



The Rheumatoid Arthritis Gut Microbial Biobank Reveals Core Microbial Species that Associate and Effect on Host Inflammation and Autoimmune Responses

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Huang, Hao-Jie, Chang Liu, Xin-Wei Sun, Rui-Qi Wei, Ling-Wei Liu, Hao-Yu Chen, Rashidin Abdugheni, et al. 2024.

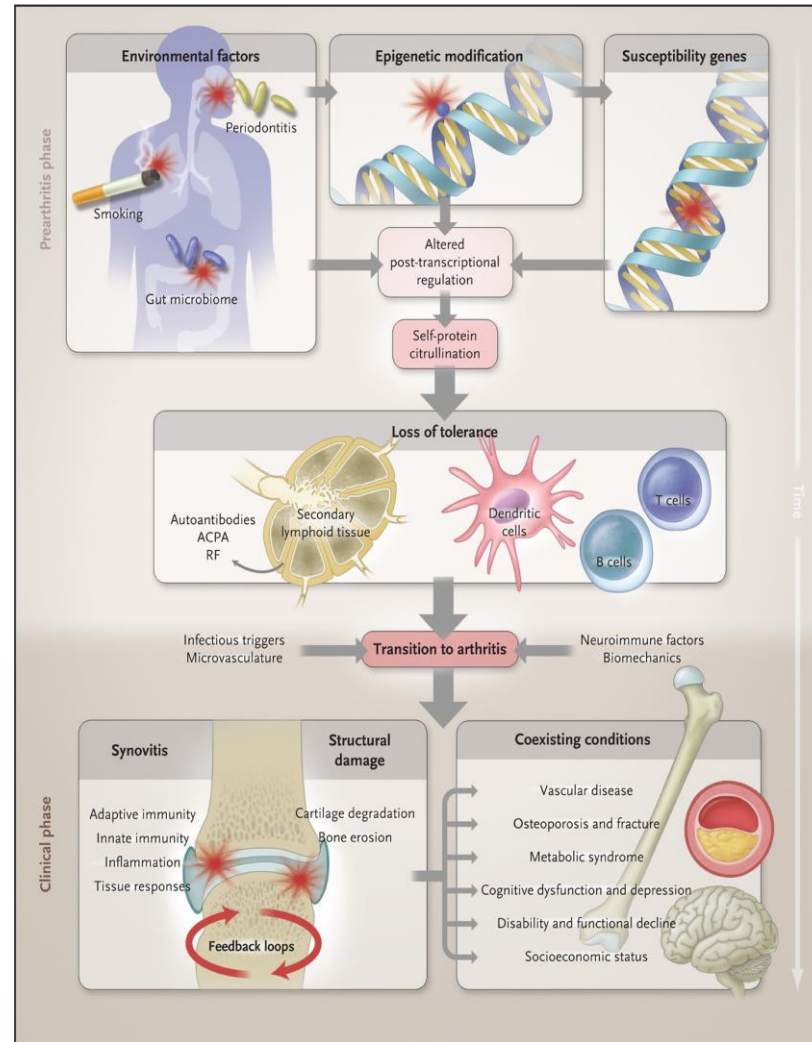
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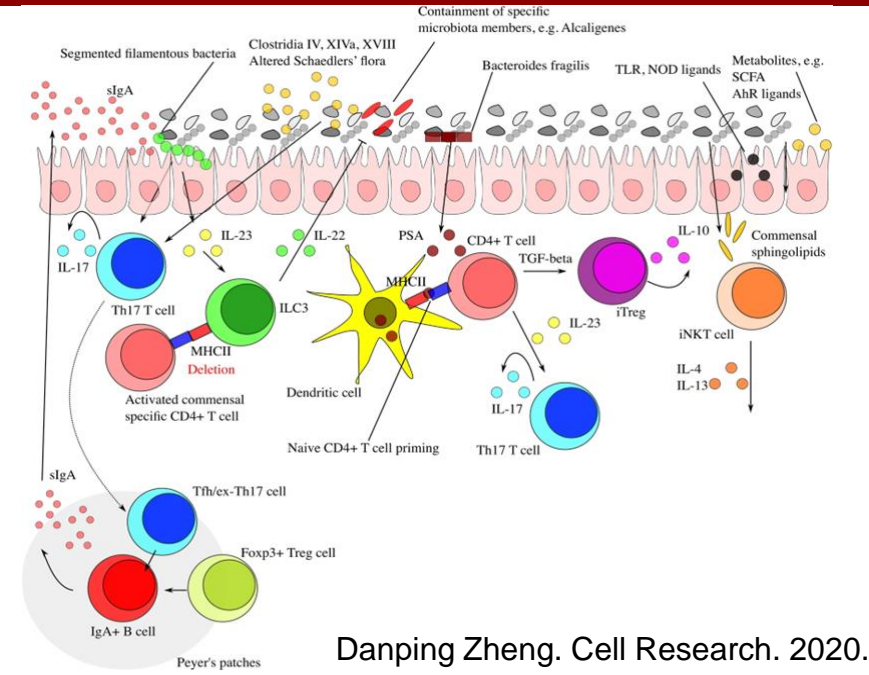
Background — Rheumatoid arthritis and gut microbes



