treatment follow-up visits with blood testing of malaria patients can be challenging in Haiti, healthcare professionals should strive to implement these goals. Implementation would enable continuous in vivo monitoring of drug susceptibility of parasites and provide real-time data to public health authorities to formulate evidence-based policy.

Acknowledgments

We thank Masami Nakatsu and Moritoshi Iwagami for providing advice on analysis of the *k13* gene and the Eiken Chemical Co., Ltd. (Tokyo, Japan), for providing technical advice on loop-mediated isothermal amplification.

S.K. was partly supported by the Research Program on the Challenges of Global Health Issues: US–Japan Cooperative Medical Sciences Program (grant 16jk0210006h0001).

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References

1. von Fricken ME, Weppelmann TA, Hosford JD, Existe A, Okech BA. Malaria treatment policies and drug efficacy in Haiti from 1955–2012. J Pharm Policy Pract. 2013;6:10. http://dx.doi.org/10.1186/2052-3211-6-10
2. Londono BL, Eisele TP, Keating J, Bennett A, Chattopadhyay C, Heyliger G, et al. Chloroquine-resistant haplotype *Plasmodium falciparum* parasites, Haiti. Emerg Infect Dis. 2009;15:735–40. http://dx.doi.org/10.3201/eid1505.081063
3. Gharbi M, Pillai DR, Lau R, Hubert V, Khairnar K, Existe A, et al.; French National Reference Center for Imported Malaria Study. Chloroquine-resistant malaria in travelers returning from Haiti after 2010 earthquake. Emerg Infect Dis. 2012;18:1346–9. http://dx.doi.org/10.3201/eid1808.111779
4. Charles M, Das S, Daniels R, Kirkman L, Delva GG, Destine R, et al. *Plasmodium falciparum* K76T *pfcrt* gene mutations and parasite population structure, Haiti, 2006–2009. Emerg Infect Dis. 2016;22:786–93. http://dx.doi.org/10.3201/eid2205.150359
5. Morton LC, Huber C, Okoth SA, Griffing S, Lucchi N, Ljolje D, et al. *Plasmodium falciparum* drug-resistant haplotypes and population structure in postearthquake Haiti, 2010. Am J Trop Med Hyg. 2016;95:811–6. http://dx.doi.org/10.4269/ajtmh.16-0214
6. Elbadry MA, Existe A, Victor YS, Memnon G, Fukuda M, Dame JB, et al. Survey of *Plasmodium falciparum* multidrug resistance-1 and chloroquine resistance transporter alleles in Haiti. Malar J. 2013;12:426. http://dx.doi.org/10.1186/1475-2875-12-426
7. Raccurt CP, Brasseur P, Cicéron M, Parke DM, Zervos MJ, Boncy J. In vivo study of *Plasmodium falciparum* chloroquine susceptibility in three departments of Haiti. Malar J. 2017;16:313. http://dx.doi.org/10.1186/s12936-017-1961-2
8. Komaki-Yasuda K, Vincent JP, Nakatsu M, Kato Y, Ohmagari N, Kano S. A novel PCR-based system for the detection of four species of human malaria parasites and *Plasmodium knowlesi.* PLoS One. 2018;13:e0191886. http://dx.doi.org/10.1371/journal.pone.0191886
9. Ménard D, Khim N, Beghain J, Adegnika AA, Shafiul-Alam M, Amodu O, et al.; KARMA Consortium. A worldwide map of *Plasmodium falciparum* K13-propeller polymorphisms. N Engl J Med. 2016;374:2453–64. http://dx.doi.org/10.1056/NEJMoa1513137
10. Carter TE, Boulter A, Existe A, Romain JR, St Victor JY, Mulligan CJ, et al. Artemisinin resistance–associated polymorphisms at the K13-propeller locus are absent in *Plasmodium falciparum* isolates from Haiti. Am J Trop Med Hyg. 2015;92:552–4. http://dx.doi.org/10.4269/ajtmh.14-0664

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Racial/Ethnic Disparities in Antimicrobial Drug Use, United States, 2014–2015

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DOI: https://doi.org/10.3201/eid2411.180762

Using a US nationwide survey, we measured disparities in antimicrobial drug acquisition by race/ethnicity for 2014–2015. White persons reported twice as many antimicrobial drug prescription fills per capita as persons of other race/ethnicities. Characterizing antimicrobial drug use by demographic might improve antimicrobial drug stewardship and help address antimicrobial drug resistance.

