PublisherInfo		
PublisherName	:	BioMed Central
PublisherLocation	:	London
PublisherImprintName	:	BioMed Central

Bacterial virulence determinants

ArticleInfo		
ArticleID	:	3666
ArticleDOI	:	10.1186/gb-2000-1-6-reports0077
ArticleCitationID	:	reports0077
ArticleSequenceNumber	:	16
ArticleCategory	:	Paper report
ArticleFirstPage	:	1
ArticleLastPage	:	4
ArticleHistory	:	RegistrationDate : 2000–10–24 Received : 2000–10–24 OnlineDate : 2000–11–26
ArticleCopyright	:	BioMed Central Ltd2000
ArticleGrants	:	

ArticleContext	:	130591166

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Abstract

A third type III secretion system involved in virulence in *Yersinia enterocolitica* has been identified.

Significance and context

The three pathogenic *Yersinia* species possess a large plasmid which is essential for their virulence. The plasmid encodes a protein secretion system (the type III system) which is involved in the secretion of 14 virulence proteins. Type III secretion systems (TTSS) are also present in numerous other animal and plant pathogenic bacteria (and in some rhizobia). The components of the secretion machinery are highly conserved and have some similarity to proteins involved in flagellum biosynthesis, from which they are thought to have evolved. The virulence proteins secreted by the *Yersinia* TTSS are secreted into eukaryotic (host) cells and disrupt a variety of cellular processes, thus causing disease. A number of chromosomal factors important for virulence have also been identified; these, in part, determine the differences in the diseases caused by each species. The flagellum biosynthetic type III machinery has also been shown to be capable of secreting virulence factors in *Y. enterocolitica*. Haller *et al.* describe the identification of a third type III secretion system in *Y. enterocolitica*. It is chromosomally encoded, is capable of secreting proteins, and has a role in virulence.

Key results

A chromosomal library of a *Y. enterocolitica* strain lacking a virulence plasmid (pYV) was screened for conserved TTSS components. From this, 15 open reading frames (ORFs) were identified with homology to TTSS components. Two ORFs with homology to transcriptional regulators of the two-component sensor-regulator family were also detected. A mutation was generated within a chromosomal gene encoding a putative TTSS component to aid the identification of any secreted proteins and to determine what conditions bring about secretion. Tests showed that the chromosomally encoded secretion system could be induced at low temperatures and could bring about the secretion of proteins independently of the plasmid-mediated secretion system.The chromosomal TTSS mutant was also tested for motility. Its motility was unaffected, and thus the chromosomal TTSS and flagellar TTSS appear to be distinct. Sequences from the chromosomal TTSS hybridized to chromosomal DNA from other (pathogenic and non-pathogenic) *Yersinia* species; the sequence was also compared with data from the

unfinished *Y. pestis* genome project and homologous sequences were found. Other *Yersinia* species (including *Y. pestis*, the cause of plague) might therefore contain chromosomal TTSS. The effects of the chromosomal TTSS on virulence were also tested. Mice were inoculated orally and intraperitoneally with the wild type or the chromosomal TTSS mutant, and the LD_{50} (lethal dose) determined. The mutant had a tenfold lower LD_{50} (compared with wild type) when inoculated orally, but there was no difference in LD_{50} values after intraperitoneal inoculation.

Links

Data from the *Yersinia pestis* genome sequencing project is available from the Sanger Centre website.

Conclusions

The chromosomal TTSS identified is responsible for the independent secretion of at least eight proteins. The induction of the system at low temperatures and the effect on virulence after oral inoculation (compared with the lack of effect after intraperitoneal inoculation) suggest a role for this system in the initial stages of infection.

Reporter's comments

The use of reporter gene constructs *in vivo* would be a nice experiment to determine at which stage of infection the chromosomal TTSS is induced, and if this fits with the proposed model. The identification of the secreted proteins will be very interesting. The authors describe a gene homologous to an effector protein from *Salmonella* which is located proximal to the chromosomal TTSS and which must be a potential candidate for the gene for one of the secreted proteins.

Table of links

Molecular Microbiology

Yersinia pestis

Sanger Centre

References

1. Haller JC, Carlson S, Pederson KJ, Pierson DE: A chromosomally encoded type III secretion pathway in *Yersinia enterocolitica* is important in virulence. Mol Microbiol. 2000, 36: 1436-1446. 0950-382X