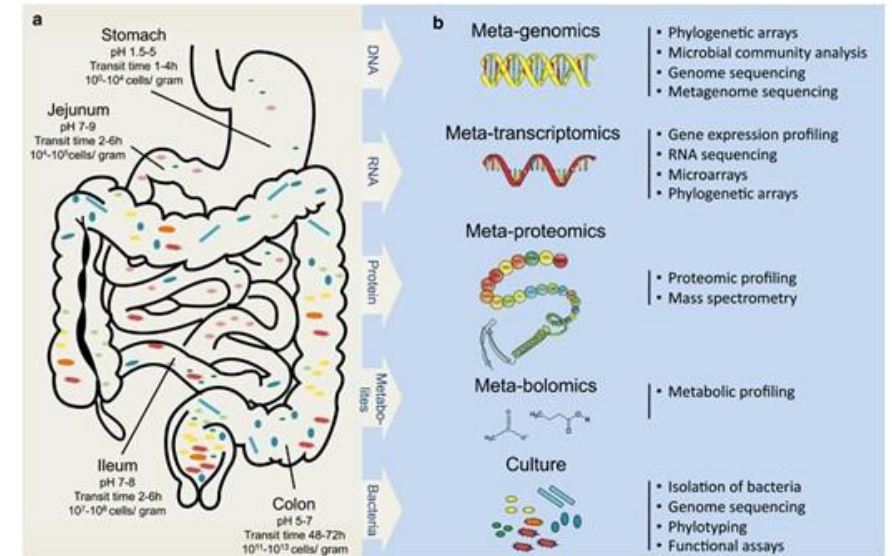
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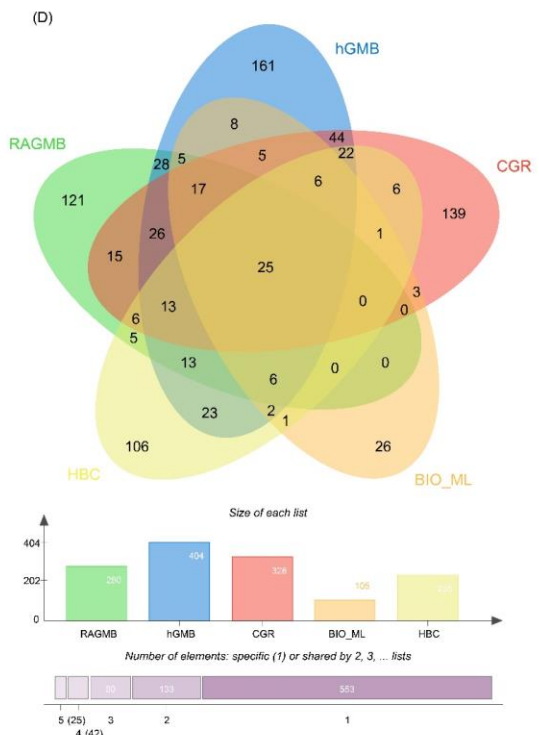
