

Title In-depth analysis of an obligate anaerobe *Paraclostridium bifermentans* isolated from uterus of *Bubalus bubalis*

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Table S1. Predicted genes from the whole genome with different gene-finding tools.

| Program | No. of genes predicted |
|-----------------------|------------------------|
| Prodigal | 3495 |
| Glimmer-3 | 3521 |
| GenemarkS+2 | 3,511 |
| MetaGeneAnn otator | 3456 |

Table S2. Genome annotation results with different platforms.

| Feature | PROKKA | RAST | DFAST | PGAP (NCBI) |
|----------|--------|------|-------|----------------|
| Genes | 3449 | 3521 | 3456 | 3511 |
| rRNAs | 5 | 6 | 1 | 3 |
| tRNAs | 55 | 54 | 36 | 55 |
| CRISPERS | 0 | 0 | 0 | 0 |

Table S3. Digital DDH values for pairwise comparisons of user genomes vs. type strain genomes.

| Query strain | Subject strain | dDDH (in %) | G+C content difference (in %) |
|---|--|-------------|----------------------------------|
| <i>Paraclostridium</i> <i>bifermentans</i> GBRC | <i>Paraclostridium dentum</i> SKVG24 T | 82.7 | 0.53 |
| <i>Paraclostridium</i> <i>bifermentans</i> GBRC | <i>Paraclostridium</i> <i>bifermentans</i> subsp. <i>muricolitidis</i> CCUG 72489 | 80.5 | 0.78 |
| <i>Paraclostridium</i> <i>bifermentans</i> GBRC | <i>Paraclostridium</i> <i>bifermentans</i> ATCC 638 | 72.5 | 0.43 |

| | | | |
|---|---|------|------|
| <i>Paraclostridium</i> <i>bifermentans</i> GBRC | <i>Paraclostridium</i> <i>benzoelyticum</i> JC272 | 66.6 | 0.57 |
| <i>Paraclostridium</i> <i>bifermentans</i> GBRC | <i>Paeniclostridium</i> <i>ghonii</i> DSM 15049 | 39.3 | 1.06 |
| <i>Paraclostridium</i> <i>bifermentans</i> GBRC | <i>Paeniclostridium</i> <i>sordellii</i> ATCC 9714 | 31.5 | 1.43 |
| <i>Paraclostridium</i> <i>bifermentans</i> GBRC | <i>Romboutsia</i> <i>ilealis</i> CRIB | 27.4 | 0.96 |
| <i>Paraclostridium</i> <i>bifermentans</i> GBRC | <i>Romboutsia</i> <i>hominis</i> FRIFI | 26.4 | 0.51 |
| <i>Paraclostridium</i> <i>bifermentans</i> GBRC | <i>Clostridium</i> <i>dakarensis</i> FF1 | 26.2 | 0.89 |
| <i>Paraclostridium</i> <i>bifermentans</i> GBRC | <i>Romboutsia</i> <i>lituseburensis</i> DSM 797 | 26 | 1.18 |

