

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

Cross-species transfer is last straw

ArticleInfo		
ArticleID	:	4888
ArticleDOI	:	10.1186/gb-spotlight-20031128-01
ArticleCitationID	:	spotlight-20031128-01
ArticleSequenceNumber	:	240
ArticleCategory	:	Research news
ArticleFirstPage	:	1
ArticleLastPage	:	2
ArticleHistory	:	RegistrationDate : 2003-11-28 OnlineDate : 2003-11-28
ArticleCopyright	:	BioMed Central Ltd2003
ArticleGrants	:	
ArticleContext	:	130594411

Cathy Holding

Email: cholding@hgmp.mrc.ac.uk

In June 2002, a strain of *Staphylococcus aureus*, resistant to the last remaining antibiotic against the methicillin-resistant *S. aureus* (MRSA), was isolated from a dialysis patient in Michigan. The vancomycin-resistant *S. aureus* (VRSA) strain was the subject of genetic analysis by Linda Weigel and colleagues at the [Centers for Disease Control and Prevention](#), and their conclusions are reported in the November 28 [Science](#). The drug resistant strain harbored a 57.9 kb multiresistance, conjugative plasmid with vancomycin resistance encoded in an integrated mobile genetic element, Tn1546, first reported in an isolate of *Enterococcus faecium*, and here identified in a co-isolate of *Enterococcus faecalis* (*Science* 2003, **302**:1569-1571).

Weigel *et al.* confirmed the identity as *S. aureus* by sequence analysis of specific genes *gyrA* and *gyrB* and rDNA and ruled out contamination with enterococci by the inability to amplify enterococcal ligases by polymerase chain reaction. Pulse field analysis confirmed the VRSA to be type USA100 - the most common type in US hospitals. Minimal inhibitory concentration was determined to be 1024 µg/ml for vancomycin, and resistance to aminoglycosides, β-lactams, fluoroquinolones, macrolides, rifampin, and tetracycline showed that it had retained its MRSA phenotype. Vancomycin resistance was observed to be conferred by *vanA*, one of several gene clusters found in *Enterococcus faecium*. Analysis of plasmids from the VRSA and *E. faecalis* co-isolates identified two plasmids, 45 and 95 kb long, and Southern blot analysis revealed a 7.1-kb fragment containing *vanA*. Filter mating studies identified the resistance plasmid as conjugative. The complete sequence has been placed in [GenBank](#).

"Genetic analyses suggest that the long-anticipated transfer of vancomycin resistance to a methicillin-resistant *S. aureus* occurred *in vivo* by interspecies transfer on Tn1546 from a co-isolate of *Enterococcus faecalis*. The VRSA plasmid was transferable to other strains of *S. aureus*, reinforcing concerns of potential widespread resistance to one of the few classes of agents still active against multidrug-resistant *S. aureus*," conclude the authors.

References

1. Vancomycin-resistant *Staphylococcus aureus*: a new model of antibiotic resistance
2. Centers for Disease Control and Prevention, [<http://www.cdc.gov/>]
3. *Science*, [<http://www.sciencemag.org/>]
4. GenBank, [<http://www.ncbi.nlm.nih.gov/Genbank/index.html>]