A tet(S/M) hybrid from CTn6000 and CTn916 recombination

We read with interest the article by Barile et al. (2012) which describes the first mosaic tet(S/M) gene encoding tetracycline resistance from foodborne strains of *Streptococcus bovis*. The mosaic tet genes described to date are hybrids of other ribosome protection type [tet(O), tet(32), tet(W)] which are particularly abundant among Firmicutes (*Lactobacillus, Bifidobacterium, Streptococcus, Clostridium*) isolated from animals (Stanton et al., 2005; Patterson et al., 2007; van Hoek et al., 2008; Palmieri et al., 2012). The origin and nomenclature of such genetically divergent mosaic tet genes remains controversial due to the lack of information about their genetic contexts and the identical size of the resulting proteins (Zheng et al., 2004, Stanton et al., 2005; Palmieri et al., 2012).

During an *in silico* analysis of the available genetic platforms containing the tet(S) gene (Novais et al., in press), we realized that the tet(S) allele located within the previously published CTn916S, identified in a *Streptococcus intermedius* human isolate (Lancaster et al., 2004; GenBank accession no. AY534326.1), is in fact a mosaic tet(S/M). When comparing Tet(S/M) sequences from *S. intermedius* (AY534326.1) with that of *S. bovis* described by Barile et al. (2012) different hybrids were observed. The Tet(S/M) from *S. intermedius* was mainly composed of Tet(S) [595 aa of Tet(S) versus 61 aa of Tet(M)] while most of the sequence from *S. bovis* corresponds to Tet(M) [611 aa of Tet(M) versus 33 aa of Tet(S)]. The analysis of the available genetic contexts of these two tet(S/M) genes, hybrids of tet genes of ribosomal protection type, also indicates that different rearrangements have occurred between orf13-orf12-tet(M)-orf6 and orf13-tet(S)-orf6 regions of genetic platforms related to CTn916 [tet(M)] and CTn6000 [tet(S)], respectively, as represented in Fig. 1.

The description of hybrid genes remains low or anecdotal despite different reports demonstrating that mosaic alleles are readily and continually generated in bacteria, often conferring new phenotypes (Mazel & Davies, 1999; Zheng et al., 2004). Transformable micro-organisms are preferential hosts for the acquisition of foreign DNA (Domingues et al., 2012; Mazel & Davies, 1999) and, thus, for generating recombinant platforms and genes between divergent sequences, as reflected in the bacterial species from which tet hybrids used to be recovered, namely from the genus *Streptococcus* (Kazimierczak et al., 2008; Palmieri et al., 2012; Barile et al., 2012). The genes reported by Barile et al. (2012) and us are the two unique tet(S/M) hybrids described to date and correspond to different recombinaltory events involving Tn916 and Tn6000 which are widely disseminated among different genera of the phylum Firmicutes (Novais et al., in press; Roberts & Mullany, 2009). The analysis and comprehensive characterization of hybrid genes is of interest for not only identifying new adaptive phenotypes (Stanton et al., 2004; Patterson et al., 2007) but also determining the dynamics of mobile genetic elements and antibiotic resistance genes among bacterial species and their genetic exchange communities (Skippenston & Ragan, 2011), as suggested by our findings, those of Barile et al. (2012) and another recent report (Palmieri et al., 2012).

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Agnès Fouet, Editor-in-Chief
Fig. 1. Schematic representation of Tn916, Tn6000 and mosaic platforms containing tet(S/M) alleles. The hybrids are (i) a platform from *Streptococcus intermedius* previously described as Tn916S and (ii) a platform from *Streptococcus bovis* described by Barile et al. (2012). *Homology with CTn916 or CTn6000 is $\geq 99\%$. **In GenBank, *S. bovis* is identified as *Streptococcus equinus*.


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