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LETTERS

Relative Risk for Ehrlichiosis and Lyme Disease Where Vectors for Both Are Sympatric, Southeastern United States

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To the Editor: The timely study on the relative risk for ehrlichiosis and Lyme disease in which the tick vectors, *Amblyomma americanum* and *Ixodes scapularis*, are sympatric notes that knowledge of tickborne diseases is "startlingly low" (*1*). The call for more research in diseases other than Lyme disease (LD) is long overdue. In the southeastern United States, 5 species of ticks bite humans (*2*). At least 11 associated human pathogens have been identified; all may cause tick paralysis (*2*,*3*).

This study also prompts comment on drawbacks. First, even where *A. americanum* ticks outnumber *I. scapularis* in high-incidence LD areas (*1*), there is no mentioned concern about inflated LD case numbers resulting from reporting patients with erythema migrans (EM) from *A. americanum* tick bites (*4*). Second, there is no evidence for or against a 1:1 transmissibility factor. Bites from infected ticks may not result in illness because of various factors. Subclinical cases may occur. Finally, LD may be reported more frequently because of EM occurrence compared with ehrlichiosis, which depends on laboratory criteria (*5*).

In addition, this study prompts pertinent observations. *A. americanum* ticks are known vectors of numerous pathogens and conditions, including several not yet reportable—for example, α gal allergy, Southern tick-associated rash illness, and Heartland virus—and no prevalence studies have been conducted, so their impact is unknown. It is notable that Monmouth County, New Jersey, USA, tests *I. scapularis* but not *A. americanum* ticks, which are more numerous, carry a greater number of pathogens, and are aggressive biters of humans.

Even though the Southeast United States has more tick species and tickborne pathogens, tick education campaigns, such as those conducted in the Northeast, are absent. The Southeast is experiencing human misery and economic impact from the increase in tick species and diseases. Attention to diseases other than LD is needed and is gratifying to see.

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Invasive Serotype 35B Pneumococci Including an Expanding Serotype Switch Lineage

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To the Editor: We read with interest the article by Chochua et al. from the Centers for Disease Control and Prevention (*1*). We appreciate that the authors cited our recent publication on the same topic from 8 children's hospitals across the United States (*2*). Our study encompassed pneumococcal serotype 35B invasive and noninvasive infections, spanning more than 2 decades. We believe, however, that their reference to our study needs some clarification. We did not report that clonal complex (CC) 156 was the major contributor to antimicrobial resistance among serotype 35B isolates, as stated by Chochua et al. We reported a predominance (69.2%) of 35B sequence type (ST) 558 among invasive isolates across the entire study period (before and after introduction of the 13-valent pneumococcal conjugate vaccine [PCV13]); 95% of the ST558 isolates were penicillin nonsusceptible. We noted that clonal expansion of ST558 was the major contributor to the increase in prevalence of serotype 35B, as did Chochua et al. Furthermore, we observed the emergence of 35B-CC156 after introduction of PCV13 and noted that 35B-CC156 isolates were multidrug-resistant (penicillin nonsusceptibility plus resistance to ≥2 non–β-lactam antimicrobial drugs), similar to previous observations of CC156 associated with other pneumococcal polysaccharide capsules (e.g., serotypes 9V and 14). Thus, the increase in multidrug resistance among serotype 35B isolates in the post-PCV13 era was strongly associated with the emergence of CC156.

Our conclusion that both clonal expansion and diversification had occurred in the post-PCV13 era is validated by the results of Chochua et al. During 2015–2016, we observed no further increase in serotype 35B. We agree with Chochua et al. that the emergence of serotype 35B is of concern and the development of a new generation pneumococcal vaccine is necessary. We will continue to monitor and report data regarding ongoing changes in pneumococci; although our study is not population based, we believe it provides reliable data that are useful for clinical, epidemiologic, and vaccine-related considerations.

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