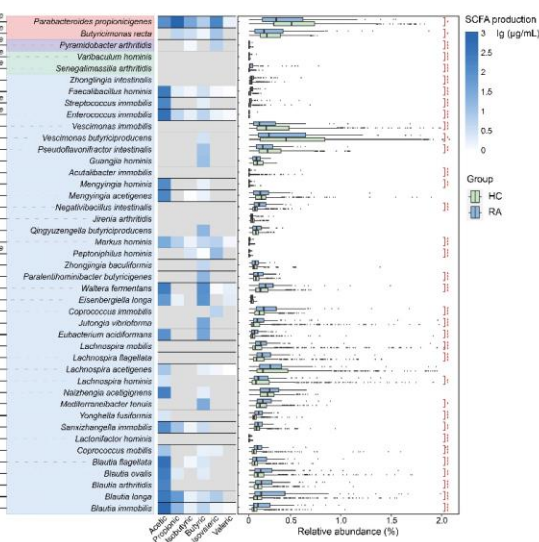
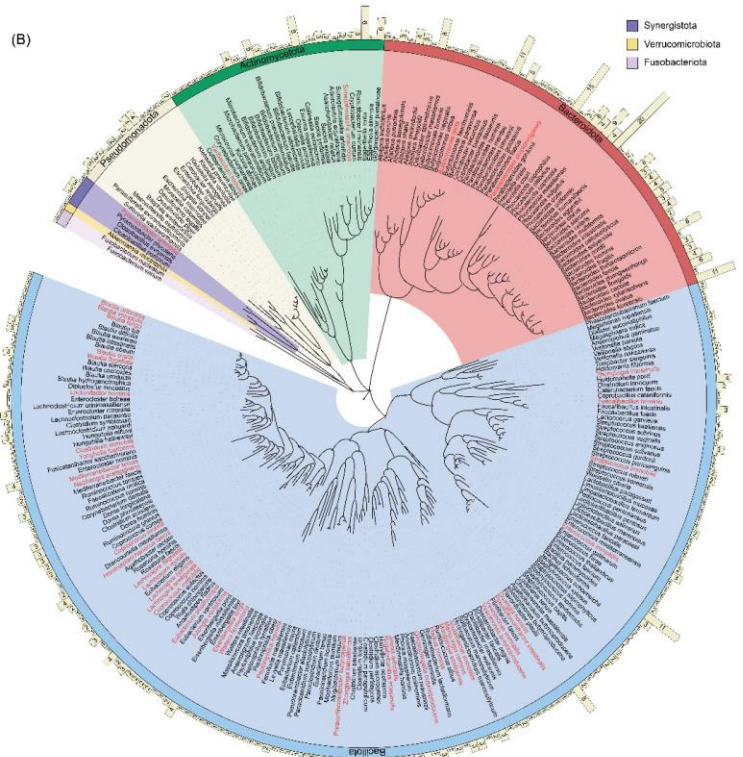
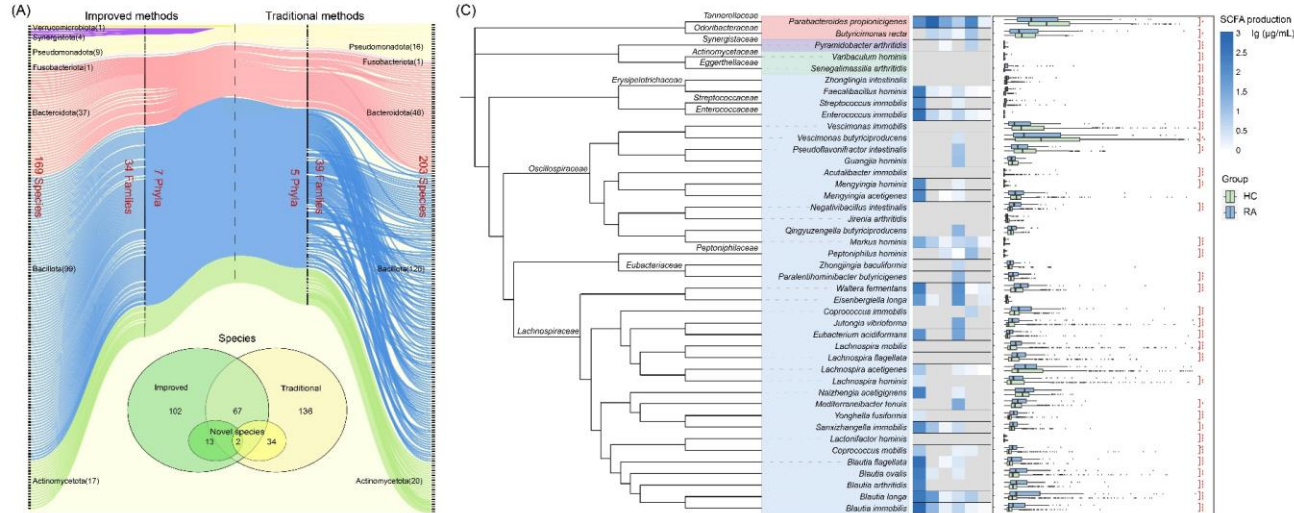
Danping Zheng. Cell Research. 2020.



