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Sabine Pereyre, Hélène Renaudin, Alain Charron, Cecile Bebear

To cite this version:
Sabine Pereyre, Hélène Renaudin, Alain Charron, Cecile Bebear. Clonal spread of Mycoplasma pneumoniae in primary school, Bordeaux, France. Emerging Infectious Diseases, Centers for Disease Control and Prevention, 2012, 18 (2), pp.343-345. 10.3201/eid1802.111379. hal-02648761

HAL Id: hal-02648761
https://hal.inrae.fr/hal-02648761
Submitted on 29 May 2020

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Table. Countries in Africa with evidence of dengue virus transmission among French Armed Forces, 1998–2010

| Country and year | No. cases | Testing method | Infection status | Dengue virus serotype |
|------------------|-----------|----------------|------------------|-----------------------|
| Cameroon, 2010   | 1         | PCR            | Confirmed        | 1                     |
| Cape Verde, 2010 | 5         | Culture        | Confirmed        | 3                     |
| Central African Republic, 1995 | 1 | Serology | Probable | Unknown |
| Chad, 1998–2001, 2003, 2006, 2009–2010 | 28 | Serology | Probable | Unknown |
| Comoros 2010     | 1         | PCR, culture   | Confirmed        | 1                     |
| Comoros 2010     | 2         | PCR            | Confirmed        | 3                     |
| Côte d’Ivoire 1999 | 1 | Culture | Confirmed | 1 |
| 2000, 2004–2007  | 11        | Serology       | Probable         | Unknown               |
| 2010             | 1         | PCR            | Confirmed        | 3                     |
| Djibouti 1998    | 4         | Culture        | Confirmed        | 1                     |
| 1998             | 24        | Serology       | Probable         | Unknown               |
| 2000             | 2         | Culture        | Confirmed        | 1                     |
| 2000             | 4         | Serology       | Probable         | Unknown               |
| 2001–2005        | 123       | Serology       | Probable         | Unknown               |
| 2005             | 1         | PCR            | Confirmed ND     | ND                    |
| 2006             | 4         | Serology       | Probable         | Unknown               |
| 2008             | 2         | Serology       | Probable         | Unknown               |
| Gabon 1998, 2006–2008 | 22 | Serology | Probable | Unknown |
| 2010             | 1         | PCR            | Confirmed        | 1                     |
| Mayotte, 2009    | 1         | Culture        | Confirmed        | 1                     |
| Senegal, 2009    | 1         | PCR            | confirmed        | 3                     |
| Somalia, 1999    | 1         | culture        |                  | 2                     |

data may be confusing because of potential cross-reactions with other flavivirus antibodies (in particular in Chad with West Nile virus).

Because of probable underreporting from the field, our reported number of confirmed dengue cases likely underestimates the actual number of cases among French troops stationed in Africa. Nonetheless, our data complement those reported by Amarasinghe et al. by demonstrating additional locations for circulation of serotype 1 (Cameroon, Djibouti, Gabon, Mayotte) and serotype 3 (Comoros). Military epidemiologic surveillance systems can detect dengue circulation where soldiers stay. Thus, these systems could serve to evaluate the risk for dengue infection in countries without local epidemiologic surveillance systems, thereby improving knowledge about dengue circulation in African countries.

Franck de Laval, Sébastien Plumet, Fabrice Simon, Xavier Deparis, and Isabelle Leparc-Goffart

Author affiliations: Epidemiologic and Public Health Military Center, Marseille, France (F. de Laval, X. Deparis); French Army Forces Biomedical Institute, Marseille (S. Plumet, I. Leparc-Goffart); and Laveran Military Hospital, Marseille (F. Simon)

DOI: http://dx.doi.org/10.3201/eid1802.111333

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Address for correspondence: Isabelle Leparc-Goffart, IRBA Marseille, Parc du Pharo, BP60109, 13262 Marseille Cedex 07, France; email: isabelle.leparcgoffart@gmail.com

Clonal Spread of Mycoplasma pneumoniae in Primary School, Bordeaux, France

To the Editor: *Mycoplasma pneumoniae* is responsible for ≈20% of all cases of community-acquired pneumonia. The most common form of the infection is tracheobronchitis, for which an etiologic diagnosis is seldom reached (1). Although tracheobronchitis is often mild, the infection is disruptive, with the cough lasting several weeks, and consumes substantial resources (2). *M. pneumoniae* infections occur endemically and epidemically worldwide, especially in children and young adults (1). In 2010, an increased incidence was reported from Denmark (3), England and Wales (4), and Israel (5). Several outbreaks have been reported in closed or semiclosed settings, as indicated on the basis of similar clinical symptoms, chest radiograph results, and detection of the bacteria (1).
Previous M. pneumoniae typing methods were based on the analysis of the gene encoding the cytadhesin P1 (MPN141) or the gene MPN528a (6). These methods only enabled the separation of isolates into 2 types and a few variants; therefore, clinical isolates were previously poorly differentiated. We recently developed a multilocus variable-number tandem repeat analysis (MLVA), based on the study of the whole genome, that can differentiate >26 distinct variable-number tandem repeat types (7). We report the use of this MLVA typing method to show evidence of a clonal spread of a unique strain of M. pneumoniae among children in a French primary school and their household contacts.

