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Occurrence of *vanB* vancomycin resistant enterococci (VRE) in a patient

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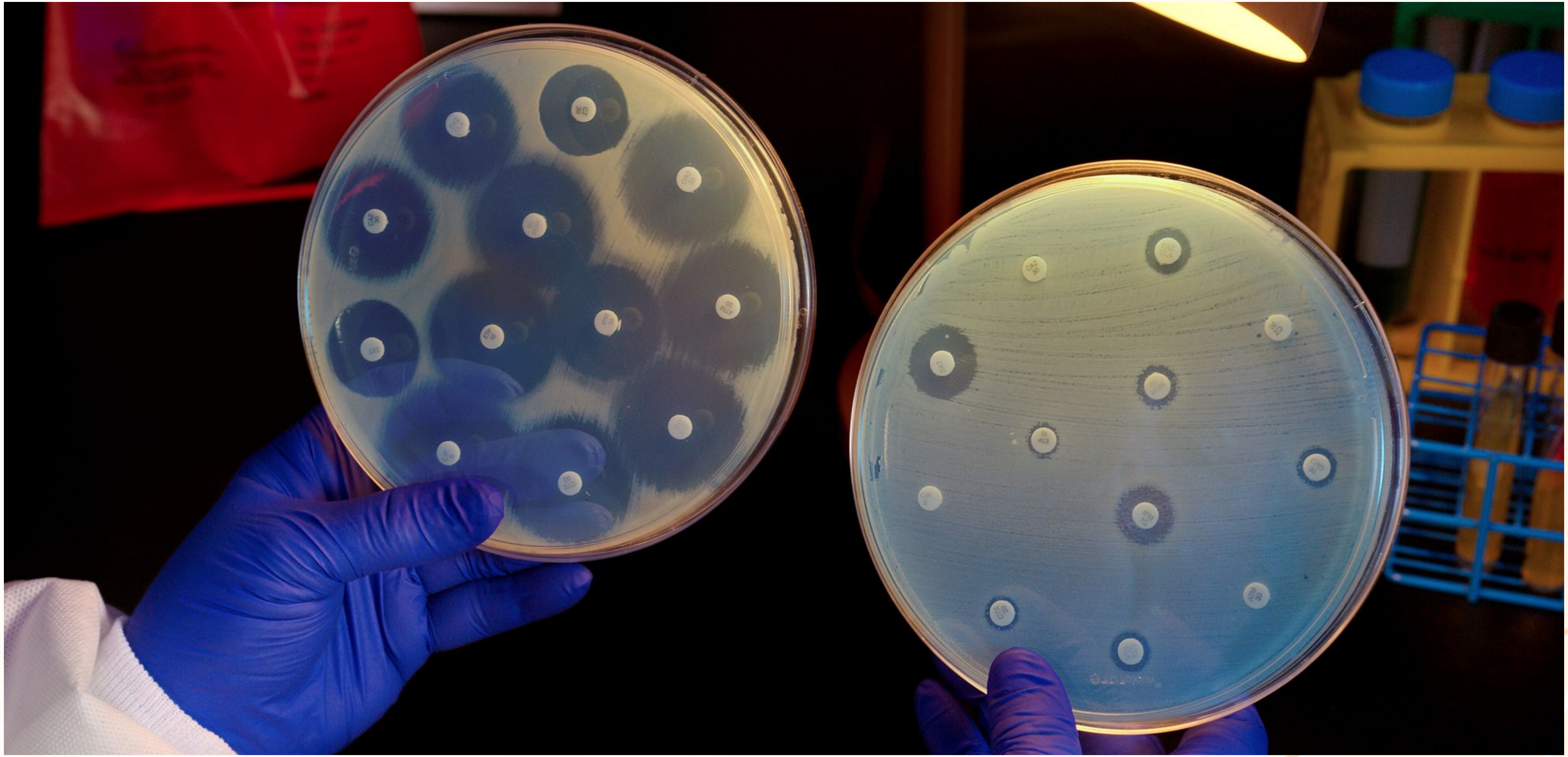
University of Tromsø – The arctic university of Norway
24.04.2017