Antimicrobial drug use varies by sex, age, and geography (*1*), and antimicrobial drug prescribing practice for specific medical conditions and age cohorts varies by patients' race/ethnicity (*2–4*). Many studies on the role of patient race/ethnicity in antimicrobial drug prescribing practice focus on acute respiratory illnesses because antimicrobial drugs are often inappropriately prescribed for these conditions. The subjective diagnostic criteria for respiratory illnesses might result in race/ethnicity influencing prescribing practice more for these illnesses than for other illnesses (*4*). Despite our increasing knowledge of the role of patient race/ethnicity in drug prescribing practice for specific

conditions, how or whether these specific effects translate into overall antimicrobial drug use by race/ethnicity remains unclear. In this report, we address this gap in knowledge by describing the extent of racial/ethnic disparities in overall antimicrobial drug prescription fill rates in the United States.

We used the nationwide Medical Expenditure Panel Survey (MEPS) to acquire data about race/ethnicity and outpatient antimicrobial drug use for 2014–2015, the latest years with data available. MEPS contains data on members of a nationally representative sample of households (*5*,*6*). A person's race/ethnicity is reported by the respondent and imputed in <0.1% of cases. Information about race and Hispanic ethnicity are collected in separate questions. Data regarding prescriptions filled at outpatient pharmacies are collected from the respondent and, if the respondent approves, verified with the filling pharmacy. Data are afterward cross-referenced and cleaned by survey preparers (*5*).

We used 2 exposure variables. The first was a categorical race/ethnicity variable with 5 values: Hispanic, non-Hispanic white only, non-Hispanic black only, non-Hispanic Asian only, and non-Hispanic other or multiple race. The second exposure variable was dichotomous and indicated whether white was the race or 1 of the races of the respondent. This exposure variable included all persons from the non-Hispanic white category, some from the Hispanic category, and some from the other or multiple race category. The main outcome was reported outpatient antimicrobial drug prescription fills per 1,000 persons per year stratified by major antimicrobial drug class (penicillins, macrolides, quinolones, sulfonamides, other). The complex survey design was accounted for when computing rates and CIs with survey package version 3.32 in R version 3.4.1 (online Technical Appendix, https://wwwnc.cdc.gov/EID/article/24/11/18-0762-Techapp1.pdf).

The reported annual outpatient prescription fill rate for all antimicrobial drugs was 373 (95% CI 358–388) fills/1,000 persons. This rate varied by race/ethnicity; non-Hispanic whites reported the highest rate, followed by persons of other or multiple race/ethnicity, Hispanics, non-Hispanic blacks, and non-Hispanic Asians (Figure, panel A). White persons reported 2.0 (95% CI 1.9–2.2)–fold more fills per capita than nonwhite persons (Figure, panel B). The reported fill rate disparity was similar for macrolides (2.0 [95% CI 1.8–2.4]–fold higher), sulfonamides (2.2 [95% CI 1.8–2.7]–fold higher), and quinolones (2.3 [95% CI 1.9–2.8]–fold higher) but smaller for penicillins (64% [95% CI 48%–82%] higher).

We found a large disparity in antimicrobial drug fill rates by race/ethnicity: white persons reported making twice as many antimicrobial drug prescription fills as persons who were not white. Disparities were apparent for each major antimicrobial drug class, rather than different drug classes being used more predominantly by persons of particular race/ethnicities.

This study is subject to several limitations. First, the survey is not a perfect measure of antimicrobial drug use. Survey respondents report medications they remember filling, subjecting results to systematic differences in respondents' abilities to recall medications (*6*). Survey preparers then obtain information about those medications from the pharmacies the respondents visited, which themselves might have systematic differences in completeness of records (*5*). Also, respondents might not have complete information about other household members' antimicrobial drug use or might choose not to disclose all antimicrobial drug use. Second, nonprescription antimicrobial drug use might be higher among minority groups (*7*), perhaps mitigating the observed disparity. Last, the survey measures reported antimicrobial drug fills and not actual use (*8*); the fill rates we report are substantially lower than those measured by others using sales data (*1*) or other national surveys (*9*).

