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Letters to the Editor

Molecular Analysis of Tn*1546* in *vanA*-Containing *Enterococcus* spp. Isolated from Humans and Poultry

The genes encoding the VanA type of vancomycin resistance in enterococci are located on elements related to Tn*1546* (1). Heterogeneity of Tn*1546* in *Enterococcus faecium* has been previously reported (3, 4, 6, 9, 10, 12, 14, 15, 16) and includes deletions, insertions, and mutations. In this study, Tn*1546* elements from 43 *vanA*-containing isolates of different enterococcal species with diverse pulsed-field gel electrophoresis (PFGE) patterns (criteria of Tenover et al. [13]) were analyzed: 30 *E. faecium* isolates (18 from chicken feces or products and 12 from human fecal samples) showing 25 unrelated PFGE patterns, 7 *Enterococcus durans* isolates with two unrelated PFGE patterns, (chicken feces or products), 5 *Enterococcus hirae* isolates (4 from chicken feces or products and 1 from a human fecal sample known to have an indistinguishable or a closely related PFGE pattern), and 1 *Enterococcus faecalis* isolate (from a chicken product).

PCR products were obtained from all isolates for the seven genes of Tn*1546* (*vanR*, *vanS*, *vanH*, *vanY* [10], *vanA* [16], *vanX* [11], and *vanZ* [8]); IS*1216V*-related sequences (6) were also demonstrated by PCR for all 43 isolates. When the *vanXY* (9) region was amplified, the expected 1,947-bp fragment was obtained with 36 of the 43 isolates; however, in all 5 *E. hirae* isolates and in 2 *E. faecium* isolates (both from chickens, with different PFGE patterns) the fragment amplified was longer than expected. Results of hybridization of *vanXY* PCR products with an IS*1216V* probe indicated that IS*1216V* was located within the *vanXY* region in these seven isolates and outside this region in the other isolates. An IS*1216V*-like sequence was first described within the intergenic *vanXY* region (5) and later both within and outside Tn*1546* (3, 6); disruption of *vanS* by IS*1216V* has been found in a clinical *E. faecium* isolate (2). Despite these reports for *E. faecium*, this is the first time that IS*1216V* has been reported within the *vanXY* region of *E. hirae*. The restriction of the IS*1216V-vanXY* association to *E. hirae* and two *E. faecium* strains isolated from chickens could suggest interspecies transmission of these transposons in animal gastrointestinal tracts.

IS*1251* sequences (6) were detected in 18 *E. faecium* isolates (13 from chickens and 5 from humans; 15 unrelated PFGE patterns) but not in the other species tested. Analysis of *vanSH* (9) amplicons and hybridization showed that IS*1251* was not included in this region. IS*1251* has been previously found in the *vanSH* intergenic region and at other sites in *E. faecium* (4, 6).

IS*1476*, first found in the *vanY* gene of an *E. faecium* isolate (9), was not detected in our strains nor in two other studies (6, 15). Recently, a 1-bp difference in *vanX* was found at position 8234, with either a G (G type) or a T (T type) (6). All our *vanA* isolates, except one (*E. faecium* from ground chicken), belonged to the G type as determined by *Dde*I digestion of the *vanX* gene PCR fragment (315 bp) (6). The G type has been associated with poultry, and the T type has been associated with porcine *E. faecium* isolates (3, 7). Both types have been found among isolates from humans in different countries (7), although we found only the G type among vancomycin-resistant enterococci isolated from humans in Spain.

In conclusion, *vanA*-containing *E. faecium*, *E. faecalis*, *E. hirae*, and *E. durans* strains of human and animal origins were found to contain similar genetic arrangements of the *vanA* gene cluster, suggesting either horizontal transfer, the existence of a common reservoir, or a predilection for insertion of certain elements at specific sites.

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B. Robredo
C. Torres*
Área Bioquímica y Biología Molecular
Universidad de La Rioja
Avenida de la Paz 105
26004 Logroño, Spain

K. V. Singh
B. E. Murray
Division of Infectious Diseases
Center for the Study of Emerging and Reemerging Pathogens
University of Texas Medical School
Houston, Texas

*Phone: 34-941-299284
Fax: 34-941-299274
E-mail: carmen.torres@daa.unirioja.es