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Bordetella holmesii in Nasopharyngeal Samples from Chilean Patients with Suspected *Bordetella pertussis* Infection

We read the article of Njamkepo et al. (5) with great interest. These authors report the finding of *Bordetella holmesii* DNA in 177 IS*481*-positive nasopharyngeal samples from French patients with suspected pertussis. They performed 4 *Bordetella* species-specific "in-house" real-time PCRs on all samples (*Bordetella pertussis*-specific *ptxA*-Pr-based PCR, *B. holmesii*-specific RecA-based PCR, BP3385-based PCR specific for *B. pertussis* and some *Bordetella bronchiseptica*, and IS*1001* PCR for *B. bronchiseptica* and *Bordetella parapertussis*). *Bordetella holmesii* DNA was detected in 20.3% of samples collected from adolescents and adults. Previously, from January 1995 (when the article describing *B. holmesii* [6] was published) to December 1998, Yih et al. (7) had also found 34 *B. holmesii* isolates in 33 positive nasopharyngeal specimens from mainly adolescent and adult patients (30 patients were 11 to 29 years old) suspected of having pertussis.

We wish to contribute to this discussion by describing our experience in the study of 99 IS*481*-positive nasopharyngeal samples (3) collected between January 2010 and August 2011 in the Molecular Microbiology Laboratory, Pontificia Universidad Católica de Chile. It is important to mention that since October 2010, Chile has been experiencing a whooping cough epidemic, with 51% of the cases in the <12-months age group (http://epi.minsal.cl/). The samples were analyzed by a real-time PCR for the housekeeping gene *recA* using the BHrecA primers described by Guthrie et al. (2). A total of 88 samples (88.9%) were negative for the *recA* gene and were considered positive for *B. pertussis* DNA. Eleven samples (11.1%) contained *B. holmesii* DNA, as determined by a positive RecA-based PCR. The *B. holmesii* diagnosis was confirmed by sequencing a 1,046-bp segment of the *recA* gene from one of the positive samples (1). Regarding age groups, our data included 51, 25, and 23 patients aged 0 to 9, 10 to 17, and 18 or more years old, respectively. *B. holmesii* infection was present in all age groups, especially in younger patients: 7 cases were in patients aged 0 to 9 years (13.7% of patients that age group), 2 were in patients aged 10 to 17 (8%), and 2 were in patients 18 or more years old (8.7%). There were 3 cases in patients younger than 12 months, including one 16-day-old newborn. Although this is a small set of samples, our data contrast with those reported by Njamkepo et al. (5) in which there were no cases in small children. These results are probably explained by the outbreak situation we mentioned earlier. In this context, a hypothetical lower rate of transmission of *B. holmesii* than of *B. pertussis* in this age group would not be the case. We agree with the authors' conclusion about the need for surveillance of *B. holmesii*, especially due to the lack of knowledge about the clinical characteristics and/or antimicrobial susceptibility of *B. holmesii* in respiratory infection.

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