Antibiotic susceptibility



Enterococcus faecium

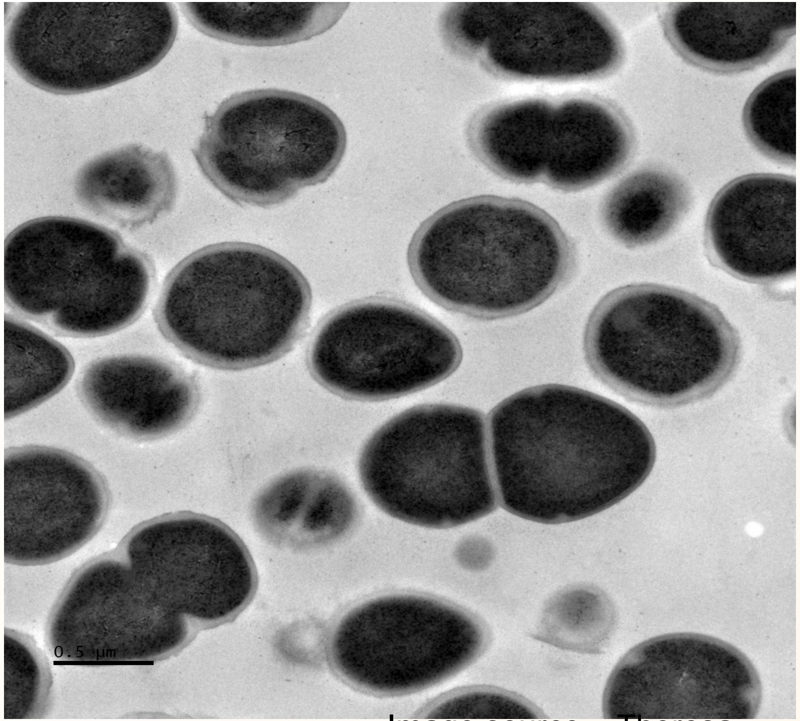
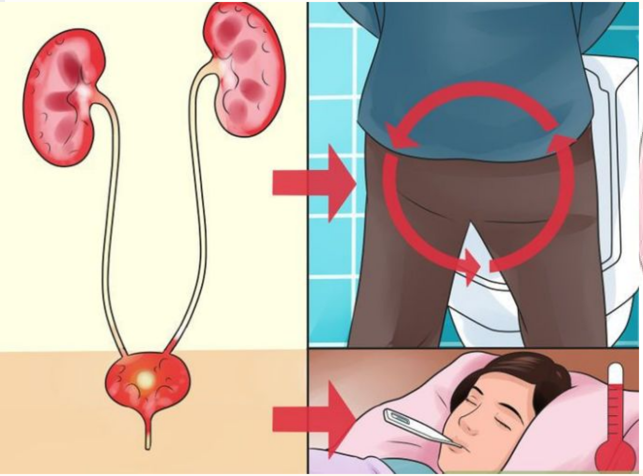
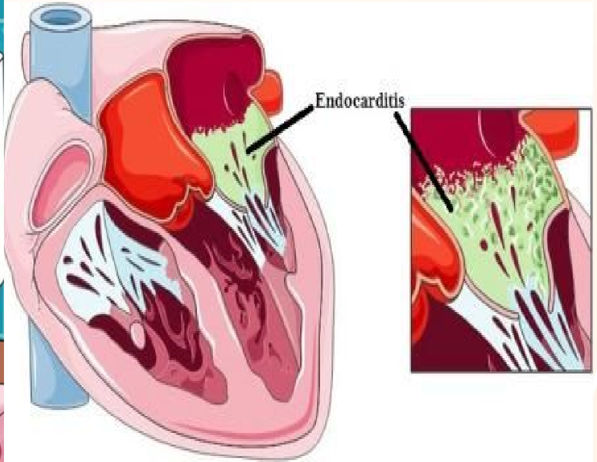


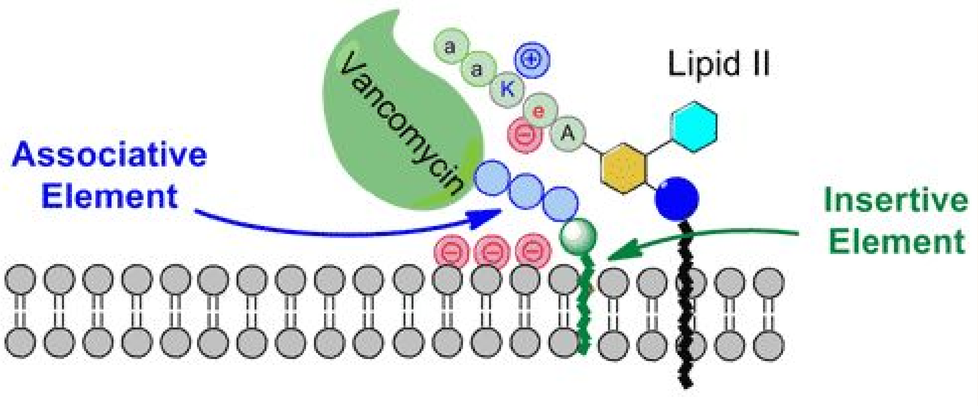
Image source – Theresa Wagner

E. faecium infections





Treatment for *E. faecium* infections



Cytoplasmic membrane of Gram-positive bacteria

Vancomycin Resistance *Enterococcus* - VRE

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doi:10.1093/jac/dks469 Advance Access publication 2 December 2012

Journal of Antimicrobial Chemotherapy

Twenty-five years of shared life with vancomycin-resistant enterococci: is it time to divorce?

