

Genetic manipulations of nonmodel gut microbes

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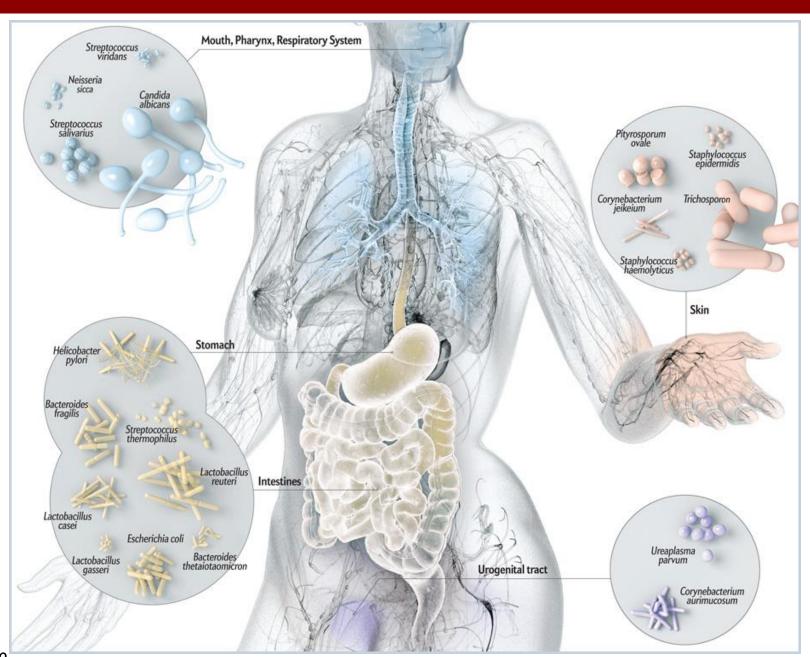
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The human microbiota



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Gut microbiota genes-Metabolites-Host biology



- Invisible organ/virtual organ
- Minor fraction of our total mass (~2 kg)
- 3.3 million genes outweigh human genes by ~150 times



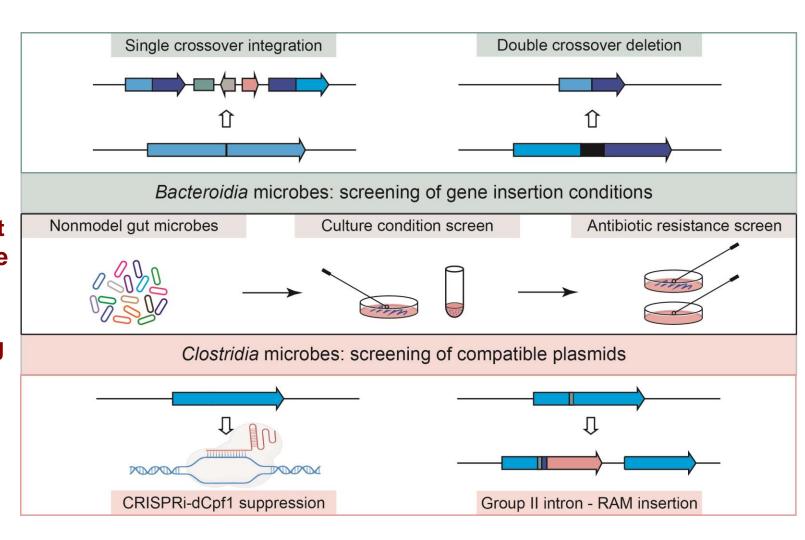
- **❖** IBD, colorectal cancer
- Obesity, type 2 diabetes, metabolic liver disease, cardio-metabolic disease
- ❖ Gut-brain axis

Gut microbiota genes → Metabolites → Host biology



Highlights

- ✓ A step-by-step genetic strategy that facilitates the study of functional genes encoded by gut commensals
- ✓ Establish genetic tools in nonmodel gut *Bacteroidia* and *Clostridia* without prior knowledge of genomic sequence
- A high-throughput genetics screening and manipulating platform for human gut microbes