Clara Belzer. ISME. 2012



Results — Construction of the RAGMB



- 11 traditional and 7 modified methods / media were used;
- RAGMB covers 601 strains in 280 species from 7 phyla, including 43 new species;
- RAGMB website: <https://www.nmdc.cn/ragmb/> ;
- The new species were analysed for identification, genome, metabolome and distribution in the population.
- RAGMB provides 121 unique species, including 8 strains from the phylum *Synergistota*, representing 4 species.

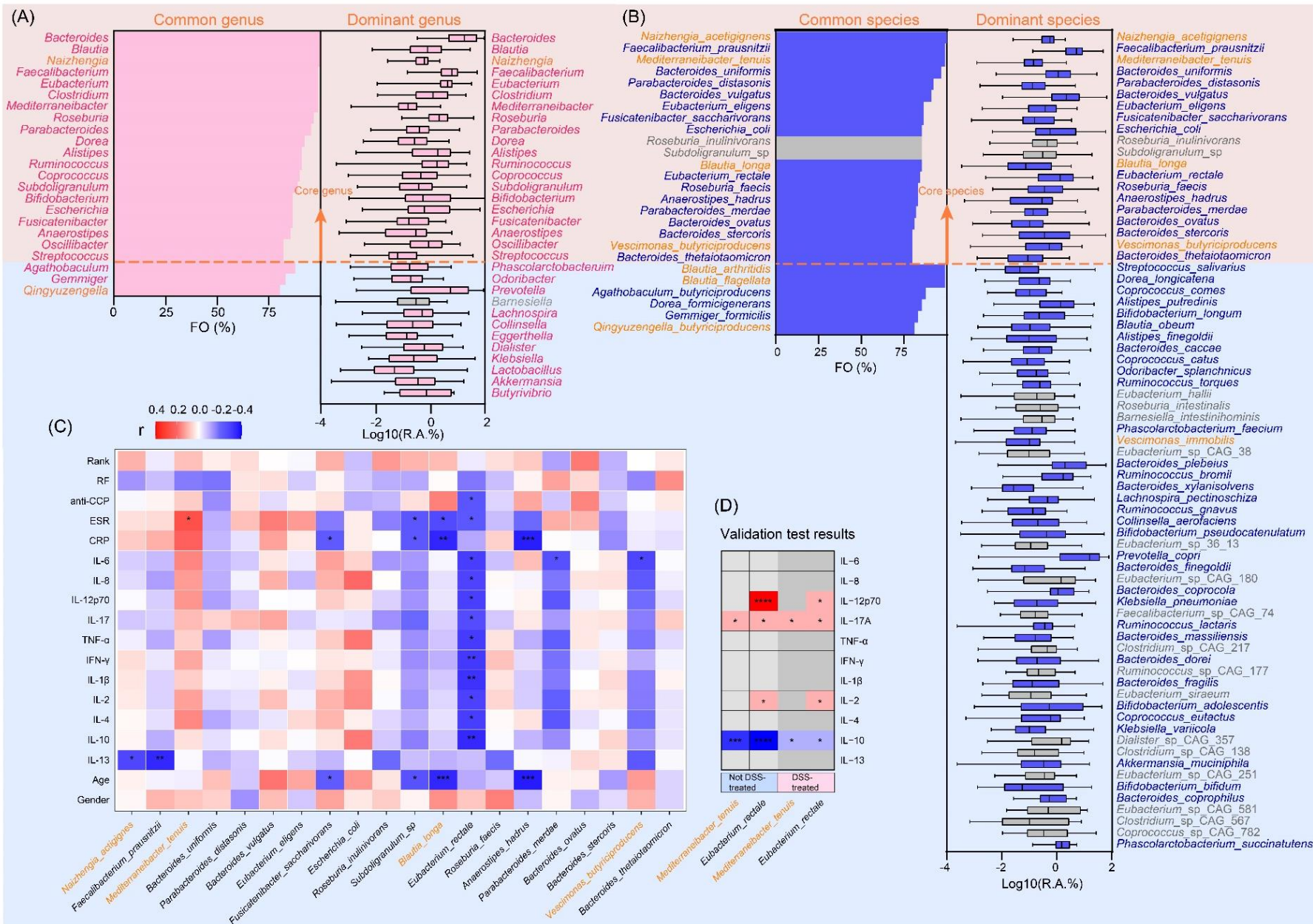


Results — RAGMB covers both high and low-abundant bacterial taxa from RA patients



- The abundance of *Bifidobacteriaceae* and *Prevotellaceae* showed significant differences between samples;
- 145 species (51.8%) were conserved in the RAGMB but were not detected by the metagenomic approach;
- The RAGMB that covered 93.2% at species level of medium- and high-abundant gut microbes with RA patients.