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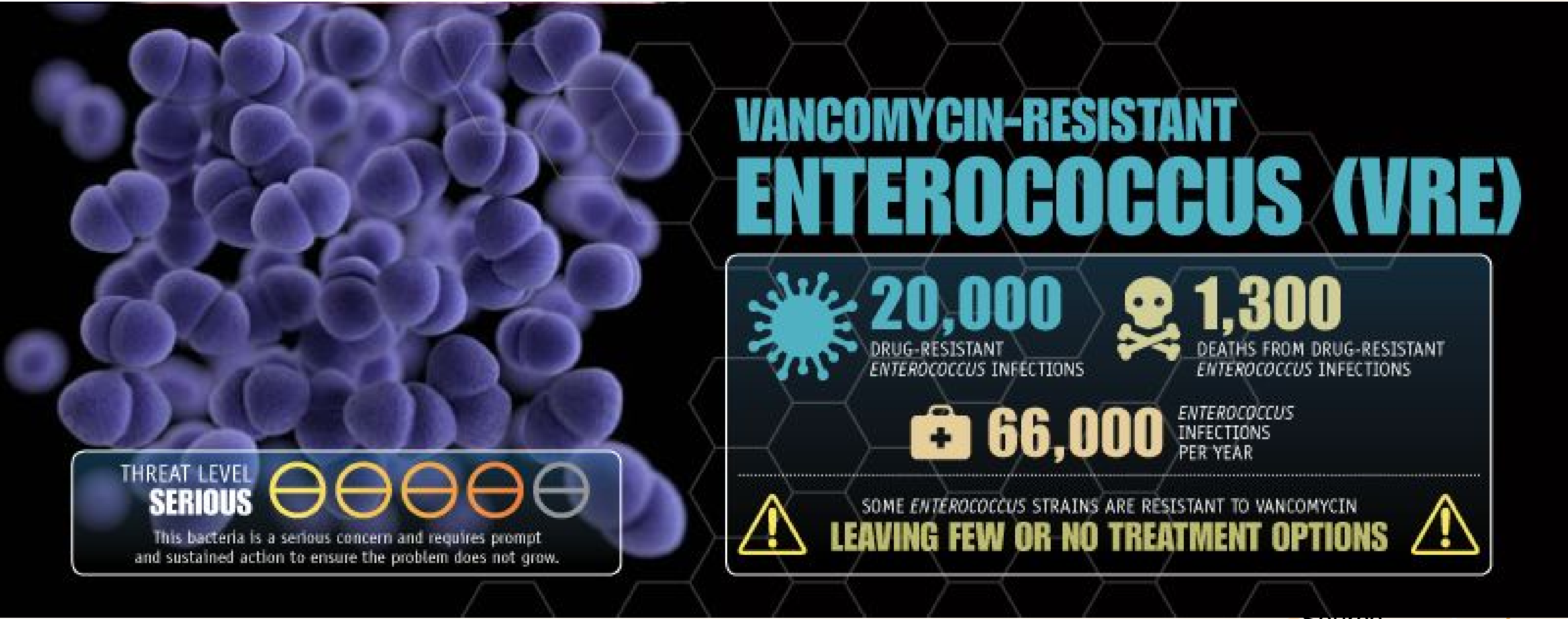
Vancomycin Resistance *Enterococcus* - VRE



VANCOMYCIN-RESISTANT
ENTEROCOCCUS (VRE)

20,000
DRUG-RESISTANT *ENTEROCOCCUS* INFECTIONS

1,300
DEATHS FROM DRUG-RESISTANT *ENTEROCOCCUS* INFECTIONS

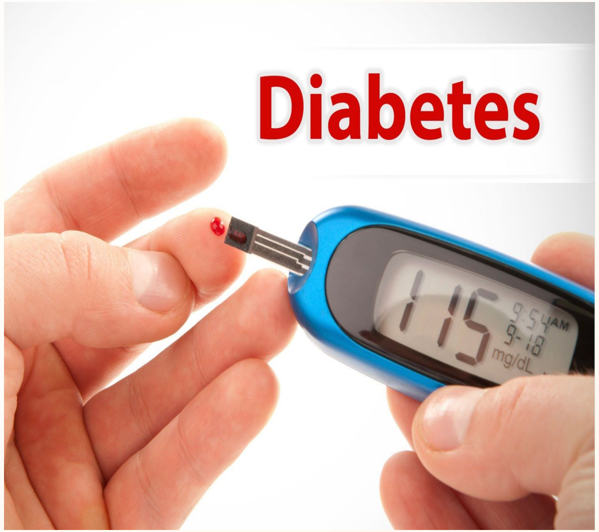
66,000
ENTEROCOCCUS INFECTIONS PER YEAR

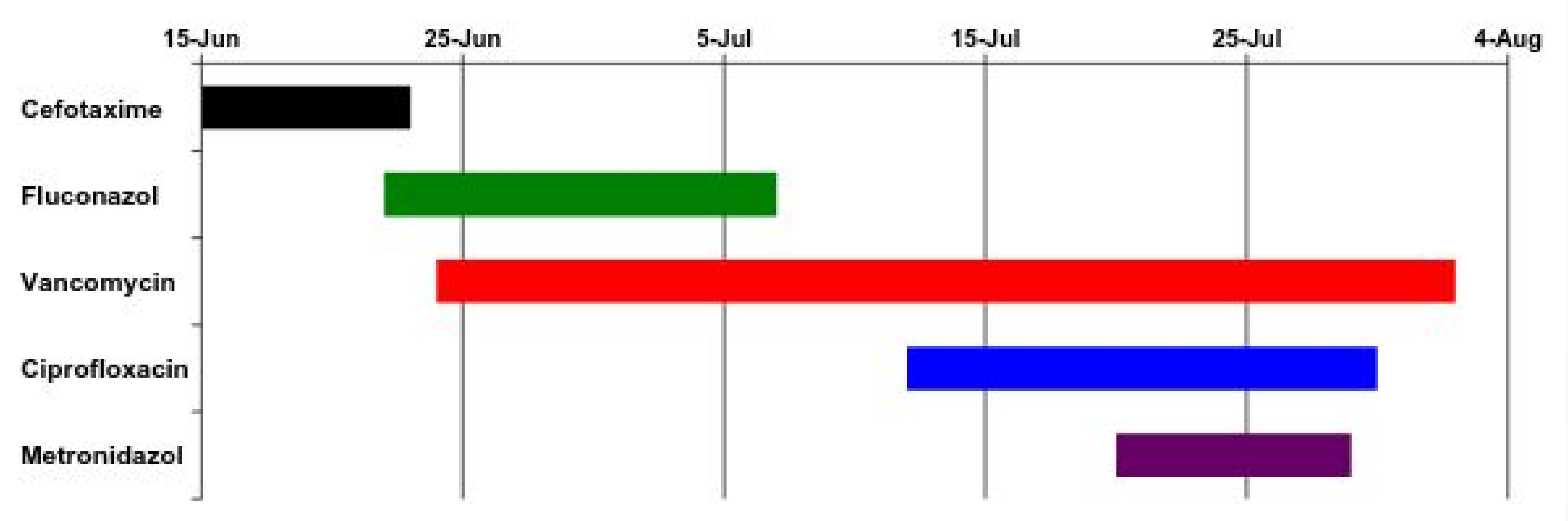
SOME *ENTEROCOCCUS* STRAINS ARE RESISTANT TO VANCOMYCIN
LEAVING FEW OR NO TREATMENT OPTIONS