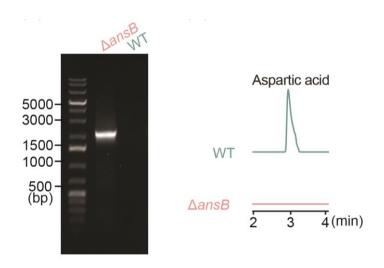




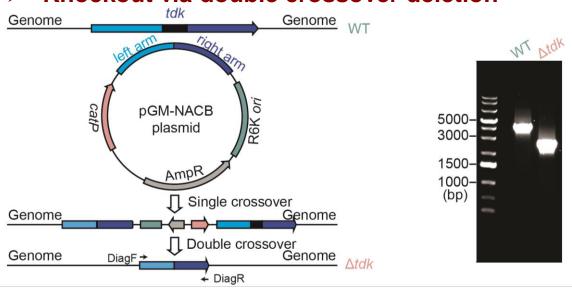
Genetic tools for nonmodel Bacteroidia microbes

Single crossover integration Screen of genetic tractability by single crossover integration 16s rRNA (or target genes) Genome Genome (or 1kb fragment of target genes) Antibiotic resistance screen Bacteroidia microbes Culture condition screen pGM-NACB/P D, G: suppress E. coli Agar plate: TSAB, BHIB, LB, CBA... ∏ Single crossover Liquid broth: Mega, RCM, CMM... Thiam: select integration A2 Genome Genome → A1 SegR DiagR

