Detection of Jamestown Canyon Virus in Mosquito Populations, Northeastern Illinois, USA, 2024

Andrew J. Mackay, Corrado Cara, Millon Blackshear, Lance E. Jones, Nicholas Jude, Donghyun Seo, Jannatul S. Promee, Aurora Marguccio, Arif Ciloglu, Chang-Hyun Kim, Chris Stone

Jamestown Canyon virus (JCV) is an underreported mosquitoborne arbovirus that can cause viral encephalitis in humans. To determine whether humans in greater Chicago, Illinois, USA, were at risk for JCV infection, we conducted surveillance on mosquito populations in suburban forest preserves with seasonal wetland habitats likely to sustain enzootic transmission. We documented the diversity and abundance of putative vector mosquito species to determine their prevalence for JCV infection. Of 11 predominantly mammalophilic mosquito taxa screened, we detected JCV in 5 species. The highest JCV prevalence was in *Anopheles punctipennis*, followed by *Aedes stimulans* group, *Ae. canadensis*, *Ae. trivittatus*, and *Coquillettidia perturbans* mosquitoes. Most detections were from mosquitoes collected in June and early July, and earliest detections were limited to *Ae. stimulans* group female mosquitoes. Our findings indicate substantial potential for human JCV exposure where urban development encroaches on natural habitats in northeastern Illinois. We urge continued surveillance for JCV.

Jamestown Canyon virus (JCV) is a member of the California serogroup of orthobunyaviruses and can cause acute febrile illness as well as neuroinvasive disease such as encephalitis or meningitis (*1*,*2*). The geographic distribution of apparent human disease in the United States is concentrated in the northeastern and upper Midwest regions; Minnesota and Wisconsin account for more than half of reported JCV cases (*1*–*3*). Although reported human infections are relatively uncommon, clinical cases likely underestimate the true intensity of transmission because most JCV infections are asymptomatic or mild, diagnostic cross-reactivity complicates confirmation, and routine testing has historically been limited (*4*). In addition, detections in a variety of mosquito species and mammalian hosts indicate that the virus has a wider geographic distribution than case counts alone suggest (*2*,*5*). Together, those observations suggest that the geographic extent of JCV transmission and rate of human exposure in the United States are likely underestimated by case-based surveillance.

Across endemic regions of the United States and Canada numerous mosquito species have been implicated as competent or regionally consequential JCV vectors (*5*). For example, *Aedes stimulans* was identified as the primary overwintering mosquito host and early season vector in northern Indiana (*6*), *Ae. canadensis* has been incriminated as the main early season mosquito vector in Connecticut (*7*), and *Ae. provocans* appears to be the key early season mosquito vector of JCV in Wisconsin, Michigan, and upper New York state (*8*–*10*). Therefore, region-specific knowledge of the possible contributions of vector species to virus maintenance and zoonotic amplification is essential for developing effective surveillance and vector management strategies, and for understanding risk for exposure in humans.

In Illinois, USA, a high incidence of mosquitoborne virus cases has been observed in recent decades, most of which were attributed to West Nile virus (*11*), and few human JCV infections were reported (*12*,*13*). Other orthobunyaviruses, namely Potosi virus, La Crosse virus, and Cache Valley virus, have been detected in mosquitoes collected from Illinois (*14*,*15*), but entomologic evidence of JCV transmission in the state is absent. In contrast, serologic surveys of white-tailed deer (*Odocoileus virginianus*), a primary JCV reservoir, indicate active transmission and suggest likely human JCV exposure in suburban forest preserve habitats in the Chicago metropolitan

Author affiliations: University of Illinois Urbana-Champaign, Prairie Research Institute, Illinois Natural History Survey, Champaign, Illinois, USA (A.J. Mackay, C. Cara, M. Blackshear, L.E. Jones, N. Jude, D. Seo, J.S. Promee, A. Marguccio, A. Ciloglu, C.-H. Kim, C. Stone); Erciyes University, Faculty of Veterinary Medicine, Kayseri, Turkey (A. Ciloglu)

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area (*12*,*16*). The discrepancy between frequent reservoir host exposure and the paucity of clinical and mosquito detections demonstrates the limitations of current surveillance and emphasizes the need for a greater understanding of the ecology and relative public health risk for JCV in the state. To characterize the enzootic transmission of JCV in northeastern Illinois, we conducted targeted sampling and testing of mosquito populations to identify mosquito species most strongly associated with virus maintenance and assess the potential implications for human exposure risk in the region.

Materials and Methods

We selected 8 suburban forest preserves adjacent to residential development in Cook, DuPage, and Lake Counties, Illinois, USA, for mosquito sampling. We selected those areas based on the presence of vernal woodland pools and other seasonal wetland habitats associated with the production of univoltine *Aedes* spp. mosquitoes and other suspected JCV vectors.