THREAT LEVEL
SERIOUS
This bacteria is a serious concern and requires prompt and sustained action to ensure the problem does not grow.

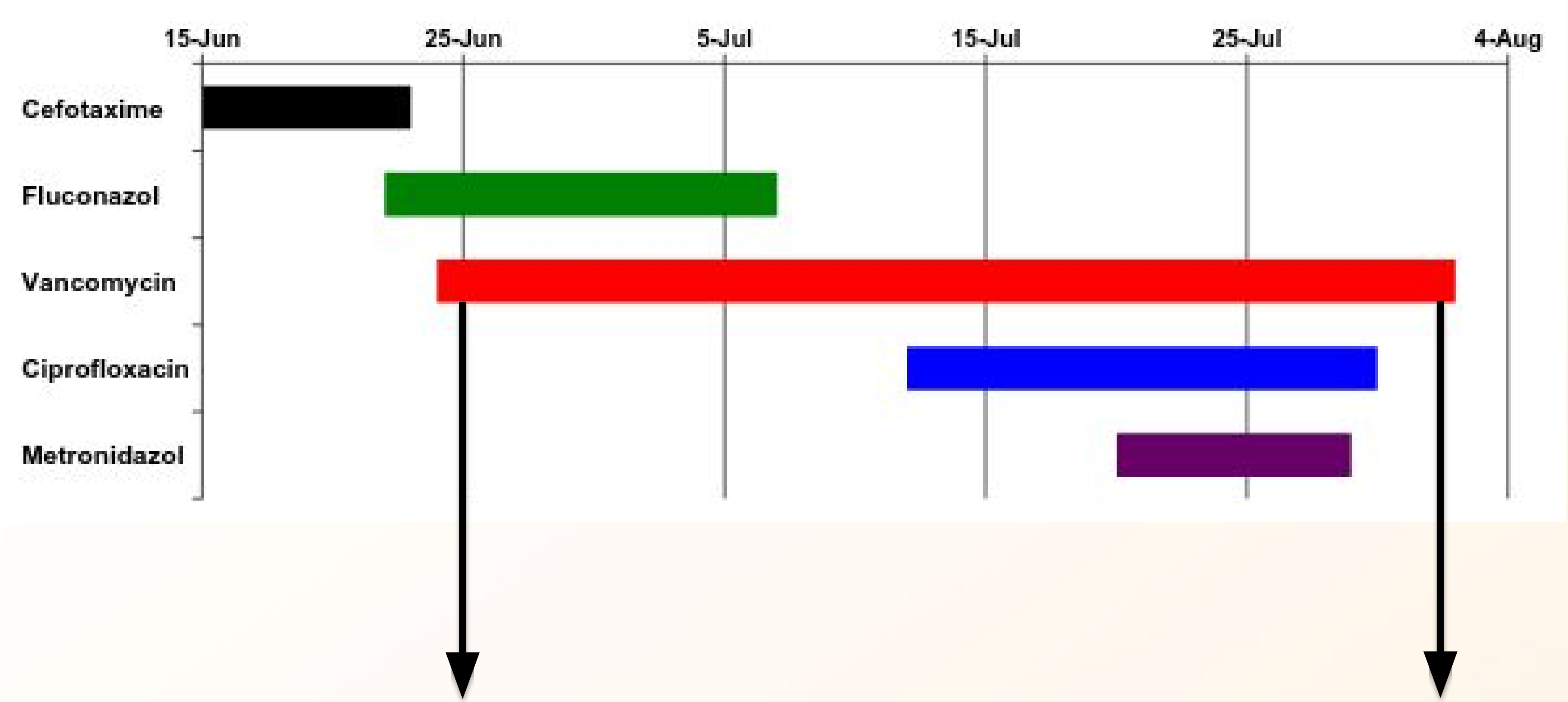
Source – CDC

Case background





- ⬛ Ventilator-associated pneumonia
- 🟩 *Candida albicans* septicemia
- 🟥 *Enterococcus faecium* septicemia
- 🟦 *Acinetobacter* sp. and *Enterobacter* sp. wound infections
- 🟪 Bacteriodes sp. wound infections