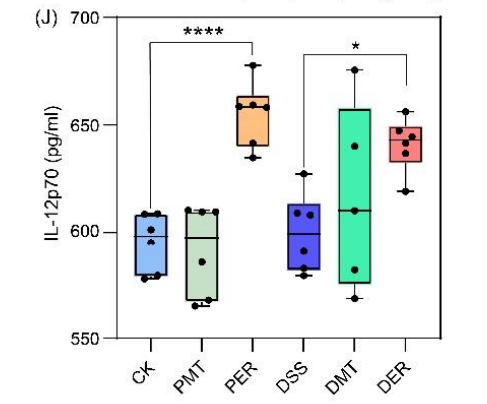
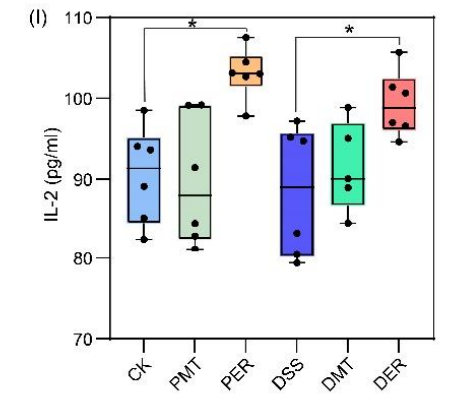
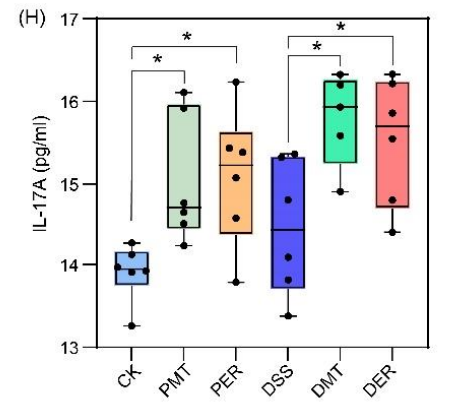
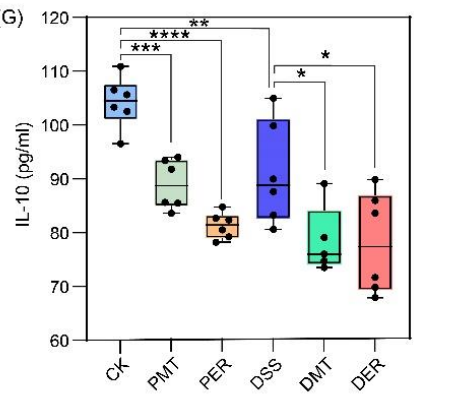
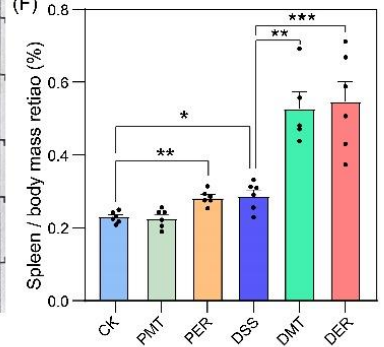
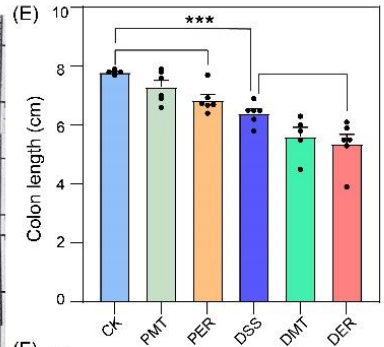
