–1.0</td>
<td>0.05</td>
</tr>
<tr>
<td>Lived in home with screened windows and doorsb</td>
<td>6/26 (23)</td>
<td>20/43 (47)</td>
<td>0.35</td>
<td>0.07–1.6</td>
<td>0.16</td>
</tr>
<tr>
<td>Lived in home from which neighbor’s house visibleb</td>
<td>2/20 (10)</td>
<td>14/38 (37)</td>
<td>0.19</td>
<td>0.03–1.29</td>
<td>0.09</td>
</tr>
<tr>
<td>Used payphone regularlya</td>
<td>6/26 (23)</td>
<td>4/44 (9)</td>
<td>3.00</td>
<td>0.71–12.67</td>
<td>0.13</td>
</tr>
<tr>
<td>Home with animals in house or yarda</td>
<td>22/28 (79)</td>
<td>42/43 (99)</td>
<td>0.17</td>
<td>0.04–0.78</td>
<td>0.02</td>
</tr>
<tr>
<td>Home with birds other than chickensa</td>
<td>16/28 (57)</td>
<td>4/44 (9)</td>
<td>13.33</td>
<td>3.00–59.18</td>
<td>0.001</td>
</tr>
<tr>
<td>Home with birds or chickens or botha</td>
<td>17/28 (61)</td>
<td>8/44 (18)</td>
<td>6.95</td>
<td>1.70–28.49</td>
<td>0.01</td>
</tr>
</tbody>
</table>

* Reported.
* Observed.

### Table 3
Factors statistically associated (P < 0.2) with recent dengue infection considered for inclusion in a multiple logistic regression, Nahiku, Maui, Hawaii, 2001; continuous variables (differences between the means of the groups)

<table>
<thead>
<tr>
<th>Factor</th>
<th>Mean for RI cases (no., SEb)</th>
<th>Mean for non-cases (no., SEb)</th>
<th>Difference of means (SEb)</th>
<th>95% CI for difference (d.f. = 34)</th>
<th>P-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Distance (ft) from house to thick vegetation</td>
<td>35 (26, 12.61)</td>
<td>16 (44, 12.61)</td>
<td>19 (12.60)</td>
<td>0–44</td>
<td>0.15</td>
</tr>
<tr>
<td>Average tree height (ft)a</td>
<td>31 (26, 3.82)</td>
<td>24 (42, 2.11)</td>
<td>7 (4.30)</td>
<td>0–16</td>
<td>0.09</td>
</tr>
<tr>
<td>Percent covered in vegetationa</td>
<td>73 (26, 8.12)</td>
<td>54 (44, 6.99)</td>
<td>19 (10.09)</td>
<td>0–39</td>
<td>0.07</td>
</tr>
<tr>
<td>Percent shadeda</td>
<td>49 (23, 10.45)</td>
<td>28 (44, 5.12)</td>
<td>21 (10.85)</td>
<td>0–43</td>
<td>0.06</td>
</tr>
</tbody>
</table>

*a* Within a 30-ft perimeter around house.

*b* Standard error.
1960s found that A. albopictus preferred to feed on humans but would feed on birds if no other host was available (Hawley, 1988; Hess et al., 1968). Some of the exposures associated with dengue infection in the initial examination of the data (Tables 2 and 3) may also have been important for acquiring infection, but the small number of people included in the study limited the power of the analysis to detect additional risk factors.

The timing of our serosurvey in relation to the peak of the dengue epidemic in Maui is an important consideration for the interpretation of our results. The diagnostic limitations of serologic tests for dengue are dependent on the interval between disease onset and blood sample collection, and the dynamics of antibody production and duration (Gubler and Sather, 1990). Optimal detection of recent cases requires serologic sampling at two or three points (early, middle and late) in the epidemic. Retrospectively, we found that our community survey was conducted 6 weeks after the peak of the epidemic and therefore would probably provide an underestimate of incidence. Even so, in Nahiku our estimate of 389 infections per 1000 population was almost twice that of the 198 laboratory-positive symptomatic cases per 1000 population that had been detected by the HDOH dengue surveillance system in this community before the survey. It is to be expected that a house-to-house serosurvey would have greater sensitivity for the detection of infections than surveillance for symptomatic cases. For the same reason, our serosurvey results combined with the HDOH data support the conclusion that no dengue transmission occurred in the Hana Subdivision during the 2001 outbreak. Because local transmission of dengue in Hawaii was last detected during the 1943–1945 DEN-1 epidemic, and our survey was conducted 6 weeks after the peak of the 2001 outbreak, it is surprising that we identified eight Hana Subdivision residents, with no history of living or traveling in dengue endemic areas, whose sera gave a specific DEN-2 reaction, one of whom was 9 years of age. This suggests that Hana Subdivision experienced DEN-2 transmission within the past 9 years. The HDOH dengue surveillance system revealed that the 2001 outbreak occurred on three Hawaiian islands. As there was no evidence of spread of dengue from one island to another, it appears that separate outbreaks have caused the three independent outbreaks (Effler et al., 2005). If this occurred in 2001, it is quite plausible that other small dengue outbreaks may have gone undetected in recent years in Hawaii.

Because only one RI was identified in the Hana Subdivision, in a person not likely to have been exposed there, it was not logical to include results from this community in helping define risk factors for infection. However, as described earlier, there are striking differences between the two communities, including the relative abundance of the vector. In all, 135 containers with mosquito larvae were found on 81% (30/37) of the Nahiku premises surveyed, while only 18 such containers were found on 28% (12/43) of the premises surveyed in the Hana Subdivision. Therefore, Nahiku’s Bretteau Index (365), the number of containers positive for mosquito larvae or pupae per 100 houses, was nearly nine times greater than that for Hana Subdivision (42). In addition, Nahiku premises were larger (2.8 vs. 0.8 acres), had twice as much thick vegetation (50 vs. 25%) and trees that were, on average, twice as tall (25 vs. 12 ft). Even after intensive educational and vector control efforts, the average number of reported anti-mosquito actions by residents of both locations remained low, and approximately 50% (42/80) of the inspected houses had larvae, evidencing the need for more effective community participation (e.g. self inspection of properties for breeding sites, self directed source reduction, increased personal protection) in controlling mosquitoes.

This outbreak was largely confined to an area with large mosquito populations and a human population without prior exposure to dengue. The most probable explanation for this is the low efficacy of A. albopictus as an epidemic vector of dengue viruses (Effler et al., 2005; Gubler, 2003). This mosquito may take blood from a variety of animals, thus decreasing the probability of transmission. Furthermore, it rarely takes blood from more than one host in a single gonotrophic cycle, which also decreases probability of transmission to humans. These factors result in low vectorial capacity and sporadic, rather than sustained, epidemic transmission.

In conclusion, we documented the spread of dengue in Nahiku (estimated recent infection rate of 39%) and identified residing in properties with birds in the house or yard (including the presence of wild birds, caged exotic birds or free-ranging domestic fowl) as significantly associated with risk of infection, probably as an indicator of an environment attractive to the vector. Although only one RI (maybe due to exposure elsewhere) was identified in the Hana Subdivision in 2001, the analysis of statewide surveillance data from the 2001 outbreak indicate the importance of considering ecological variables to identify populations at risk of dengue transmission. These results suggest that, just as there are many undetected dengue infections for every case identified by surveillance, there may also be a number of undetected dengue outbreaks for every recognized epidemic in areas with the necessary vector, susceptible human population and newly introduced virus.

Conflicts of interest statement
The authors have no conflicts of interest concerning the work reported in this paper.

References
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