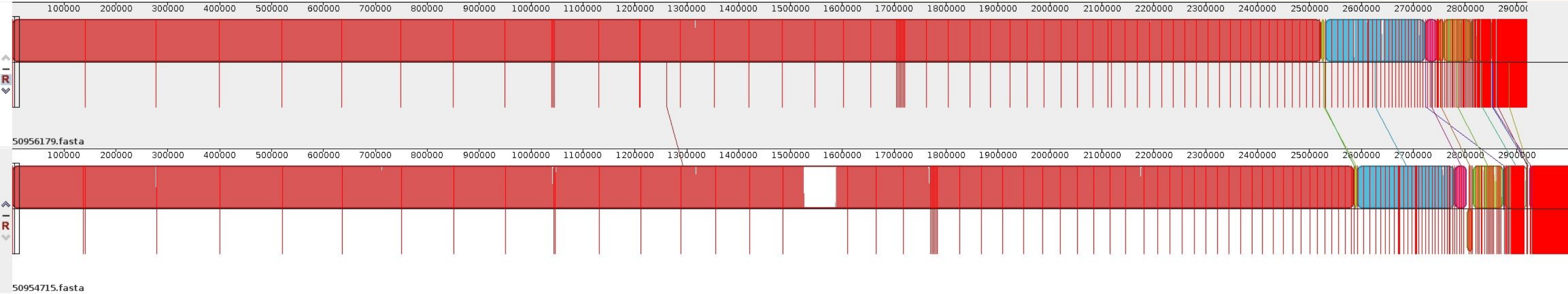


Van $^{\text{Susceptible}}$

Van $^{\text{Resistant}}$

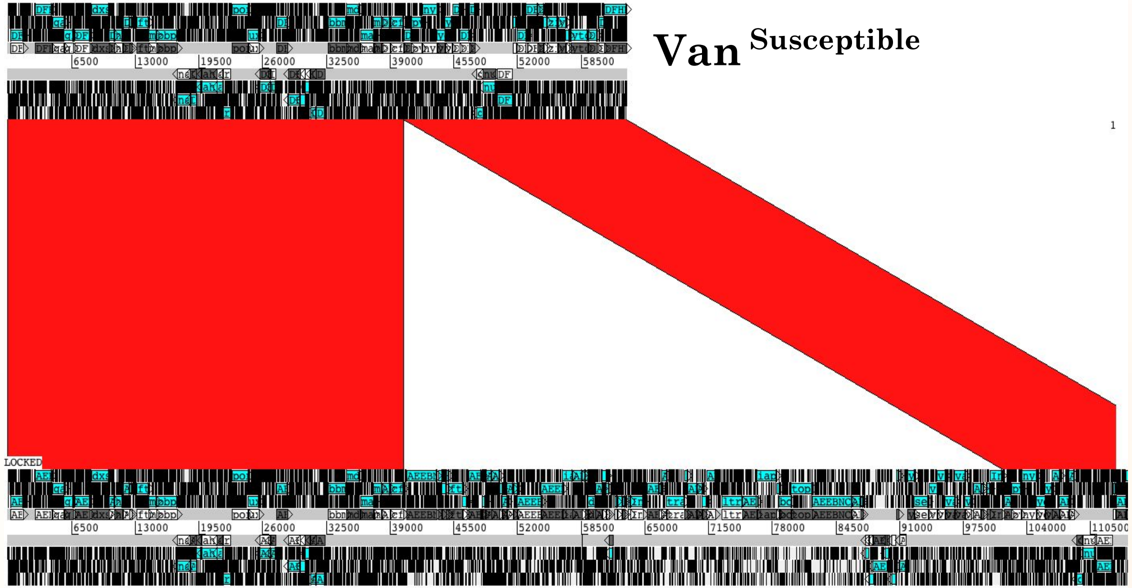
Comparison – whole genome

Van Susceptible



Van Resistant

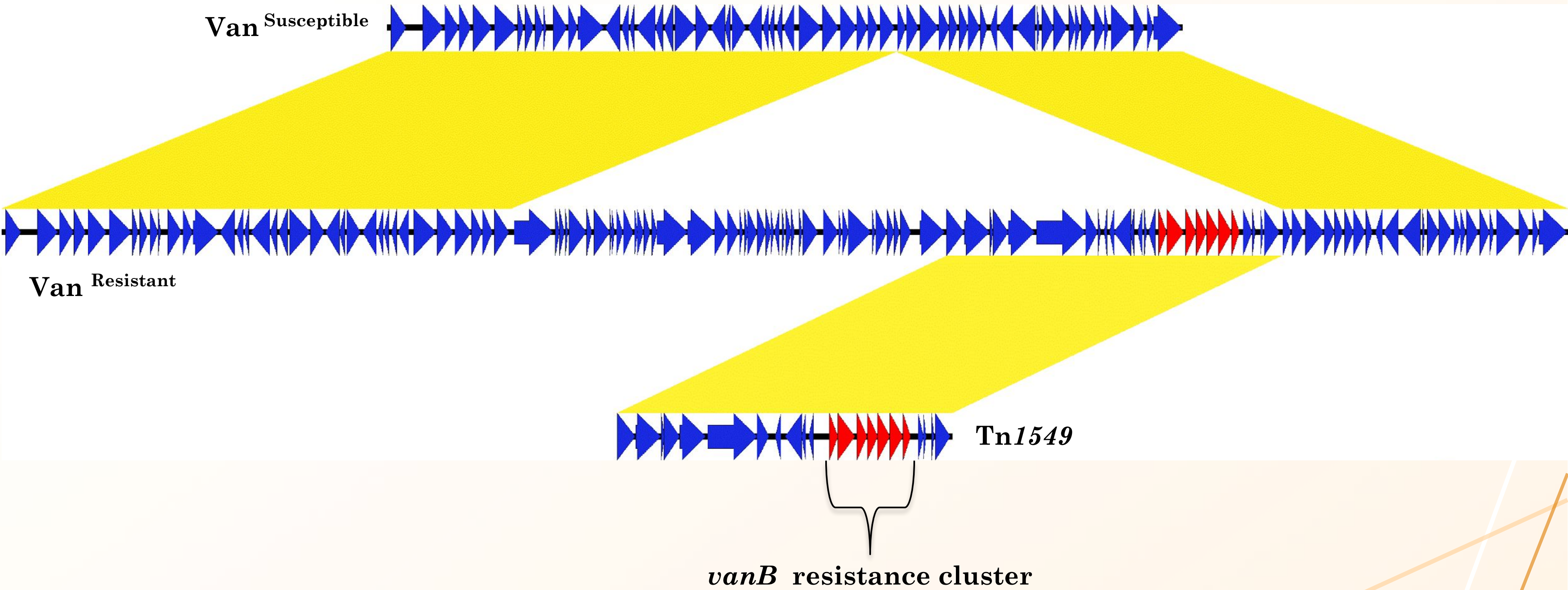
Comparison



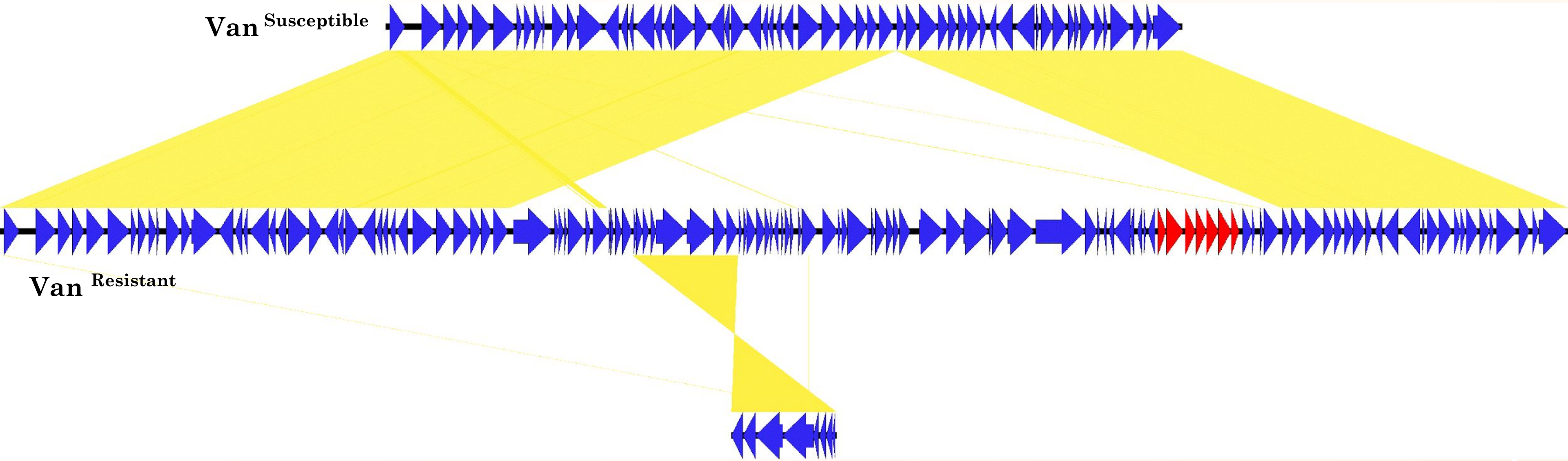
Van Susceptible

Van Resistant

Comparison against bacterial genomes



Comparison against bacterial genomes

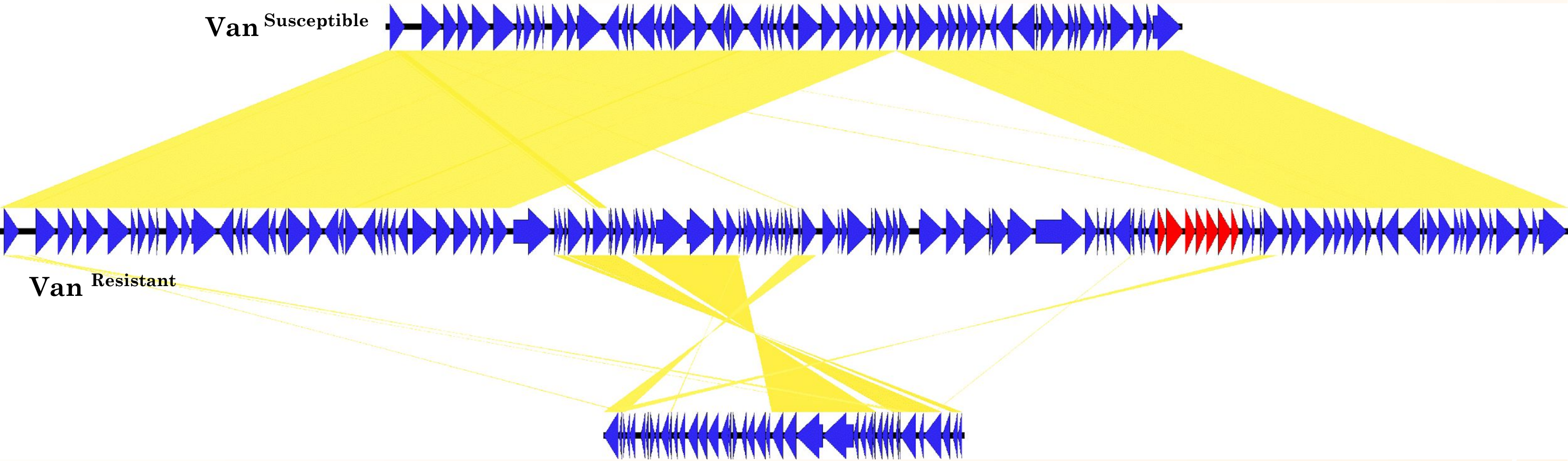


Van Susceptible

Van Resistant

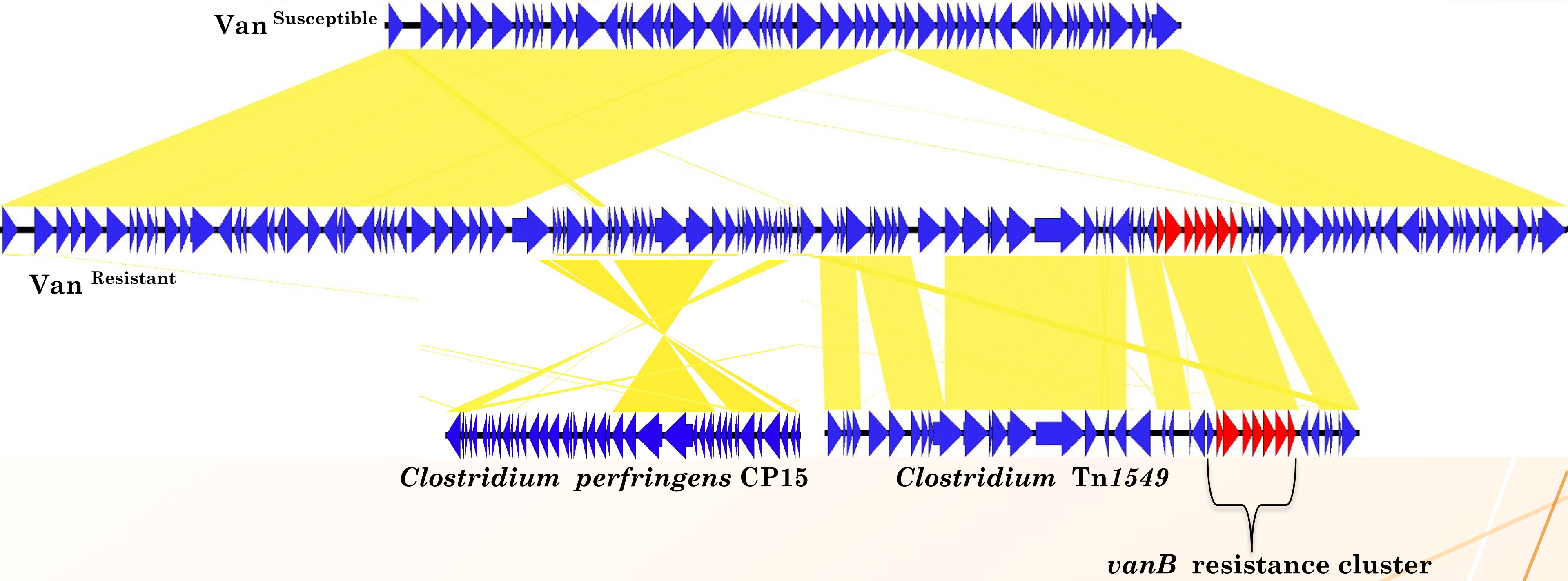
Eubacterium sp. Marseille-P3177

Comparison against bacterial genomes

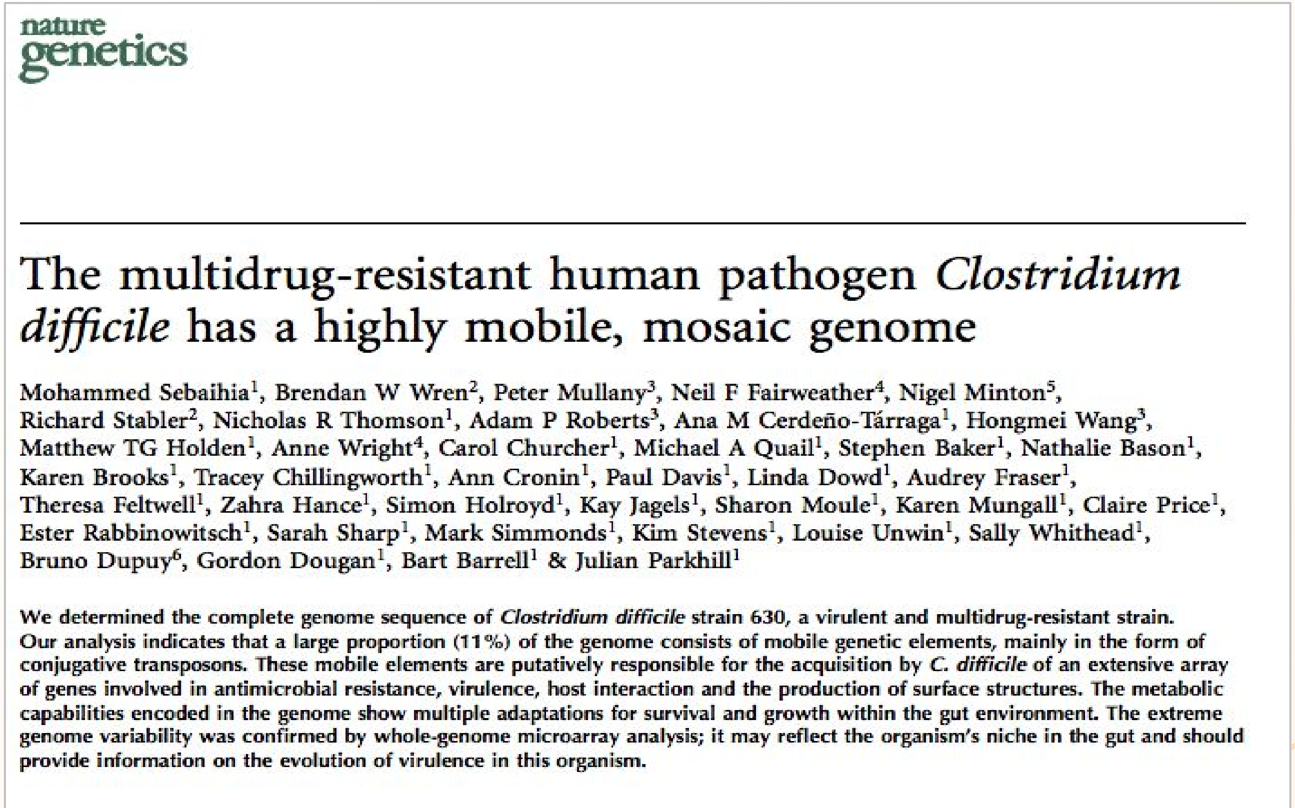


Clostridium perfringens CP15

Comparison against bacterial genomes



Gene transfer



nature genetics

The multidrug-resistant human pathogen *Clostridium difficile* has a highly mobile, mosaic genome

