

MS02 Infection and Disease/hot structures

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Structural and Functional Characterization of TraA, the Relaxase a Gram-positive Type IV Secretion System (T4SS)
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Abstract

The occurrence of multi-resistant strains among pathogenic bacteria, in particular those causing nosocomial infections, is one of the most pressing problems of our health system. Bacterial conjugation is one important route of DNA transfer between bacteria and mediates the rapid spread of bacterial resistances within bacterial communities. Type IV secretion systems (T4SS) are responsible for the efficient transport of nicked, single-stranded plasmid DNA across the cell walls of the donor as well as the recipient cell (1). The T4SS from the antibiotic resistance plasmid pIP501, occurring in *Enterococci* and related Gram-positive bacteria, is encoded within a single operon comprised of 15 putative transfer factors. The 1st open reading frame encodes TraA, a relaxase, which causes a single-strand DNA cleavage at the *nic* site of the origin of transfer, *oriT*, of plasmid pIP501 and initiates the transfer of the nicked DNA strand. Here we present the crystal structure of the N-terminal domain comprising the relaxase activity, which shows structural homology with NES, the nicking enzyme in *S. aureus*. (2) The solution structure of both the N-terminal domain and full-length TraA are investigated by SAXS and CD spectroscopy methods.

References

- (1) Alvarez-Martinez CE, and Christie PJ (2009) Biological diversity of prokaryotic type IV secretion systems. *Microbiol Mol Biol Rev* 73, 775-808.
- (2) Edwards JS, et al. (2013) Molecular basis of antibiotic multiresistance transfer in *Staphylococcus aureus*. *Proc Natl Acad Sci U S A* 110, 2804-2809.