Sampling of adult mosquitoes began during the first week of May 2024. At each site, we placed 3 dry ice–baited light traps from the Centers for Disease Control and Prevention (CDC) near seasonal wetlands, using an average nearest-neighbor distance of 209 meters between traps. At 1 of the CDC light trap locations, we co-located 2 BG-Sentinel traps (Biogents, https://eu.biogents.com) containing ≈3 pounds of dry ice ≥30 meters from the CDC light trap and from each other. One BG-Sentinel trap contained a UV-LED light and BG-skin lure (Biogents); the other was baited with octenol, a host kairomone attractive to many mammalophilic *Aedes* and *Anopheles* species mosquitoes suspected of contributing to JCV transmission. We conducted trapping for ≈24 hours per sampling event at 2-week intervals during May–August (9 collection dates per site), corresponding to the expected period of maximum JCV infection rates in vector populations. In September and October, we reduced sampling frequency to a single ≈24-hour sampling event per site per month.

We transported collected mosquitoes to the laboratory on dry ice, sorted and identified mosquitoes on chill tables, and stored at mosquitoes −80°C until RNA extraction. We made identifications on the basis of morphologic characteristics and used taxonomic keys (*17*,*18*). For *Ae. stimulans* group (*Ae. stimulans*, *Ae. excrucians*, *Ae. fitchii*) mosquitoes, we identified female specimens that had light-colored scales covering at least one third of the surface area of the proboscis as *Ae. stimulans* (*17*) and classified all other specimens as unidentified *Ae. stimulans* group. We pooled adult female mosquito specimens from 11 species or species groups identified as potential JCV vectors by trap date, location, and taxa before RNA extraction and subsequently screened for JCV by real-time reverse transcription PCR (RT-PCR). We considered all remaining taxa unlikely to contribute substantially to zoonotic transmission on the basis of ≥1 of the following criteria: prior evidence of incompetence for JCV transmission (e.g., *Ae. vexans* [*6*], 44.3% of total female mosquitoes collected); reported lack or infrequent detection of JCV infection in previous surveys of field populations; low frequency of mammalian blood feeding; seasonal activity that is temporally misaligned with the enzootic amplification period; or insufficient sample sizes. In addition, the number of *Ae. trivittatus* mosquito pools tested was limited to a maximum of 5 per trap sample.

Pools contained an average of 36.4 female specimens. Minimum pool size was 5, and maximum pool size was 30 for *Ae. stimulans* group, *Ae. grossbecki*, *Culiseta inornata* mosquitoes and 50 for all other species. We extracted RNA from pools and screened for JCV by using the JCV132FAM and JCV231cFAM primer-probe sets (*19*). We defined positive samples as those with a cycle threshold (Ct) value <37 after setting a threshold level at 0.2 for ≥1 primer set. We confirmed positive samples by sequencing using Orthobunyavirus CAL/BWA group forward and reverse primers (*20*). We compared sequences to available sequences in GenBank BLAST (https://blast.ncbi.nlm.nih.gov) and considered those that showed the highest percentage of identity to JCV as confirmed positive. We deposited partial small segment sequences obtained from RT-PCR–positive samples into GenBank (accession nos. PX962933–71).

We used the PoolTestR version 0.1.3 package (https://github.com/AngusMcLure/PoolTestR) in R (The R Project for Statistical Computing, https://www.r-project.org) to calculate maximum-likelihood estimates (MLEs) of infection rate. We also fit generalized linear models comparing fixed effects of month of collection and taxonomic group on infection within the *Ae. stimulans* group using the PoolReg function in PoolTestR (*21*). We calculated the vector index (VI) value for May–July for each tested species at each collection site as the product of MLE of infection and the average number of female specimens collected per CDC light trap sample (*22*). As a proxy for overall JCV exposure risk at each collection site, we then summed individual VI values for each species to generate a cumulative VI value.

Table 1. MLEs of Jamestown Canyon virus infection rate in female mosquitoes, northeastern Illinois, USA, 2024*

Species	No. female mosquitoes	No. pools		MLE of infection rate/1,000 mosquitoes (95% CI)
		Tested	Positive	
Aedes canadensis	2,469	71	1	0.407 (0. 023–1.790)
Ae. cinereus	3,760	104	0	0 (0–0.511)
Ae. grossbecki	357	20	0	0 (0–5.366)
Ae. sticticus	263	17	0	0 (0–7.277)
Ae. stimulans group†	19,752	709	16	0.819 (0.481–1.289)
Ae. trivittatus	14,974	324	5	0.337 (0.121–0.723)
Anopheles punctipennis	9,190	221	9	1.003 (0.482–1.808)
An. quadrimaculatus sensu lato	3,483	103	0	0 (0–0.551)
An. walkeri	259	17	0	0 (0–7.389)
Coquillettidia perturbans	19,298	417	2	0.104 (0.017–0.321)
Culiseta inornata	112	11	0	0 (0–17.003)

*MLE, maximum-likelihood estimate.
†Includes both *Ae. stimulans* and unidentified *Ae. stimulans* group specimens.