Mohammed Sebaihia[1], Brendan W Wren[2], Peter Mullany[3], Neil F Fairweather[4], Nigel Minton[5], Richard Stabler[2], Nicholas R Thomson[1], Adam P Roberts[3], Ana M Cerdeño-Tárraga[1], Hongmei Wang[3], Matthew TG Holden[1], Anne Wright[4], Carol Churcher[1], Michael A Quail[1], Stephen Baker[1], Nathalie Bason[1], Karen Brooks[1], Tracey Chillingworth[1], Ann Cronin[1], Paul Davis[1], Linda Dowd[1], Audrey Fraser[1], Theresa Feltwell[1], Zahra Hance[1], Simon Holroyd[1], Kay Jagels[1], Sharon Moule[1], Karen Mungall[1], Claire Price[1], Ester Rabbinowitsch[1], Sarah Sharp[1], Mark Simmonds[1], Kim Stevens[1], Louise Unwin[1], Sally Whithead[1], Bruno Dupuy[6], Gordon Dougan[1], Bart Barrell[1] & Julian Parkhill[1]

We determined the complete genome sequence of *Clostridium difficile* strain 630, a virulent and multidrug-resistant strain. Our analysis indicates that a large proportion (11%) of the genome consists of mobile genetic elements, mainly in the form of