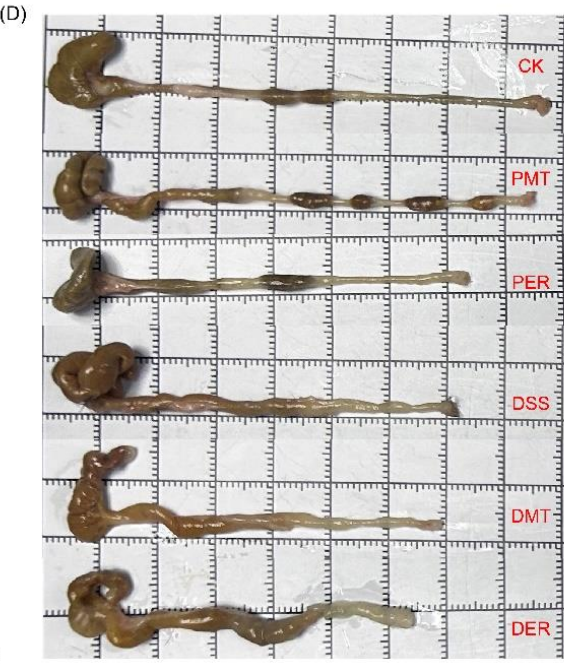
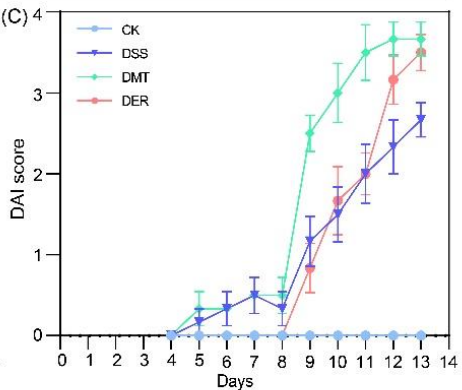
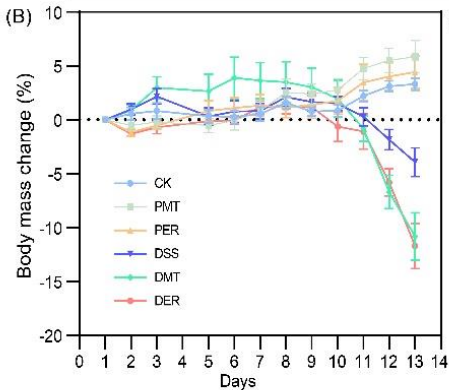
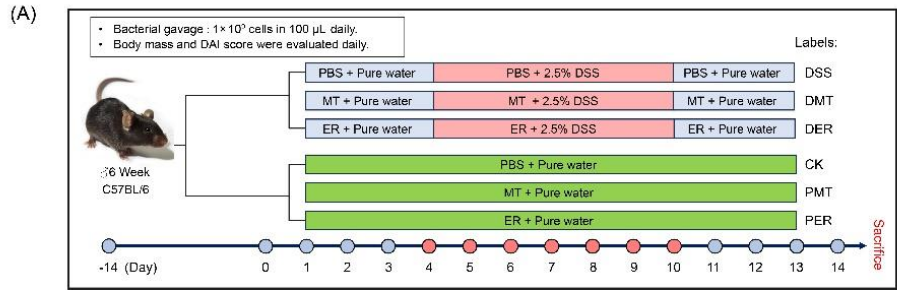
Results — Core gut microbial species and their correlation with RA clinically used indices