Results

During May 1–October 22, 2024, we collected and identified 213,996 female mosquitoes and 16,374 male mosquitoes to the species, species group, or genus level (Appendix Table, https://wwwnc.cdc.gov/EID/article/32/12/26-0243-App1.pdf). From those, we grouped a subset of 73,917 female specimens from 11 mosquito taxa into 2,029 pools for JCV screening (Table 1).

We detected JCV RNA in a total of 33 pools, representing 5 taxa. The highest MLE of infection was in *An. punctipennis* and *Ae. stimulans* group female mosquitoes, followed by *Ae. canadensis*, *Ae. trivittatus*, and *Cq. perturbans* female mosquitoes. We detected JCV in *Ae. stimulans* group female mosquitoes at all sampled locations, but the spatial distribution of JCV detection in *An. punctipennis* mosquitoes was more limited (Figure 1). The earliest JCV detection was in a pool

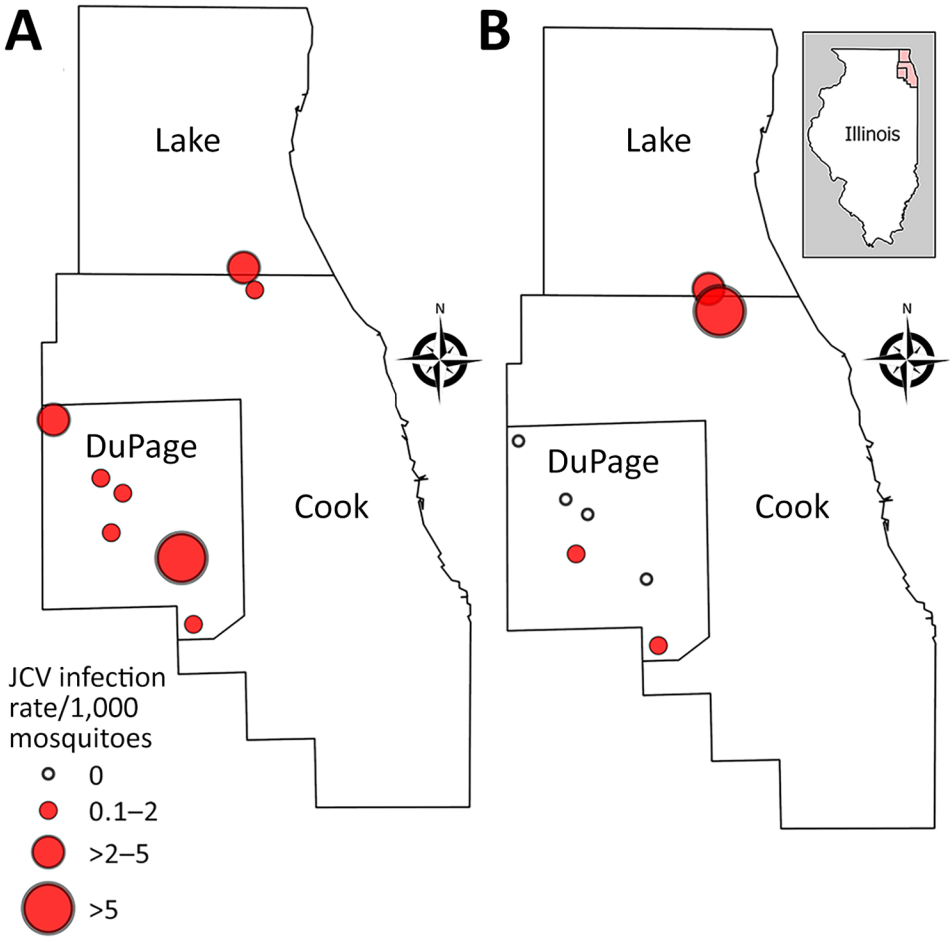


Figure 1. Maximum-likelihood estimates of infection from study of detection of Jamestown Canyon virus in mosquito populations, northeastern Illinois, USA, 2024. Maps show estimates per 1,000 mosquitoes adult female specimens collected from forest preserves in 3 counties during May–July 2024. A) Prevalence among *Aedes stimulans* group mosquitoes; B) prevalence among *Anopheles punctipennis* mosquitoes. Inset shows region of Illinois surveyed.

of *Ae. stimulans* group female mosquitoes collected on May 24. Infection prevalence in the *Ae. stimulans* group mosquitoes increased through June and July (Table 2), and we noted a significantly greater MLE of infection in July than in May (p = 0.012). We did not detect JCV in any mosquito specimens collected after July 23. Within the *Ae. stimulans* mosquito group, we observed a significantly lower MLE of infection in female mosquitoes not classified to the species level, compared with those that were presumptively identified as *Ae. stimulans* (p = 0.049) (Table 3). Cumulative VI values for May–July were variable (range 0.05–0.25) across sampling locations (Figure 2) and suggest a low to moderate seasonal risk for human exposure to JCV-infected mosquitoes.

