To the Editor—We read with interest the article by Sassi et al published in Clinical Infectious Diseases [1]. They investigated Pneumocystis jirovecii genotypes involved in Pneumocystis pneumonia (PCP) outbreaks among renal transplant recipients. To that aim, they used fragment length polymorphisms of the major surface glycoprotein gene family. This work revealed that the same P. jirovecii genotype was involved in 2 outbreaks, 1 in Zurich [2] and 1 in Munich [3], whereas another genotype was linked to a Japanese outbreak [4]. It was likely that the most predominant genotype in the area was not involved in the 2 European outbreaks because unlinked control cases were infected with different genotypes. The authors concluded that there may have been an increased virulence of the outbreak genotypes in renal transplant recipients, and that the Zurich and Munich outbreaks may have had a common source of infection. These observations provided new insights into the transmission patterns of this opportunistic pathogen, but analysis of other outbreaks is needed in order to better understand the issue and improve prevention measures.

We reinvestigated the genotypes involved in 2 other PCP outbreaks among renal transplant recipients that occurred in Europe – 1 in Frankfurt [5] and 1 in Lyon [6]. To compare the genotypes of the different outbreaks, we considered the most frequently used method of typing, which is the sequencing of 4 genomic loci. These loci included the internal...
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