

APPLIED MICROBIOLOGY AND BIOTECHNOLOGY

Therapeutic applications of gut microbes in cardiometabolic diseases:
current state and perspectives

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Table S1. Altered gut microbial compositions associated with hypertension

Table S2 Altered Intestinal Microbiota Composition Associated with Atherosclerosis

Table S1. Altered gut microbial compositions associated with hypertension

First Author (Ref. #), Year	Sample	Technique	Increase in hypertension	Decrease in hypertension
Mell et al. [1], 2015	Dahl salt- resistant rats	16S	Plasma acetate and heptanoate	S24-7, <i>Veillonellaceae</i>
Gomez-Arango et al. [2], 2016	obese pregnant women	16S		<i>Butyrate-producing bacteria Odoribacter</i>
Jackson et al. [3], 2019	756 hypertensive patients, 1790 controls	16S	<i>Lactobacillaceae,</i> <i>Streptococcaceae</i>	<i>Dehalobacteriaceae,</i> <i>Christensenellaceae,</i> <i>Oxalobacteraceae,</i> <i>Mollicutes,</i> <i>Rikenellaceae,</i> <i>Clostridia,</i> <i>Anaeroplasmataceae,</i> <i>Peptococcaceae</i>
Huart et al. [4], 2019	38 hypertensive patients, 7 pre- hypertensive patients, 9 controls	16S	<i>Clostridium sensu stricto</i>	<i>Ruminococcaceae,</i> <i>Clostridiales</i>
Verhaar et al. [5], 2020	4672 subjects	16S	<i>Streptococcus</i>	<i>Roseburia,</i> <i>Clostridium sensu stricto,</i> <i>Roseburia hominis, Romboutsia,</i> <i>Ruminococcaceae,</i> <i>Enterorhabdus</i>
Iñaki Robles et al.[6], 2021	8 DOCA-salt rats	16S	<i>lactate-producing bacteria</i>	<i>Oscillospira</i>
Larissa et al. [7], 2021	hypertensive rats induced by high-fat diet	16S	<i>Lactobacillales,</i> <i>Clostridiales,</i> <i>Enterobacteriales</i>	<i>Bacteroidales,</i> <i>Desulfovibrionales,</i> <i>Methanobacteriales,</i> <i>Gastranaerophilales,</i> <i>Selenomonadales.</i>
Chao-Yue et al. [8], 2021	Spontaneously hypertensive rats	16S	<i>the ratio between Firmicutes and Bacteroidetes</i>	

Haicui et al. [9], 2022	hypertensive rats	16S	<i>Proteobacteria</i>	<i>Bacteroidales_S24-7</i>
Georgianna et al. [10], 2022	hypertensive rats induced by high-fat diet	16S	<i>Lachnospiraceae</i> , <i>Clostridiaceae I</i> , <i>Peptostreptococcaceae</i> , <i>Enterobacteriaceae</i>	<i>Ruminococcaceae</i> , <i>Methanobacteriaceae</i> , <i>Muribaculaceae</i>
Lin et al.[11], 2022	L-NAME-induced hypertensive rats	16S	<i>Christensenellaceae</i> , <i>Streptococcaceae</i> , UUG-010	

Table S2 Altered Intestinal Microbiota Composition Associated with Atherosclerosis and coronary artery disease

First Author (Ref. #), Year	Sample	Technique	Increase in CVD	Decrease in CVD
Yin et al.[12], 2015	141 stroke/TIA patients vs. 94 asymptomatic control subjects	16S rRNA	<i>Enterobacteriaceae</i> <i>Proteobacteria</i> <i>Escherichia/Shigella</i>	<i>Bacterioidetes</i> <i>Bacteroidales</i> <i>Bacteroidaceae</i> <i>Bacterioides</i>
Feng et al. [13], 2016	59 CAD patients vs. 43 healthy control subjects	Fecal metagenome	<i>Streptococcus sp.</i> M334 and M143 <i>Clostridium sp.</i> HGF2	
Jie et al.[14], 2017	218 ACVD and 187 healthy controls.	Fecal Metagenomic	<i>Streptococcus and Escherichia</i>	<i>Bacteroides and Prevotella</i>
Kasahara et al.[15],2018	Atherosclerotic murine model	16S sequencing		<i>Roseburia</i>
Zhiyang et al. [16], 2021	Atherosclerotic mice model	16S sequencing	<i>Helicobacter spp.</i>	
Xiao-Lin et al. [17], 2022	Atherosclerotic mice model	16S sequencing	<i>Firmicutes</i>	<i>Bacterioidetes</i>

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