Whether differences in antimicrobial drug use and race/ethnicity lead to disparities in antimicrobial drug resistance is unclear. We expect that disparities in use, regardless of their cause, will lead to disparities in the proportions of carried bacteria that are antimicrobial drug–resistant. Absolute rates of antimicrobial drug–resistant

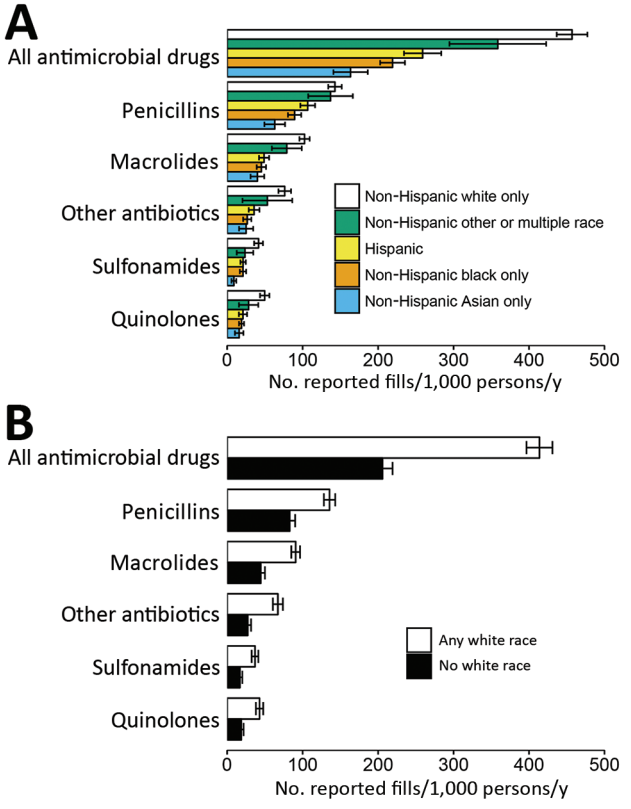

Figure. Annual antimicrobial drug use reported by Medical Expenditure Panel Survey respondents, by race/ethnicity, United States, 2014–2015. Error bars indicate 95% CIs. A) Drug use by race/ethnicity category. B) Drug use among persons who reported white as their race or 1 of their races and among those who did not.

infections, however, might follow different patterns (*10*). For example, higher macrolide use among white persons might lead to macrolide resistance in a greater proportion of *Streptococcus pneumoniae* bacteria carried by whites, but if white persons have fewer *S. pneumoniae* infections, then they would incur a lower absolute rate of macrolide-resistant *S. pneumoniae* infections. Further studies comparing antimicrobial drug use, antimicrobial drug resistance, and disease prevalence by race/ethnicity will be critical for addressing this question and improving antimicrobial drug stewardship.

S.W.O. was supported by cooperative agreement U54GM088558 from the National Institute of General Medical Sciences.

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References

1. Hicks LA, Bartoces MG, Roberts RM, Suda KJ, Hunkler RJ, Taylor TH Jr, et al. US outpatient antibiotic prescribing variation according to geography, patient population, and provider specialty in 2011. Clin Infect Dis. 2015;60:1308–16.
2. Goyal MK, Johnson TJ, Chamberlain JM, Casper TC, Simmons T, Alessandrini EA, et al.; Pediatric Care Applied Research Network. Racial and ethnic differences in antibiotic use for viral illness in emergency departments. Pediatrics. 2017;140:e20170203. http://dx.doi.org/10.1542/peds.2017-0203
3. Steinman MA, Landefeld CS, Gonzales R. Predictors of broad-spectrum antibiotic prescribing for acute respiratory tract infections in adult primary care. JAMA. 2003;289:719–25. http://dx.doi.org/10.1001/jama.289.6.719
4. Gerber JS, Prasad PA, Localio AR, Fiks AG, Grundmeier RW, Bell LM, et al. Racial differences in antibiotic prescribing by primary care pediatricians. Pediatrics. 2013;131:677–84. http://dx.doi.org/10.1542/peds.2012-2500
5. Hill SC, Roemer M, Stagnitti MN. Methodology report #29. Outpatient prescription drugs: data collection and editing in the 2011 medical expenditure panel survey. 2014 Mar [cited 2018 May 7]. https://meps.ahrq.gov/data_files/publications/mr29/mr29.shtml
6. Hill SC, Zuvekas SH, Zodet MW. Implications of the accuracy of MEPS prescription drug data for health services research. Inquiry. 2011;48:242–59. http://dx.doi.org/10.5034/inquiryjrnl_48.03.04
7. Zoorob R, Grigoryan L, Nash S, Trautner BW. Nonprescription antimicrobial use in a primary care population in the United States. Antimicrob Agents Chemother. 2016;60:5527–32. http://dx.doi.org/10.1128/AAC.00528-16
8. Tamblyn R, Eguale T, Huang A, Winslade N, Doran P. The incidence and determinants of primary nonadherence with prescribed medication in primary care: a cohort study. Ann Intern Med. 2014;160:441–50. http://dx.doi.org/10.7326/M13-1705
9. Fleming-Dutra KE, Hersh AL, Shapiro DJ, Bartoces M, Enns EA, File TM Jr, et al. Prevalence of inappropriate antibiotic prescriptions among US ambulatory care visits, 2010–2011. JAMA. 2016;315:1864–73. http://dx.doi.org/10.1001/jama.2016.4151
10. Kanjilal S, Sater MRA, Thayer M, Lagoudas GK, Kim S, Blainey PC, et al. Trends in antibiotic susceptibility in *Staphylococcus aureus* in Boston, Massachusetts, from 2000 to 2014. J Clin Microbiol. 2017;56:e01160-17. http://dx.doi.org/10.1128/JCM.01160-17