Discussion

In this study, we detected JCV in ≥5 mosquito species collected from suburban forest preserves. On the basis of their seasonal abundance, infection prevalence, and previously reported host range and competence for JCV transmission (*6*,*23*), we suspect that *An. punctipennis* and *Ae. stimulans* group mosquitoes are the primary enzootic vectors of JCV in northeastern Illinois. However, other species that have demonstrated vector competence, such as *Ae. canadensis* and *Cq. perturbans* (*23*), might play a secondary role in transmission. Estimates of JCV infection in *Ae. stimulans* group and *An. punctipennis* female mosquitoes observed in our study are comparable with rates reported from other regions where human cases are frequently reported (*7*,*24*,*25*). The seasonal peak in JCV infection observed in the *Ae. stimulans* group and *An. punctipennis* mosquitoes in July also coincided with the timing of peak human JCV disease reporting in the United States (*13*).

The white-tailed deer is considered the principal vertebrate amplifying host of JCV in the northeastern and upper midwestern United States. Experimental studies have shown that deer develop viremias after JCV infection, and reported titers are consistent with levels capable of infecting competent mosquito vectors (*26*,*27*). High seroprevalence has also been documented in free-ranging populations, suggesting frequent exposure to infected mosquitoes (*16*,*28*,*29*). Previous blood-meal analyses indicate that the 5 mosquito taxa we found to be infected with JCV (*Ae. canadensis*, *Ae. stimulans* group, *Ae. trivittatus*, *An. punctipennis*, and *Cq. perturbans*) commonly obtain blood meals from white-tailed deer (*6*,*24*,*30*), providing an ecologic mechanism for virus amplification and maintenance. In addition, studies have suggested positive associations between deer abundance and human incidence of JCV disease (*31*,*32*), supporting the relevance of deer-mediated amplification in areas containing competent JCV vectors. Although we did not sample vertebrate hosts in this study, the widespread detection of JCV-infected mosquitoes across sites is consistent with an active deer–mosquito enzootic transmission cycle occurring throughout suburban natural areas in northeastern Illinois.

Ae. stimulans group mosquitoes are represented by ≥3 morphologically similar species in Illinois: *Ae. excrucians*, *Ae. fitchii*, and *Ae. stimulans* (*33*). In this study, JCV was most frequently detected in specimens of *Ae. stimulans* group mosquitoes, representing nearly half (16/33) of total JCV-positive pools and exhibiting higher infection rates relative to most other taxa screened. That pattern suggests that mosquitoes of the *Ae. stimulans* group likely play a central role in amplification of JCV in northeastern Illinois. In addition, we observed the first seasonal detections of JCV infection in that group, indicating that they might be involved with initiating annual transmission. Vertical transmission of JCV has previously been demonstrated in *Ae. stimulans* mosquitoes (*6*) and is considered an overwintering mechanism for the virus in temperate regions (*34*).

In this study, we applied a simple criterion to distinguish *Ae. stimulans* adult female mosquitoes from the other 2 species within the *Ae. stimulans* group. We used that rationale because many other diagnostic adult morphological characteristics used to differentiate species in *Ae. stimulans* group mosquitoes are considered either ambiguous (*17*) or impractical when processing large numbers of trap-collected specimens on a cold chain under low magnification. Although our threshold for classifying mosquito specimens as *Ae. stimulans* was intentionally conservative and likely resulted in many *Ae. stimulans* female mosquitoes being included in pools of unidentified *Ae. stimulans* group female mosquitoes, we observed a ≈2.8-fold

Table 2. MLEs of infection rates between *Aedes stimulans* and unidentified *Ae. stimulans* group female specimens from study of Jamestown Canyon virus in mosquito populations, northeastern Illinois, USA, 2024*

Collection month	No. pools		MLE of infection rate/1,000 mosquitoes (95% CI)
	Tested	Positive	
May	317	2	0.219 (0.036–0.677)
June	300	9	1.083 (0.521–1.952)
July	91	5	2.386 (0.856–5.122)

*MLE, maximum-likelihood estimate.

Table 3. Comparison of MLEs of infection rates between *Aedes stimulans* and unidentified *Ae. stimulans* group female specimens from study of Jamestown Canyon virus in mosquito populations, northeastern Illinois, USA, 2024*

Identification class	No. pools		MLE of infection rate/1,000 mosquitoes (95% CI)
	Tested	Positive	
Aedes stimulans	140	6	1.667 (0.663–3.374)
Unidentified *Ae. stimulans* group	597	10	0.604 (0.303–1.059)

*MLE, maximum-likelihood estimate.

higher infection rate in pools of mosquito specimens identified as *Ae. stimulans*, compared with pools containing *Ae. stimulans* group female mosquitoes not identified to the species level. That finding might be notable because *Ae. stimulans* mosquitoes have been confirmed to be competent for transmitting JCV (*6*), but vector competence has not been demonstrated for *Ae. excrucians* and *Ae. fitchii* mosquitoes (*23*). However, uncertainty in species-level identification limits interpretation of that comparison. Additional studies incorporating molecular identification and experimental competence assays might be required to better resolve the relative contributions of *Ae. stimulans*, *Ae. excrucians*, and *Ae. fitchii* mosquitoes to JCV transmission in northeastern Illinois.

