Rotavirus G12 in Spain: 2004–2006

Rotavirus G12 en España: 2004–2006

To the Editor,

We have carefully read the interesting article by Sánchez-Fauquier et al.[1] and agree that surveillance of the rotavirus genotypes that cause acute gastroenteritis would be of great interest for Public Health. Because a rotavirus vaccine is available on the market and has recently been licensed in several countries, surveillance of circulating rotavirus genotypes and strains would now be particularly opportune.[2] Surveillance would allow us to determine whether changes are occurring or not in the genotypes that cause winter epidemics and to study their possible association with vaccines. Examples of such changes are replacement of the currently predominant genotypes (G1–G4 and G9) by others that, at the present moment, are considered unusual, or the spread of new strains due to genetic recombination, the development of escape mutations to vaccines, or the introduction of zoonotic strains in the human population.[3,4]

However, we would like to clarify a point made in the study by Sánchez-Fauquier et al.[1] concerning the presence in Spain of rotavirus G12, which is considered an emerging genotype, due to its global spread in the first few years of the current century.[3,5] Rotavirus G12 was not first detected in Spain in 2008, as indicated in the study by Sánchez-Fauquier et al.[1] Cases of human infection by rotavirus G12 ($n=4$) were detected in Gipuzkoa in 2004 and 2005.[6,7] Three of these strains (G12[P8]) were analyzed in a phylogenetic tree of the VP7 region of rotavirus together with more than 40 G12 [P8] strains, which were also detected in the Basque Country during the winter epidemic of 2010–2011, in which G12[P8] were predominant.[7] The strains detected in Gipuzkoa in 2004–2005 were grouped with strains from Hungary and Slovenia and those detected in 2010–2011 were closer to others from Southeast Asia, suggesting distinct introductions in the population.[7] When referring to this epidemic, Sánchez-Fauquier et al.[1] cite an Australian study,[8] instead of the original work.[7] In addition, Halaihel et al.[9] also described rotavirus G12[P8] detection before 2008 in Spain, in this case in the feces of pigs in the farms of Aragón in 2006. This finding is interesting, as it suggests G12 rotavirus transmission between humans and pigs.[3] These comments serve to clarify an aspect of an otherwise excellent study by Sánchez-Fauquier et al.[1]

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Sugerencias sobre el análisis molecular microbiológico *post mortem*

Suggestions on* post mortem *molecular microbiology analysis

Sr. Editor:

Hemos leído con interés, por su utilidad en las competencias analíticas de Microbiología Clínica, la revisión publicada por Fernández-Rodríguez et al.[1] titulada «Análisis microbiológico *post mortem*». Al hilo de la misma, querríamos expresar algunas puntualizaciones. La significación microbiológica en la analítica *post mortem* es clave para el análisis y la emisión de informes microbiológicos realizados en el ámbito de una autopsia que además conllevan en ocasiones connotaciones legales. Existe escasa literatura de microbiología *post mortem* necesaria para una mejor comprensión de las enfermedades infecciosas a nivel patogénico y su papel como causantes de mortalidad[2,3]. Las utilidades de esta práctica microbiológica *post mortem* tienen la mayoría de las veces fines diagnósticos que ayudan a esclarecer la causa de la muerte. Otras veces son fines epidemiológicos o de investigación (infecciones nosocomiales, prevalencia de patógenos, resistencias antibióticas, racimos epidemiológicos...)[4]. A este respecto, el protocolo de la SEIMC dedicado a dicha analítica[5] debe servir para unificar criterios a la hora de interpretar resultados y emitir informes *post mortem*. La mayoría de barreras (físicas, funcionales, etc.) dejan de ser eficaces durante el periodo preagónico y *post mortem*, permitiendo una diseminación microbiana parcial o total[4]. Estos procesos, aunque inevitables, pueden reducirse pero nunca eliminarse, y tampoco evaluar el grado de contaminación *post mortem* a partir del tiempo de conservación del cadáver. El mayor problema radica en la toma de muestras, y en menor medida en su transporte o en las técnicas microbiológicas. Aunque se postula que la toma de muestras no se debe retrasar más de 24 h después de la muerte, la realidad hospitalaria hace que la toma de muestras se demore aún más desde el fallecimiento[6]. La sensibilidad de las técnicas moleculares ha supuesto numerosas ventajas para los laboratorios de Microbiología Clínica pero en absoluto mejoran la validez de