chromosomally. However, one of the conserved systems on the *Staph. aureus* chromosome is located between genes that encode a putative ABC transporter and glycerate kinase, whereas the system in *L. monocytogenes* is downstream of a gene encoding a glycosyl hydrolase. The common carriage of Fst-like TA systems on resistance plasmids in particular is potentially significant in terms of the maintenance of antimicrobial resistance in important Gram-positive pathogens.

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Prevalence of Fst-like toxin–antitoxin systems – author's response

The work of Kwong, Jensen and Firth (above) dramatically expands the pAD1 *par*-like family of RNA-regulated toxin–antitoxin (TA) systems described in our recent study (Weaver *et al.*, 2009). While the primary sequences of these systems are highly diverse, important interacting and regulatory structures are clearly conserved. These results would appear to contradict an earlier report indicating that, while several proteic TA systems are widespread among enterococci, *par*-like sequences are rare (Moritz & Hergenrother, 2007). However, given the sequence diversity of the *par*-like systems identified, it is not surprising that the PCR-based screening approach used by Moritz & Hergenrother (2007) failed to amplify any of the *par*-like loci. This information should be considered in future surveys designed to

determine the distribution of other type I TA systems.

Our work and that described above should also be viewed in the larger context of RNA-regulated, probably membrane-localized, small peptide toxins, which were originally reviewed by Fozo *et al.* (2008). While the number of Gram-positive representatives in their sample was limited, it is now clear that such peptides are widespread in Gram-positive bacteria and are likely to play roles at least as important as their counterparts in Gram-negative bacteria. Finally, while most of the *par*-like loci appear to be associated with mobile elements, the association of some of the chromosomally located loci with genes involved in basic carbon metabolism is intriguing. Since the function of many chromosomally encoded TA systems has been elusive and controversial, it would be worth determining if regulation of these elements is integrated with basic cellular metabolism.

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