Correspondence

Polymorphisms in Pneumocystis jirovecii Strains in Spanish Children with Cystic Fibrosis

To the Editor—In a recent study, Beard et al. [1] analyzed lung tissue samples obtained at autopsy from colonized infants and samples from HIV-positive adults with Pneumocystis pneumonia (PCP) for the presence of Pneumocystis jirovecii and compared the distributions of the genotypes of the mitochondrial large subunit (mtLSU) rRNA gene and the dihydropteroate synthase (DHPS) gene. Different rates of mtLSU rRNA genotypes were observed between these populations, suggesting the existence of 2 independent cycles of transmission (1 during childhood and 1 during HIV infection in adults). In addition, the authors speculated that infection with specific strains may occur during childhood.

The primary limitations of this study were the different geographical locations of the groups that were studied and the absence of a colonized, non–HIV-infected adult group, which did not allow for comparisons between colonized populations of adults and children. The different geographical locations included in Beard et al.’s study might explain the differences that were found in the distributions of mtLSU rRNA polymorphisms. In addition, colonized adults may have a genotype pattern that is similar to that in colonized infants but different from that in adults with PCP.

In a recent molecular epidemiological study of colonized Spanish adults with different chronic pulmonary diseases and Spanish adults with PCP, polymorphisms in the mtLSU rRNA and DHPS genes of P. jirovecii were analyzed [2]. A comparison of the mtLSU rRNA region indicated that genotype 1 (85C/248C) occurred more often in patients with AIDS than in patients with chronic pulmonary disease. Rates of genotype 2 (85A/248C) were similar in all patients. Genotype 3 (85T/248C) occurred more frequently in patients with chronic pulmonary disease than in patients with PCP. These results indicate that the mtLSU rRNA genotype pattern in Spain is different from the one found in the United States [3]. However, this study did not include colonized infants.

Recently, the prevalence of P. jirovecii colonization was reported in a cohort of patients with cystic fibrosis (CF) [4]. These data are in accordance with those in the study by Beard et al., who found that genotype 3 was more frequent in colonized children than in HIV-positive adults.

Furthermore, we have typed a homogeneous cohort (from the same geographical area) of 42 patients with CF, between 1 and 36 years old, who were colonized with P. jirovecii, as well as 27 HIV-infected adults with PCP. To compare the distribution of mtLSU rRNA genotypes, we examined 3 groups: adults with PCP and 2 groups of patients with CF, divided according to age: 14 years old (21 children) and >14 years old (21 patients). Figure 1 summarizes the results. As we described elsewhere [2], the rate of genotype 1 was higher in adults with PCP than in patients with CF. In contrast to the results obtained by Beard et al., genotype 2 was expressed less often in Spain, and it was found in all groups at a similar rate. Analysis of the rate of genotype 3 showed a concordance with the results obtained by Beard et al. In HIV-infected patients with PCP, the rate of genotype 3 was 14.8%, which was significantly lower than the rates of 42.8% and 47.6% that were found in children with CF and adults with CF, respectively. Finally, genotype 4 (85C/248T) was not found, but a lower rate, <10%, of strains with mixed polymorphisms was detected.

These observations suggest that there is a different pattern of mtLSU rRNA gene expression between colonized patients with CF, irrespective of age, and patients with PCP. These findings are in agreement with the results obtained by Beard et al. and support the concept of a different cycle of transmission and infection in immunocompetent children and in immunosuppressed patients with PCP. However, when colonized patients with CF were divided by age, we found an identical pattern of mtLSU rRNA gene expression among them, and this pattern was similar to that described in immunocompetent infants in the United States.

Thus, differences in genotype distribution might be due to the status of underlying diseases, rather than age, in patients in the United States. Further studies should clarify whether variations in rates
of \textit{P. jiroveci} genotypes are related to underlying disease.

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References


Viremia and Clinical Manifestations in Children with Rotavirus Infection

To the Editor—We read with interest the recent article by Fisher et al. investigating rotavirus antigenemia in patients hospitalized for acute diarrhea during a major outbreak of enteritis [1]. Antigenemia was demonstrated by EIA in 30 (42.8%) of 70 children and was confirmed by reverse-transcription polymerase chain reaction (RT-PCR) in 12 (66.6%) of 18 children. Rotavirus antigen levels were commonly detected on the first day of illness, peaked 1–3 days after symptom onset, and remained positive beyond 1 week only in a minority of convalescent children. Interestingly, an association between antigen detection in the serum and severity of clinical symptoms was suggested, since (1) there was a nonsignificant tendency for severity of illness to be associated with higher serum optical density values, as assayed by EIA; (2) in 1 of 2 deceased children, viral RNA was demonstrated in the serum; and (3) antigenemia was higher in children with primary infection than in those with subsequent infection, and it is well known that primary infection is usually more severe [2]. Unfortunately, no detailed data on extraintestinal involvement and its potential association with antigenemia were provided. This is an interesting issue, since the extraintestinal spread of the virus may occur through the blood [3].

In light of this, we would like to mention the results of our recent investigation on 54 immunocompetent children hospitalized for acute diarrhea who were prospectively evaluated by nested RT-PCR for the presence of rotavirus RNA [4]. Viral RNA was detected in the blood of 9 (64.3%) of 14 children with documented rotavirus infection but in no child with diarrhea of other origin. The presence of rotavirus RNA in the blood was associated with high fever and/or evidence of extraintestinal involvement. However, severe clinical manifestations were absent in all children. This finding suggests that viremia by itself is not the major determinant of severe illness.

Taken together, both the study by Fisher et al. and our study indicate that viremia is common in rotavirus-infected children. We suggest that future targeted studies should clarify whether specific rotavirus strains or a higher viral load are more frequently associated with severe and/or extraintestinal manifestations.

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References


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\textbf{Legionella Bacteria in Aerosols: Sampling and Analytical Approaches Used during the Legionnaires Disease Outbreak in Pas-de-Calais}

Between November 2003 and February 2004, an outbreak of legionnaires disease occurred in the Pas-de-Calais region of northern France. There were 18 deaths among the total of 86 cases found within a radius of ∼10 km around a petrochemical plant that was the probable source of contamination [1].

From January to March 2004, we sampled aerosols produced by industrial cooling towers and by an industrial sludge water treatment basin to search for \textit{Legionella} bacteria by use of a new experimental method. To date, management of this serious biological risk has relied solely on the monitoring of water quality. The only known contamination vector is the aerosol, and the transfer function between contaminated water and air remains unknown. Our contribution, which is based on the collection of large volumes of aerosols and the detection of \textit{Legionella} bacteria by fluorescent in situ hybridization (FISH), offers an interesting new approach, leading to