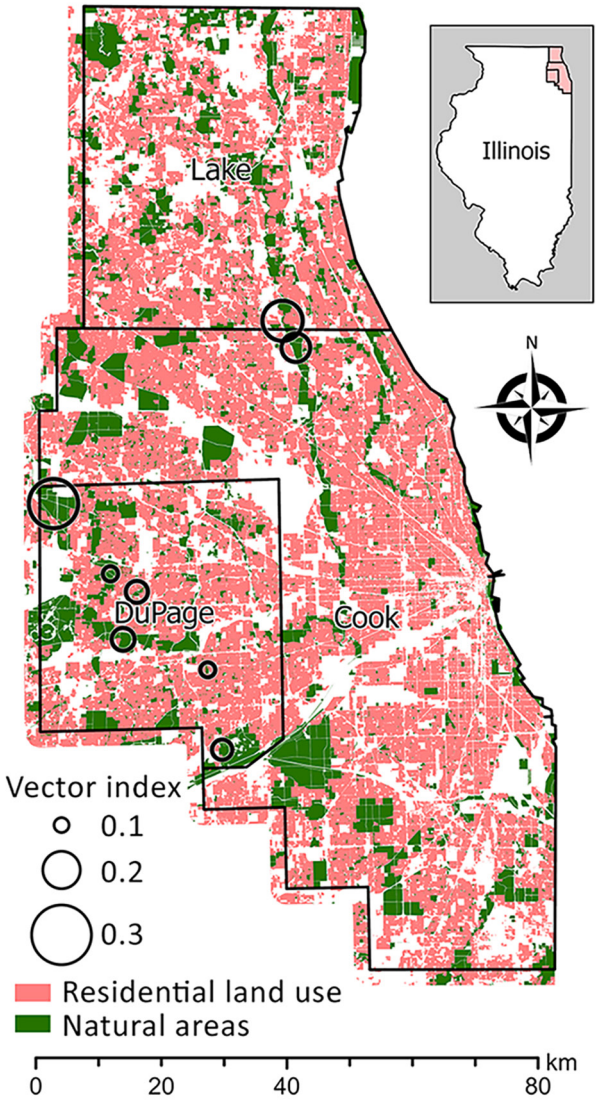


Figure 2. Cumulative vector index values for 11 mosquito species tested for Jamestown Canyon virus, northeastern Illinois, USA, 2024. Map shows distribution of mosquito vectors in 3 counties overlaid with urbanized residential land use data from the 2020 Land Use Inventory for Northeastern Illinois (Chicago Metropolitan Agency for Planning, https://datahub.cmap.illinois.gov) and natural areas data from the Illinois Protected Natural Lands database (Prairie State Conservation Coalition, https://prairiestateconservation.org). Inset shows region of Illinois surveyed.

The greater Chicago area has an extensive wildland-urban interface (Figure 2) that might enable enzootic JCV transmission and increase the risk for spillover into human hosts. Forest preserves, conservation districts, and other protected natural lands occupy ≈10% of the land area in Cook, Lake, and DuPage Counties (*35*), and many contain seasonal wetlands potentially productive for univoltine *Aedes* species mosquitoes and other putative JCV vectors. In addition, those natural areas typically support high white-tailed deer densities because of abundant forage, limited predation, and prohibitions on public firearm hunting (*36*). Forest preserves and other natural areas within those 3 counties collectively host >70 million human visits annually (*37*,*38*), and adjacent residential development is often within the reported maximum flight range (≈2–14 km) of *Ae. stimulans* group, *An. punctipennis*, and other JCV mosquito vector species (*39*,*40*). Paradoxically, despite evidence of prevalent enzootic transmission and potential for frequent human exposure to JCV vector mosquitoes in the greater Chicago area, locally acquired human JCV infections are not commonly recognized within Illinois. Only 3 cases of neuroinvasive disease have been reported in Illinois residents, 1 each in 1983, 2019, and 2024, and 1 case of nonneuroinvasive disease was reported in 2023 (*12*,*41*). Subsequent epidemiologic investigations concluded the 3 most recent cases were likely a result of out-of-state JCV exposure (S. Kerr, Illinois Department of Public Health, pers. comm., email, 2025 Sep 17). The rarity of reported clinical illness in northeastern Illinois might be related to a lack of active disease surveillance and awareness among clinicians. Alternatively, because substantial variability in neurovirulence among JCV isolates in vertebrate hosts has been previously documented (*42*),

lack of apparent disease in Illinois might indicate that JCV strains circulating in this region express a relatively lower neuropathogenicity.

