community-acquired *S. aureus* infections in children, methicillin-resistant isolates produced more cases of pneumonia than methicillin-susceptible strains and infection severity was associated with PVL production.[4]

MRSA pneumonia often presents with unilateral consolidation, pneumatoceles and pleural effusion[8] and is more common in younger infants. At our hospital we found no cases of CA-MRSA pneumonia in infants over the age of 6 months. In children over the age of 2 years, the radiological findings, need for surgery and complications of MRSA pneumonia are similar to those observed in infants.[6]

MRSA carrier status increases the risk of pneumonia caused by this strain up to six-fold,[3] and the rate of intrafamilial spread is very high.[6] MRSA colonisation in Spain is more common among the immigrant population, especially among immigrants from South America.[9] There is an ongoing spirited debate regarding the need for decolonisation in children and their family members. Decolonisation seems to be well advised in children with risk factors, such as premature infants, immunosuppressed children or patients admitted to intensive care units, and their relatives.

The American Academy of Pediatrics recommends the use of vancomycin or clindamycin in suspected cases of MRSA pneumonia.[10] Once advantage of clindamycin is that it is active against PVL, but experience in actual cases of pneumonia is very limited and there may be resistant isolates. Vancomycin shows poor tissue penetration and its toxicity requires the use of serial loading doses. Linezolid is an excellent alternative, since its activity against MRSA is similar to that of vancomycin and it shows adequate penetration into lung tissue and antitoxic activity. Although the use of linezolid in paediatrics is *off-label*, pharmacokinetic and safety studies have demonstrated that it is a well-tolerated drug, with adequate plasma concentrations at the established doses, and that it also allows sequential administration due to its excellent oral bioavailability.

To conclude, MRSA must be suspected as the causative agent in cases of CAP with radiological signs of clinical deterioration (necrosis and pleural effusion) despite conventional empirical antibiotic therapy, especially in infants born to immigrant families. Linezolid is a good alternative to vancomycin in these patients.

Appendix. Supplementary material. Supplementary data

Supplementary material associated with this article can be found in the online version available at https://doi.org/10.1016/j.eimce.2019.04.008.

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Imported cryptosporidiosis caused by *Cryptosporidium hominis* IbA13G3 in Spain. The relevance of molecular-based surveillance

Criptosporidiosis importada por Cryptosporidium hominis *IbA13G3. La relevancia de la vigilancia basada en métodos moleculares*

Cryptosporidium is the most common diarrhoea-causing protozoan parasite globally. *Cryptosporidium* infections primarily affect children aged <24 months in the sub-Saharan Africa and South Asia, where three out of four reported cases were due to *C. hominis*.[1] Based on sequence analysis of the 60-kDa glycoprotein (*GP60*) gene, *C. hominis* has been demonstrated to comprise nine (Ia-Ik) subtype families with marked differences in geographical distribution.[2,3]

In middle August 2018 two Spanish-borne siblings complaining of gastrointestinal symptoms (a 2 years-old boy and a 12-years old girl) from a Nigerian family were attended at the María Jesús Hereza primary health centre (Leganés, Madrid). Both children had just returned from a 2-month family trip to Nigeria, where acute, non-bloody watery diarrhoea initiated. Three consecutive, soft stool specimens were obtained from each patient and submitted

