

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

The Staphylococcus aureus genome

ArticleInfo		
ArticleID	:	4060
ArticleDOI	:	10.1186/gb-spotlight-20010423-03
ArticleCitationID	:	spotlight-20010423-03
ArticleSequenceNumber	:	131
ArticleCategory	:	Research news
ArticleFirstPage	:	1
ArticleLastPage	:	2
ArticleHistory	:	RegistrationDate : 2001-04-23 OnlineDate : 2001-04-23
ArticleCopyright	:	BioMed Central Ltd2001
ArticleGrants	:	
ArticleContext	:	130592211

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Following the recent publication of the *Streptococcus pyogenes* genome, Makoto Kuroda and colleagues at Juntendo University, Tokyo, have published the entire genome of another medically important pathogenic bacterium, *Staphylococcus aureus* in the 21 April issue of *Lancet*. *S. aureus* is a gram-positive bacterium carried by about 30% of the healthy human population. But in hospitalized patients it is the major cause of severe hospital-acquired infections, with some strains now resistant to the most powerful antibiotics available.

Kuroda *et al.* used random shot-gun sequencing to determine the genome of two related *S. aureus* strains (N315, which is methicillin resistant, and Mu50, vancomycin resistant). They found an elaborate combination of genes, many seemingly acquired by lateral gene transfer, demonstrating a remarkable ability to acquire potentially useful genes from a variety of organisms. Their findings include:

- 70 candidates for new virulence factors;
- antibiotic resistance genes carried either by plasmids or by mobile genetic elements including a unique resistance island;
- three separate new pathogenicity island families for toxic-shock-syndrome toxin, exotoxin and enterotoxin;
- clusters of exotoxin and enterotoxin genes closely linked with other gene clusters encoding putative pathogenic factors;
- a repeated duplication of genes encoding superantigens, explaining the ability of *S. aureus* to infect people of diverse genetic backgrounds and elicit severe immune reactions.

Careful investigation of the newly identified gene products will improve our understanding of the biology of staphylococci and may help in the fight against these life-threatening organisms.

References

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