The first limitation of this study is that our targeted screening approach excluded some abundant and mammalophilic mosquito species such as *Ae. vexans*, *Psorophora ferox*, and *Culex salinarius*, which might have resulted in underestimation of the diversity of potential JCV vectors in our study region. However, although JCV infection infrequently has been detected in those species (*43*), their limited seasonal synchrony with the enzootic amplification period, low infection prevalence in prior field studies, and reported low vector competence limit their potential role in JCV transmission. Further work screening the entire mosquito community in this region for JCV could clarify their possible role in JCV transmission. Second, sampling was restricted in temporal and spatial scope, because we conducted collections during a single transmission season and at a limited number of sites within the greater Chicago area, intentionally selecting sites to represent habitats most likely to support enzootic transmission, which might not represent broader landscape conditions and risk levels in northeastern Illinois. Finally, uncertain morphologic identification of *Ae. stimulans* mosquitoes limits accurate species-level inference within this group. Future investigations incorporating broader geographic and temporal sampling and improved species-level identification of mosquito vectors could clarify the ecology of JCV transmission and the factors influencing human exposure risk in the state.

In conclusion, this study provides evidence of active and widespread enzootic JCV transmission in mosquito populations from suburban forest preserves in northeastern Illinois, a region where locally acquired human infections remain infrequently recognized. Despite relatively low to moderate VI values, the broad distribution of infected vectors across sites and the proximity of those habitats to residential development suggest a plausible risk for human exposure that might be underrecognized. Further research is needed to determine whether and to what extent unrecognized human exposure to JCV-infected mosquito bites might be occurring in northeastern Illinois. Our findings underscore the need for greater public health awareness and vector surveillance for JCV, particularly in areas where residential development borders fragments of undeveloped land that support habitats favorable for both primary spring *Aedes* spp. mosquito vectors and reservoir white-tailed deer hosts.

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About the Author

Dr. Mackay is an associate research scientist with the Illinois Natural History Survey in the Prairie Research Institute at the University of Illinois Urbana-Champaign. His research interests include the ecology and behavior of vector mosquitoes, and environmental factors influencing spatial and temporal patterns of mosquito-borne disease risk.

References

1. Pastula DM, Hoang Johnson DK, White JL, Dupuis AP II, Fischer M, Staples JE. Jamestown Canyon virus disease in the United States—2000–2013. Am J Trop Med Hyg. 2015;93:384–9. https://doi.org/10.4269/ajtmh.15-0196
2. Coleman KJ, Chauhan L, Piquet AL, Tyler KL, Pastula DM. An overview of Jamestown Canyon virus disease. Neurohospitalist. 2021;11:277–8. https://doi.org/10.1177/19418744211005948
3. Matkovic E, Hoang Johnson DK, Staples JE, Mora-Pinzon MC, Elbadawi LI, Osborn RA, et al. Enhanced arboviral surveillance to increase detection of Jamestown Canyon virus infections, Wisconsin, 2011–2016. Am J Trop Med Hyg. 2019;100:445–51. https://doi.org/10.4269/ajtmh.18-0575
4. Woods TA, Johnson SF, Evans AB, Peterson KE. Neutralizing antibodies against California serogroup orthobunyaviruses in human serum samples, Montana, USA. Emerg Infect Dis. 2025;31:699–709. https://doi.org/10.3201/eid3104.241520
5. Shepard JJ, Armstrong PM. Jamestown Canyon virus comes into view: understanding the threat from an underrecognized arbovirus. J Med Entomol. 2023;60:1242–51. https://doi.org/10.1093/jme/tjad069
6. Boromisa RD, Grimstad PR. Virus-vector-host relationships of *Aedes stimulans* and Jamestown Canyon virus in a northern Indiana enzootic focus. Am J Trop Med Hyg. 1986;35:1285–95. https://doi.org/10.4269/ajtmh.1986.35.1285
7. Andreadis TG, Anderson JF, Armstrong PM, Main AJ. Isolations of Jamestown Canyon virus (Bunyaviridae: Orthobunyavirus) from field-collected mosquitoes (Diptera: Culicidae) in Connecticut, USA: a ten-year analysis, 1997–2006. Vector Borne Zoonotic Dis. 2008;8:175–88. https://doi.org/10.1089/vbz.2007.0169
8. Boromisa RD, Grayson MA. Incrimination of *Aedes provocans* as a vector of Jamestown Canyon virus in an