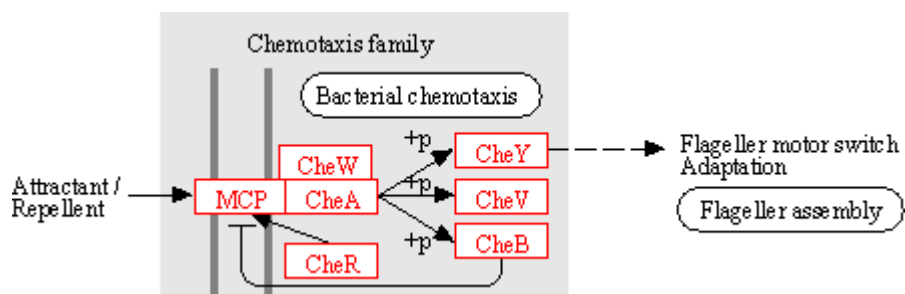
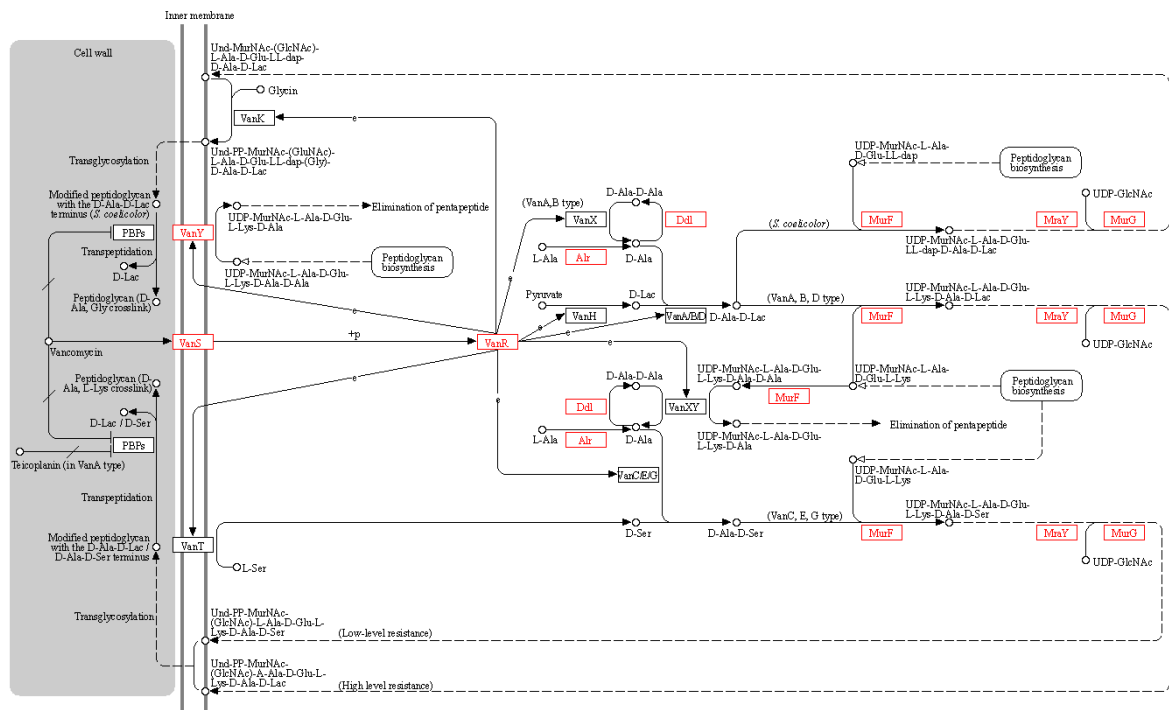


Figure S1. Flagellar assembly of strain GBRC in a hydrophobic environment where cheW is purine-binding chemotaxis protein, MCP; aerotaxis receptor, CheA; two-component system, CheR; chemotaxis protein methyl transferase, CheB; Protein-glutamate, CheV; two-component system.

VANCOMYCIN RESISTANCE



Vancomycin resistance operon types

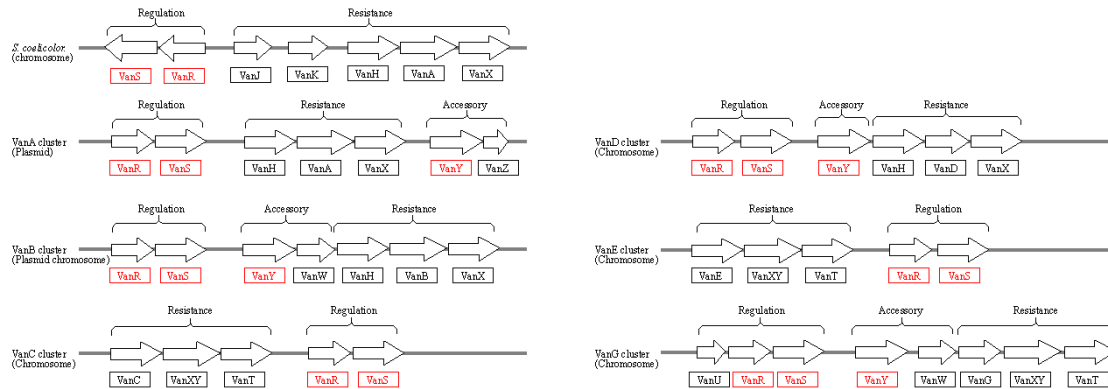


Figure S2. KEGG pathway for vancomycin resistance mechanism