- The RA core microbiome consists of 20 bacterial species;
- *Mediterraneibacter tenuis* and *Eubacterium rectale* are significantly associated with clinical diagnostic indicators.



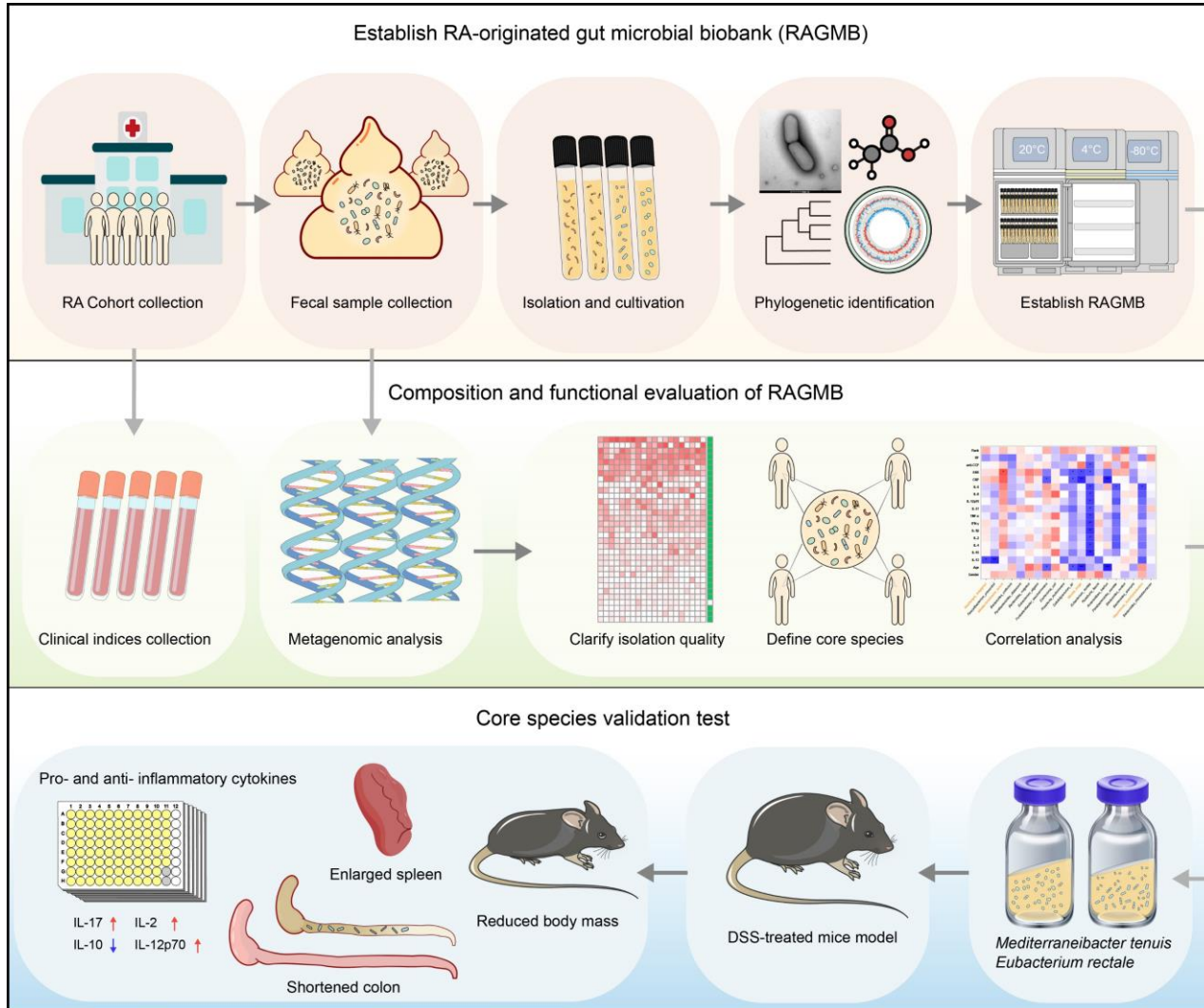
Results — The *M. tenuis* and *E. rectale* exacerbated inflammatory responses in mice