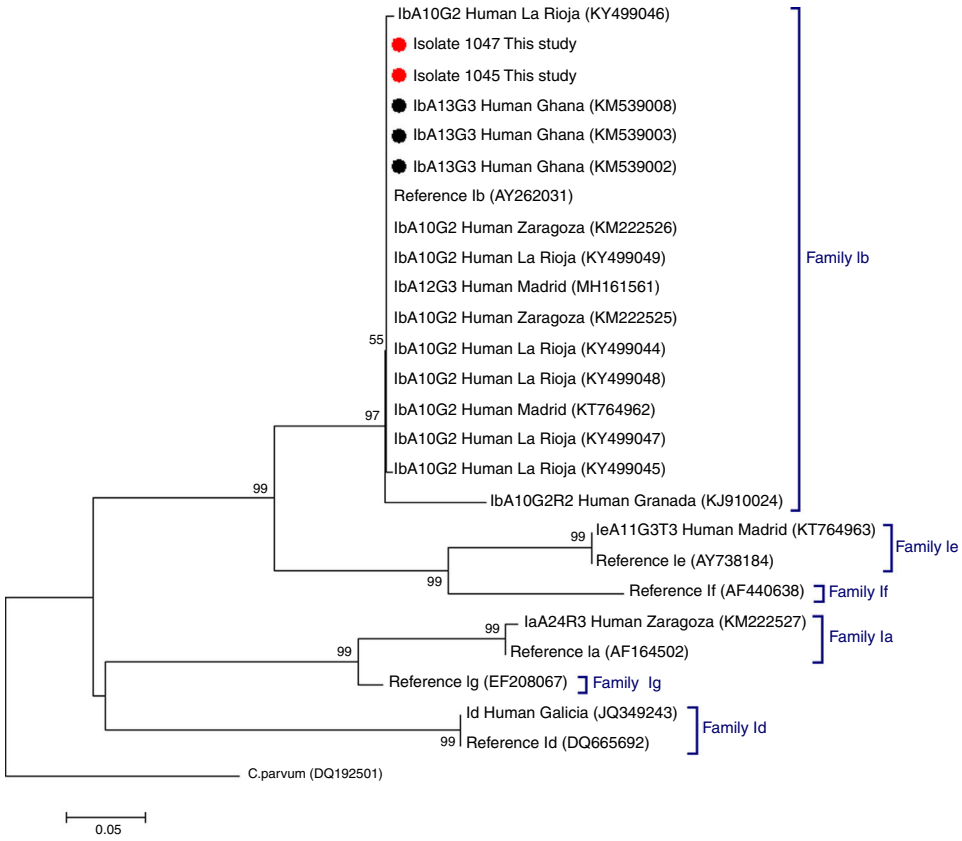

Fig. 1. Phylogenetic tree depicting evolutionary relationships among *C. hominis* IbA13G3 sequences at *GP60* from human isolates generated in the present study (represented by red filled circles) and other available surveys (represented by black filled circles). Representative sequences of *C. hominis* subtype families previously identified in different Spanish regions were also included in the analysis for comparative purposes. The analysis was inferred using the Neighbor-Joining method. Bootstrapping values over 50% from 1.000 replicates are shown at the branch points. The evolutionary distances were computed using the Kimura 2-parameter method. The rate variation among sites was modelled with a gamma distribution (shape parameter = 2). *C. parvum* was used as outgroup taxa.

to the Microbiology Service of the University Hospital Severo Ochoa (Leganés, Madrid) for routine coproparasitological investigation including copro-culture and a commercially available solid phase qualitative immunochromatographic test for giardiosis/cryptosporidiosis (X/Pect *Giardia*/*Cryptosporidium*, Santa Fe, USA). Copro-cultures were negative but all six samples tested positive to *Cryptosporidium* by the rapid screening test. No microscopic examination was conducted. Pooled aliquots of the stool samples were shipped to the Spanish National Centre for Microbiology at Majadahonda (Madrid) for diagnosis confirmation and genotyping analyses. Genomic DNA was extracted and purified using the QIAamp® DNA stool mini test kit (Qiagen, Hilden, Germany). Molecular detection and characterisation of the samples was achieved by PCR amplification of the *GP60* marker.[4] Amplicons of the expected size (~870 bp) were directly submitted for sequencing. Sequence analyses confirmed the presence in both samples of *C. hominis* IbA13G3, a very rare subtype not previously reported in Spain to date. A representative nucleotide sequence of the subtype obtained was submitted to the GenBank® public repository under the accession number MK105902. Duration of gastrointestinal complaints lasted for two weeks after diagnosis and remitted spontaneously without specific treatment.

C. hominis IbA13G3 was initially reported in four Peruvian HIV-positive individuals in 2007.[5] Subsequent molecular epidemiological surveys conducted in Nigeria allowed the identification of this subtype in community ($n = 7$)[6] and clinical ($n = 1$)[7] paediatric populations, and in HIV-infected persons ($n = 2$).[8] Additionally, the IbA13G3 subtype accounted for 19% ($n = 17$) of all *Cryptosporidium* genetic variants detected in children from rural Ghana, only second after the IIcA5G3a subtype.[9] Based on these molecular data a West African origin for *C. hominis* IbA13G3 has been suggested, but not conclusively proven, by some authors.[5,7] As expected, our phylogenetic analysis based on the *GP60* gene demonstrated that the IbA13G3 sequences generated in the present study and those available at GenBank from Ghana[9] clustered together in a well-defined group within the family subtype Ib. In order to enable direct comparison, reference sequences and representative sequences of the most frequent *C. hominis* family subtypes circulating in different Spanish human populations were also included in the analysis (Fig. 1).

In summary, we identified the presence of *C. hominis* IbA13G3 in two returning travellers from Nigeria, the geographical area where this *Cryptosporidium* subtype seems more prevalent. To the best of our knowledge the IbA13G3 subtype has been only detected so far in West African countries and Peru, so this is the first report of the occurrence of this *Cryptosporidium* subtype in Europe. These and previous[10,11] findings by our laboratory highlight the relevance of conducting active, molecular-based surveillance for the investigation of travel-related morbidity as an essential component of global public health surveillance.

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Competing interests

The authors declare that they have no competing interests.

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