Knockout via single crossover integration

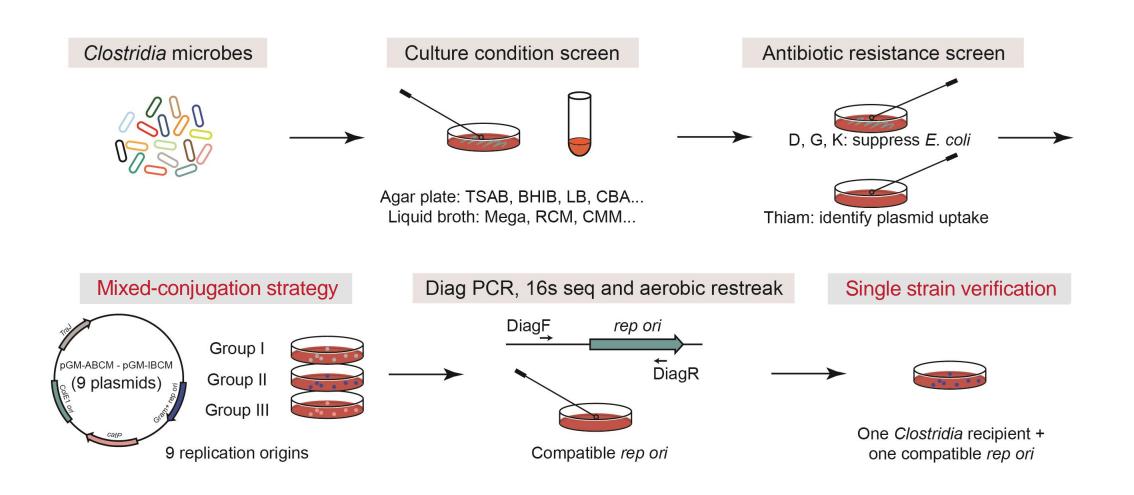


Knockout via double crossover deletion



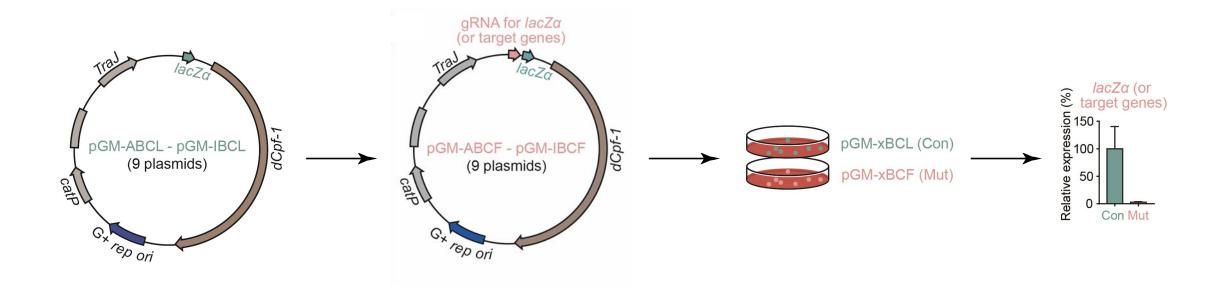


Gene transfer method for nonmodel *Clostridia* microbes



CRISPRi-dCpf1 system for Clostridia microbes

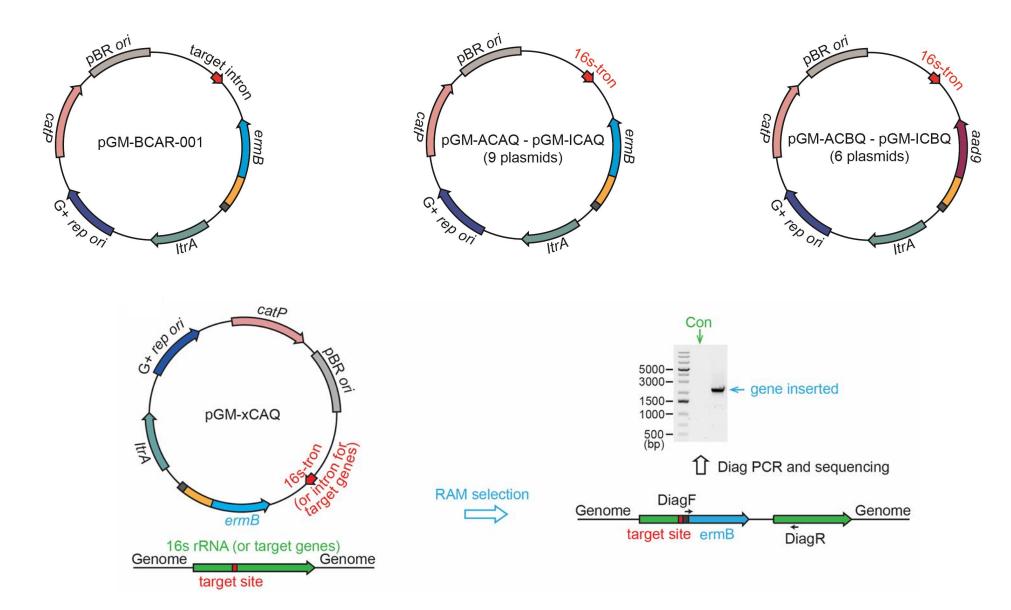
CRISPRi-dCpf1 system combined with report gene lacZα





Group II intron system for Clostridia microbes

Group II intron system-mediated gene insertion





Summary

- ☐ In this protocol, we introduced an efficient and generalizable approach to establish genetic tools in nonmodel gut microbes.
- □ For Bacteroidia microbes, genetic tractability was screened using single crossover integration, and gene knockout could be performed via single crossover insertion and double crossover deletion developed based on this.
- ☐ For Clostridia microbes, plasmids with compatible replication origin were firstly identified, then CRISPRi-dCpf1-mediated suppression and Group II intron-induced insertion genetic systems were developed.

iMeta: Integrated meta-omics to change the understanding of the biology and environment













"<u>iMeta</u>" (IF **23.7**) is a Wiley partner journal launched by iMeta Science Society of scientists in bioinformatics and metagenomics in 2022. It aims to publish high-quality papers targeting a broad and diverse audiences. Its scope is similar to that of Nature Biotechnology, Nature Microbiology, Cell Host & Microbe. It unique features include video submission, bilingual publishing, and social media dissemination with 500,000 followers. It has been published 190+ papers and been cited for 3400+ times since 2022, and indexed by <u>ESCI</u>, <u>PubMed</u>, <u>Google</u>, and <u>Scopus</u>.

"<u>iMetaomics</u>" is sister journal of "iMeta" launched in 2024, with target IF>10, and its scope is similar to Microbiome, ISME J, Nucleic Acids Research, Briefings in Bioinformatics, and Bioinformatics. All submissions are welcomed!



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