• *Mediterraneibacter tenuis* and *Eubacterium rectale* exacerbated the host's inflammatory response, including shortened colon length, enlarged spleen, decreased plasma levels of IL-10 and increased levels of IL-17A.



Conclusions



- An rheumatoid arthritis (RA)-originated gut microbial biobank (RAGMB) was established, comprising 601 bacterial strains representing 280 species (including 43 novel species) across 7 bacterial phyla.
- RAGMB covers 93.2% of medium- and high-abundant RA gut microbe species from isolated samples.
- The RA core microbiome consists of 20 bacterial species, with *Mediterraneibacter tenuis* and *Eubacterium rectale* showing significant correlations with clinical indices.
- RA core species *Mediterraneibacter tenuis* and *Eubacterium rectale* exacerbate inflammatory responses, including shortened colon length, enlarged spleen and altered plasma cytokine levels.

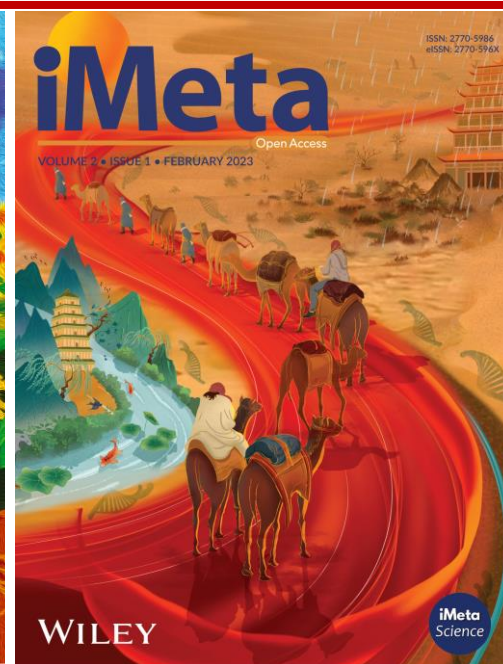
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