enzootic focus of northeastern New York. J Am Mosq Control Assoc. 1990;6:504–9.
9. Farquhar MR, Thrun NB, Tucker BJ, Bartholomay LC. Outbreak investigation: Jamestown Canyon virus surveillance in field-collected mosquitoes (Diptera: Culicidae) from Wisconsin, USA, 2018–2019. Front Public Health. 2022;10:818204. https://doi.org/10.3389/fpubh.2022.818204
10. Heard PB, Zhang MB, Grimstad PR. Isolation of Jamestown Canyon virus (California serogroup) from *Aedes* mosquitoes in an enzootic focus in Michigan. J Am Mosq Control Assoc. 1990;6:461–8.
11. Rosenberg R, Lindsey NP, Fischer M, Gregory CJ, Hinckley AF, Mead PS, et al. Vital signs: trends in reported vectorborne disease cases—United States and Territories, 2004–2016. MMWR Morb Mortal Wkly Rep. 2018;67:496–501. https://doi.org/10.15585/mmwr.mm6717e1
12. Grimstad PR, Calisher CH, Harroff RN, Wentworth BB. Jamestown Canyon virus (California serogroup) is the etiologic agent of widespread infection in Michigan humans. Am J Trop Med Hyg. 1986;35:376–86. https://doi.org/10.4269/ajtmh.1986.35.376
13. Centers for Disease Control and Prevention. Historic data (2011–2024): Jamestown Canyon virus [cited 2025 Sep 19]. https://www.cdc.gov/jamestown-canyon/data-maps/historic-data.html
14. Mitchell CJ, Haramis LD, Karabatsos N, Smith GC, Starwalt VJ. Isolation of La Crosse, Cache Valley, and Potosi viruses from *Aedes* mosquitoes (Diptera: Culicidae) collected at used-tire sites in Illinois during 1994–1995. J Med Entomol. 1998;35:573–7. https://doi.org/10.1093/jmedent/35.4.573
15. Mitchell CJ, Smith GC, Karabatsos N, Moore CG, Francy DB, Nasci RS. Isolations of Potosi virus from mosquitoes collected in the United States, 1989–94. J Am Mosq Control Assoc. 1996;12:1–7.
16. Hollis-Etter KM, Montgomery RA, Etter DR, Anchor CL, Chelsvig JE, Warner RE, et al. Environmental conditions for Jamestown Canyon virus correlated with population-level resource selection by white-tailed deer in a suburban landscape. PLoS One. 2019;14:e0223582. https://doi.org/10.1371/journal.pone.0223582
17. McDaniel IN, Webb DR. Identification of females of the Aedes stimulans group in Maine including notes on larval characters and attempts at hybridization. Ann Entomol Soc Am. 1974;67:915–8. https://doi.org/10.1093/aesa/67.6.915
18. Darsie RF, Ward RA. Identification and geographical distribution of the mosquitoes of North America, north of Mexico. Gainesville (FL): University Press of Florida; 2005.
19. Hughes HR, Kenney JL, Russell BJ, Lambert AJ. Laboratory validation of a real-time RT-PCR assay for the detection of Jamestown Canyon virus. Pathogens. 2022;11:5. https://doi.org/10.3390/pathogens11050536
20. Lambert AJ, Lanciotti RS. Consensus amplification and novel multiplex sequencing method for S segment species identification of 47 viruses of the *Orthobunyavirus, Phlebovirus*, and *Nairovirus* genera of the family Bunyaviridae. J Clin Microbiol. 2009;47:2398–404. https://doi.org/10.1128/JCM.00182-09
21. McLure A, O'Neill B, Mayfield H, Lau C, McPherson B. PoolTestR: An R package for estimating prevalence and regression modelling for molecular xenomonitoring and other applications with pooled samples. Environ Model Softw. 2021;145:105158. https://doi.org/10.1016/j.envsoft.2021.105158
22. Nasci RS, Doyle M, Biggerstaff BJ, LeBailly A. Calculation and application of a vector index (VI) reflecting the number of WN virus infected mosquitoes in a population. Presented at: 71st Annual Meeting of the American Mosquito Control Association; Vancouver, British Columbia, Canada; April 3–7, 2005.
23. Heard PB, Zhang MB, Grimstad PR. Laboratory transmission of Jamestown Canyon and snowshoe hare viruses (Bunyaviridae: California serogroup) by several species of mosquitoes. J Am Mosq Control Assoc. 1991;7:94–102.
24. Poggi JD, Conery C, Mathewson A, Bolton D, Lovell R, Harrington LC, et al. Jamestown Canyon virus (Bunyavirales: Peribunyaviridae) vector ecology in a focus of human transmission in New Hampshire, USA. J Med Entomol. 2023;60:778–88. https://doi.org/10.1093/jme/tjad046
25. Ngo KA, Maffei JG, Koetzner CA, Zink SD, Payne AF, Backenson PB, et al. Surveillance and genetic analysis of Jamestown Canyon virus in New York State: 2001–2022. Am J Trop Med Hyg. 2023;109:1329–32. https://doi.org/10.4269/ajtmh.23-0392
26. Issel CJ, Trainer DO, Thompson WH. Experimental studies with white-tailed deer and four California group arboviruses (La Crosse, Trivittatus, snowshoe hare, and Jamestown Canyon). Am J Trop Med Hyg. 1972;21:979–84. https://doi.org/10.4269/ajtmh.1972.21.979
27. Watts DM, Tammariello RF, Dalrymple JM, Eldridge BF, Russell PK, Top FH Jr. Experimental infection of vertebrates of the Pocomoke Cypress Swamp, Maryland with Keystone and Jamestown Canyon viruses. Am J Trop Med Hyg. 1979;28:344–50. https://doi.org/10.4269/ajtmh.1979.28.344
28. Dupuis AP, Prusinski MA, Russell A, O'Connor C, Maffei JG, Oliver J, et al. Serologic survey of mosquito-borne viruses in hunter-harvested white-tailed deer (*Odocoileus virginianus*), New York State. Am J Trop Med Hyg. 2020;104:593–603. https://doi.org/10.4269/ajtmh.20-1090
29. Murphy RK. Serologic evidence of arboviral infections in white-tailed deer from central Wisconsin. J Wildl Dis. 1989;25:300–1. https://doi.org/10.7589/0090-3558-25.2.300
30. Molaei G, Andreadis TG, Armstrong PM, Diuk-Wasser M. Host-feeding patterns of potential mosquito vectors in Connecticut, U.S.A.: molecular analysis of bloodmeals from 23 species of *Aedes, Anopheles, Culex, Coquillettidia, Psorophor*a, and *Uranotaenia*. J Med Entomol. 2008;45:1143–51. https://doi.org/10.1093/jmedent/45.6.1143
31. Grimstad PR, Calisher CH, Harroff RN, Wentworth BB. Jamestown Canyon virus (California serogroup) is the etiologic agent of widespread infection in Michigan humans. Am J Trop Med Hyg. 1986;35:376–86. https://doi.org/10.4269/ajtmh.1986.35.376
32. Rocheleau JP, Michel P, Lindsay LR, Drebot M, Dibernardo A, Ogden NH, et al. Risk factors associated with seropositivity to California serogroup viruses in humans and pet dogs, Quebec, Canada. Epidemiol Infect. 2018;146:1167–76. https://doi.org/10.1017/S0950268818001000
33. Ross HH. (Herbert H, Horsfall WR. A synopsis of the mosquitoes of Illinois (Diptera, Culicidae). Illinois natural history survey, biological notes vol. 52. Urbana: State of Illinois, Department of Registration and Education, Natural History Survey Division; 1965.
34. Bergren NA, Kading RC. The ecological significance and implications of transovarial transmission among the vector-borne bunyaviruses: a review. Insects. 2018;9:173. https://doi.org/10.3390/insects9040173
35. Openlands. Forest preserve and conservation districts in northeastern Illinois: meeting the challenges of the 21st Century [cited 2025 Sep 18]. https://www.csu.edu/cerc/documents/ForestPreserveDistrictStudy.pdf

