

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

Lining-up Listeria genomes

ArticleInfo		
ArticleID	:	4236
ArticleDOI	:	10.1186/gb-spotlight-20011026-01
ArticleCitationID	:	spotlight-20011026-01
ArticleSequenceNumber	:	307
ArticleCategory	:	Research news
ArticleFirstPage	:	1
ArticleLastPage	:	2
ArticleHistory	:	RegistrationDate : 2001-10-26 OnlineDate : 2001-10-26
ArticleCopyright	:	BioMed Central Ltd2001
ArticleGrants	:	
ArticleContext	:	130592211

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Listeriosis is caused by the ingestion of pathogenic *Listeria monocytogenes* in contaminated food. In the October 26 [Science](#), Glaser *et al.* report a comparative analysis of *Listeria* genomes aimed at identifying virulence genes (*Science* 2001, **294**:849-852). They sequenced the genomes of two *Listeria* strains; pathogenic *L. monocytogenes* EGD-e and a non-virulent species *L. innocua*. *L. monocytogenes* contains a single circular chromosome of 2.9 Mb, while *L. innocua* has a 3 Mb chromosome and an 80 kb plasmid. The two genomes encode similar numbers of genes: almost 3000 open reading frames, of which a third code for proteins with no known, or predicted, function. The two genomes encode large numbers of putative surface proteins, transport proteins and transcriptional regulators. Many of these are likely to account for virulence and for the adaptability of *Listeria* species to diverse environmental conditions. Glaser *et al.* identified hundreds of strain-specific genes, which are clustered in islets. They conclude that their study "opens new avenues for post-genomic analysis of the life-styles of *L. monocytogenes* in the environment and the infected host."

References

1. *Listeria* pathogenesis and molecular virulence determinants.
2. *Science*, [<http://www.sciencemag.org>]