conjugative transposons. These mobile elements are putatively responsible for the acquisition by *C. difficile* of an extensive array of genes involved in antimicrobial resistance, virulence, host interaction and the production of surface structures. The metabolic capabilities encoded in the genome show multiple adaptations for survival and growth within the gut environment. The extreme genome variability was confirmed by whole-genome microarray analysis; it may reflect the organism's niche in the gut and should provide information on the evolution of virulence in this organism.

Gene transfer

Antimicrobial Agents and Chemotherapy

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Antimicrob Agents Chemother. 2006 Mar; 50(3): 1054–1062. PMCID: PMC1426432
doi: 10.1128/AAC.50.3.1054-1062.2006

Transfer of Vancomycin Resistance Transposon Tn*1549* from *Clostridium symbiosum* to *Enterococcus* spp. in the Gut of Gnotobiotic Mice

Aline Launay,[1] Susan A. Ballard,[2] Paul D. R. Johnson,[2] M. Lindsay Grayson,[2] and Thierry Lambert[1,*]

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HELSE NORD

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WE CARE – AND SHARE RESPONSIBILITY TOGETHER

UNN

BLAST result

Functions of the genes in this regions

- Hypothetical protein – 50
- Van genes
- DNA translocase FtsK
- putative endopeptidase p60
- **Daunorubicin/doxorubicin** resistance ATP-binding protein DrrA
- Conjugal transfer protein TraG
- Group II intron-encoded protein LtrA
- putative endopeptidase p60
- **Bacteriocin BCN5**
- DNA topoisomerase 3
- putative transcriptional regulatory protein YedW
- Signal-transduction histidine kinase senX3
- D-alanyl-D-alanine carboxypeptidase
- D-specific alpha-keto acid dehydrogenase
- D-alanyl-D-alanine dipeptidase
- Transposase from transposon Tn916