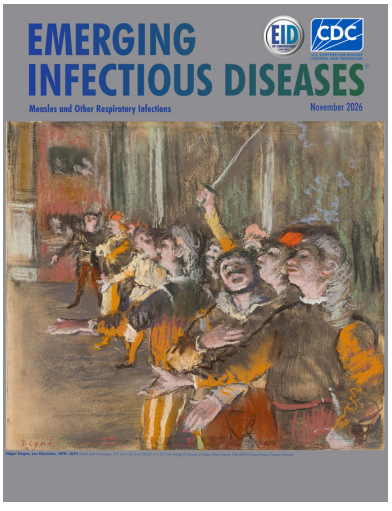
36. Witham JH, Jones JM. White-tailed deer abundance on metropolitan forest preserves during winter in northeastern Illinois. Wildlife Soc Bull. 1990;18:13–6.
37. Forest Preserve District of Cook County. Illinois. 2024 Executive budget recommendation [cited 2025 Sep 15]. https://fpdcc.com/downloads/budget/2024/FPCC-Budget-Recommendation-2024-101723.pdf
38. Forest Preserve District of DuPage County. 2024 year in review [cited 2025 Sep 15]. https://www.dupageforest.org/hubfs/DuPage2022/About%20Us/Transparency%20Portal/Documents/2024%20Year%20in%20Review.pdf
39. Verdonschot PFM, Besse-Lototskaya AA. Flight distance of mosquitoes (Culicidae): a metadata analysis to support the management of barrier zones around rewetted and newly constructed wetlands. Limnologica. 2014;45:69–79. https://doi.org/10.1016/j.limno.2013.11.002
40. Clarke LJ. Studies of the flight range of mosquitoes. J Econ Entomol. 1943;36:121–2. https://doi.org/10.1093/jee/36.1.121
41. Centers for Disease Control and Prevention. Jamestown Canyon virus historic data (2011–2024) [cited 2025 Sep 19]. https://www.cdc.gov/jamestown-canyon/data-maps/historic-data.html
42. Bennett RS, Nelson JT, Gresko AK, Murphy BR, Whitehead SS. The full genome sequence of three strains of Jamestown Canyon virus and their pathogenesis in mice or monkeys. Virol J. 2011;8:136. https://doi.org/10.1186/1743-422X-8-136
43. McMillan JR, Armstrong PM, Andreadis TG. Patterns of mosquito and arbovirus community composition and ecological indexes of arboviral risk in the northeast United States. PLoS Negl Trop Dis. 2020;14:e0008066. https://doi.org/10.1371/journal.pntd.0008066

Address for correspondence: Andrew Mackay, University of Illinois Urbana-Champaign, 1812 S Oak St, M/C 652, Champaign IL 61820, USA; email: amackay@illinois.edu

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