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Aquaculture and Florfenicol Resistance in *Salmonella enterica* Serovar Typhimurium DT104

To the Editor: In a letter recently published in Emerging Infectious Diseases, Smith (*1*) discussed evidence that he mistakenly believes to undermine the hypothesis that the florfenicol resistance gene present in some isolates of the epidemic *Salmonella enterica* serovar Typhimurium DT104 strain originated from a florfenicol resistance plasmid present in *Vibrio damsela* (*Pasteurella piscicida*) that infected fish farms in Japan in the 1990s (*2*). Smith correctly states that the florfenicol resistance gene was present in *S. enterica* serovar Typhimurium DT104 strains isolated in the United States in 1985, before the gene was documented in *V. damsela* in Japan (*1*,*3*). He is also correct in noting that this particular florfenicol resistance gene was detected in a plasmid in *Klebsiella pneumoniae* in France in 1969 (*1*,*4*).

However, an earlier report by Briggs and Fratamico (*5*) clearly established that the florfenicol resistance genes and the tetracycline resistance genes *tetG* and *tetR* in the *Salmonella* genomic island 1 (SGI1) were surrounded by non–antimicrobial-drug resistance DNA. This DNA is homologous to DNA sequences in plasmids PASPPFLO and pJA8122 (see Figure 1 and Table 2 in reference 5) (*5*–*7*). In addition to antimicrobial drug resistance genes, PASPPFLO and pJA8122 contain cloned DNA segments of indigenous R plasmids found in *V. damsela* and *V. anguillarum*, respectively; these cloned DNA segments span sequences that extend beyond their florfenicol resistance and *tetR*/*tetG* genes (*5*–*7*). For example, the region of the florfenicol resistance gene in SGI1 contains 763 nt of the non–antimicrobial-drug resistance portion of the original *V. damsela* plasmid; the region of *tetR*/*tetG* contains 468 nt of the non–antimicrobial-drug resistance DNA segment of the *P. piscicida* plasmid (*5*–*7*).

The presence of these non–antimicrobial-drug resistance R plasmid DNA sequences in SGI1 constitutes a molecular signature that firmly establishes the aquaculture origin of the florfenicol resistance and the *tetR*/*tetG* genes in the *S. enterica* serovar Typhimurium DT104 strain studied by Briggs and Fratamico and in the SGI1 of other bacteria (*5*). These R plasmid DNA sequences in SGI1 also confirm direct or indirect horizontal gene transfer between bacteria in the aquaculture environment and *S. enterica* serovar Typhimurium DT104 (*5*–*7*).

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In Response: In his letter (*1*), Cabello makes 2 observations regarding the debate concerning the origin of the *flo*R gene in *Salmonella enterica* serovar Typhimurium DT104. The first observation is that the plasmid PASPPFLO contained cloned segments of an indigenous *Vibrio damsela* plasmid. However, PASPPFLO is not the name of a plasmid but is the GenBank locus identifier associated with the sequence (GenBank accession no. D37826) of a 3,745-bp region of the *V. damsela* plasmid pSP92088 that contained pp-*flo* (*2*,*3*).

The second observation is that sequences flanking the *floR* gene in *S. enterica* serovar Typhimurium DT104 (GenBank accession no. AF071555) are homologous to those flanking the pp-*flo* gene sequenced from the *V. damsela* plasmid pSP92088 (*4*). On the basis of this homology, he seems

to assume that these flanking sequences must have originated in *V. damsela* and, therefore, that they constitute a molecular signature that firmly establishes the aquaculture origin of this florfenicol resistance. What Cabello does not mention is that sequences flanking a wide range of *floR* genes, including those in plasmid R55 (GenBank accession no. AF332662), are also homologous to those found in *S. enterica* serovar Typhimurium DT104 (*5*,*6*).

These data suggest that during horizontal transfer between species and genera, the association of *floR* with its flanking regions has been conserved (*5*,*6*). However, the data provide no evidence for postulating a unique association of these flanking sequences with *V. damsela*, and, therefore, do not provide evidence for an aquaculture origin of *floR*. If Cabello believes that sequences flanking *floR* in *S. enterica* serovar Typhimurium DT04 constitute a molecular signature that firmly establishes the aquaculture origin of *floR* in *S. enterica* serovar Typhimurium DT104, he should provide some explanation as to how this signature was also present in the R55 plasmid detected in a *Klebsiella pneumoniae* strain isolated in 1969 (*5*,*7*).

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