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## Comparing *Enterococcus* genomes

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Jonathan B Weitzman

Email: jonathanweitzman@hotmail.com

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Enterococci form part of our natural intestinal flora, but also cause antibiotic-resistant infections in hospitals. In the June 13 *Nature*, Shankar *et al.* describe an analysis of different *Enterococcus faecalis* strains, one from a hospital ward outbreak in the mid-1980s, MMH594, and the other from the first vancomycin-resistant isolate, V583 (*Nature* 2002, **417**:746-750). Genomic comparisons revealed that the V583 isolate lacks a 17 kb region containing virulence genes, such as the cytolysin operon. Further comparison with the sequence of the non-infection-derived OG1 strain showed that the clinical isolates have a genomic insertion of around 150 kb. This element contains over one hundred genes encoding transposases, transcriptional regulators and virulence-associated proteins. The characterization of this novel pathogenicity island should be of benefit for diagnosis and for the identification of new drug targets.

## References

1. *Nature* , [<http://www.nature.com>]
2. Multiple-drug resistant enterococci: the nature of the problem and an agenda for the future.
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