In January 2011, 6 children (4–9 years of age), who attended the same primary public school in Bordeaux, France, reported fever, pharyngitis, rhinorrhea, and dry cough that later became mucoid. One of the children was admitted to the pediatric ward of the University Hospital of Bordeaux, and atypical pneumonia was confirmed by radiologic testing. A diagnosis of tracheobronchitis was confirmed by general practitioners for the 5 other children. Three of the children were administered β-lactam antimicrobial drugs that did not modify the course of the illness. An additional child (4 years of age), a first cousin of one of the 6 case-patients, also received a diagnosis of tracheobronchitis after repeated contact with his cousin.

Throat swab or blood samples were obtained from the 7 children, and throat swab samples were obtained from the household members of 4 of their families. DNA was extracted from throat specimens, and a TaqMan real-time PCR was performed to detect M. pneumoniae as described (8). MLVA typing was performed on the same DNA extracts, according to the method of Dégrange et al. (7). M. pneumoniae–specific IgM and IgG in serum specimens were assessed by ELISA. PCR was used to detect Bordetella pertussis, B. parapertussis, Chlamydia pneumoniae, Streptococcus pneumoniae, and viruses commonly responsible for respiratory tract infections. In France, 10% of M. pneumoniae isolates are resistant to macrolides (9); thus, we used real-time PCR and melting curve analysis to detect macrolide resistance–associated mutations in the 23S rRNA gene (9).

The 7 children were confirmed to be positive for M. pneumoniae infection by PCR or by the presence of M. pneumoniae–specific IgM (Figure). No other respiratory tract pathogens were found. In all cases, MLVA determined the strain type to be 34572, also called MLVA type J (7); this finding suggests clonal spread of a specific M. pneumoniae strain. No macrolide resistance–associated mutation was found in the 23S rRNA gene. All children were treated with roxithromycin or clarithromycin and rapidly recovered, although PCR results remained positive for up to 6 weeks in subsequent throat samples. This length of persistence is in accordance with a previous study showing that the median time for carriage of M. pneumoniae DNA was 7 weeks after disease onset and that adequate treatment did not shorten this period (10).

M. pneumoniae DNA was also found in throat swab specimens of 3 household contacts (2 adults and a 1-year-old child) in 3 separate
families (Figure). The MLVA type was determined in 1 contact; it also was MLVA type J, suggesting that carriage in this contact was related to spread of the same clone. Of interest, none of these 3 household members had respiratory symptoms. Nilsson et al. (10) also reported a high frequency of M. pneumoniae DNA carriage in household contacts; however, in contrast to contacts in our study, all of the household contacts in the study by Nilsson et al. had ongoing or recent respiratory tract symptoms.

In summary, we report an outbreak of M. pneumoniae infections confirmed by MLVA, a discriminatory typing method. MLVA typing revealed the clonal spread of a single M. pneumoniae type J strain in children attending the same primary school and in their household contacts. The cases we identified may represent only a small proportion of the actual cases, which were likely underestimated due to mild symptoms, poor knowledge of M. pneumoniae infections by general practitioners, and lack of PCR availability. We showed that MLVA typing of M. pneumoniae can be used to detect clonal spread and outbreaks. This approach might also be useful for studying the worldwide emergence of M. pneumoniae macrolide resistance and for finding resistant clones with the potential for spreading.

Acknowledgments

We thank Florence Bernard for technical assistance.

This study was supported by internal funding.

Sabine Pereyre, Hélène Renaudin, Alain Charron, and Cécile Bébéar

Author affiliations: Université de Bordeaux, Bordeaux, France; Institut National de la Recherche Agronomique, Bordeaux; and Centre Hospitalier Universitaire de Bordeaux, Bordeaux

DOI: http://dx.doi.org/10.3201/eid1802.111379

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Address for correspondence: Sabine Pereyre, USC Infections Humaines à Mycoplasmes et Chlamydia, Université Bordeaux Segalen, Bât 2B, 146 Rue Léo Saignat, 33076 Bordeaux, France; email: sabine.pereyre@u-bordeaux2.fr

Risk for Emergence of Dengue and Chikungunya Virus in Israel

To the Editor: In recent years, Aedes albopictus, a mosquito vector of dengue and chikungunya viruses, has rapidly expanded in Europe. Since 2007, the presence of viremic patients with imported cases of dengue and chikungunya virus infection has resulted in several incidences of autochthonous transmission of the viruses in Italy, France, and Croatia (1–4).

A. albopictus mosquitoes have invaded Israel since 2002. A recent national survey showed wide distribution of the mosquito in Israel (5), and dengue and chikungunya virus infection are increasingly reported in travelers from Israel who return home from trips to other countries (6,7). We looked for overlap between the distribution areas of A. albopictus mosquitoes in Israel and the living areas of travelers who have returned to Israel with acute dengue or chikungunya virus infections. We discuss the possibility of autochthonous transmission of these viruses in Israel.

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