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Congenital Zika Virus Infection with Normal Neurodevelopmental Outcome, Brazil

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DOI: https://doi.org/10.3201/eid2411.180883

We describe a case of a 20-month-old girl with probable congenital Zika virus infection and normal neurodevelopment, despite microcephaly and abnormal neuroimaging. This case raises questions about early prognostic markers and draws attention to the need for investigation in suspected Zika cases, even if the child's early neurodevelopment is normal.

Zika virus is a mosquitoborne RNA virus (genus *Flavivirus*, family Flaviviridae) that was first isolated in 1947 from monkeys in the Zika Forest in Uganda (*1*). In November 2015, there was an outbreak of congenital microcephaly in the northeast states of Brazil (*2*). Further confirmation of this syndrome's relationship with Zika virus infection during pregnancy was then possible (*3*). Congenital Zika syndrome has been recognized as a new clinical entity (*4,5*). Most published case series focus on the picture of severely affected infants (*6,7*). We describe a case of a child with probable congenital Zika virus infection whose neurodevelopment was normal, despite

Article DOI: https://doi.org/10.3201/eid2411.180762

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Technical Appendix

We excluded persons with zero survey weight (variables PERWT14F and PERWT15F in the full-year consolidated data files). The categorical race variable was drawn from the RACETHX variable in the full-year consolidated data files, which encodes the 5 categories listed in the main text. The dichotomous white race variable was drawn from the RACEWX variable in the same file, which encodes 3 categories: only white race reported, white race and other races reported, and white race not reported. Antimicrobial drug fills were identified in the prescribed medicines file by matching the category identifications with any of the therapeutic class (TC) variables (e.g., TC1, TC1S1, TCS1_2) (Technical Appendix Table). CIs for the ratio X/Y between the fill rates X and Y for 2 different exposure groups were estimated by simulation. One million random deviates x_i were sampled from a normal distribution, with mean μ_X and standard deviation σ_X, where μ_X is the point estimate for X and σ_X is the standard error on X derived accounting for the complex survey design. One million deviates y_i were analogously sampled by using the point estimate and variance for Y. The 2.5%–97.5% interval of the distribution of the 1 million simulated ratios ($r_i = x_i/y_i$) was reported as the 95% CI for the ratio X/Y. The point estimate for the ratio is the mean of r_i. Code to reproduce the results is available at https://github.com/gradlab/abx-race.

Technical Appendix Table. Antimicrobial drugs included in study of racial/ethnic disparities in antimicrobial drug use, United States, 2014–2015

Multum Lexicon category ID no.	Antimicrobial drug description
002	Amebicide
008	Carbapenems
009	Cephalosporins
010	Leprostatic agents
011	Macrolides
012	Miscellaneous
013	Penicillins
014	Quinolones
015	Sulfonamides
016	Tetracyclines
017	Urinary anti-infective drugs
018	Aminoglycosides
240	Lincomycin derivatives

ID, identification.