



Bacteria: Black and White or Maybe Gray?

Ramin Mazaheri Nezhad Fard ^{1,*}

¹Department of Pathobiology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran

*Corresponding author: Department of Pathobiology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran. Tel: +982142933208, Email: raminmazaheri@gmail.com

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Dear Editor,

Bacteria are traditionally categorized into two broad categories of pathogenic and non-pathogenic. Many infectious diseases in humans and animals are caused by pathogenic bacteria, including respiratory, gastrointestinal, genitourinary, and central nervous system infections, as well as plant infections. Therefore, they are well-known. However, only a minority of bacteria species are pathogenic. This category includes free-living, commensal, and probiotic bacteria, which are beneficial for the body. Hence, we naturally tend to the latter and try to avoid the former. But does this categorization work properly always? In another word, are all pathogens in the first category harmful? While those in the second category are completely safe? Furthermore, should pathogens socially be pictured as absolute evils while non-pathogens are addressed as pure angels? We discussed this issue shortly to clarify the actual missions of the bacteria in life. Although pathogenic bacteria are generally recognized as harmful microorganisms, even these microorganisms are sometimes useful! While evidence regarding the benefits of pathogens for their hosts are limited, several studies have investigated the pathogen's role in the coevolution of the host cells. Furthermore, the regulation of the host immune responses is another role of the pathogens (1). Similar to pathogenic bacteria, non-pathogenic bacteria also may cause problems in specific conditions. For example, in those with weakened or failed immune system (e.g., those who receive chemotherapy), members of the human microflora (e.g., probiotics) may cause a wide spectrum of diseases (e.g., type-2 diabetes, which is probably caused by translocation of gut microbiota to other tissues and the relative inflammation) (2). Besides, there are studies which demonstrated that gut microbiota may induce insulin resistance through *Prevotella* and *Bacteroides* spp. Furthermore, gut microbiota may affect type-2 diabetes via amino

acid metabolism. Imbalances in the gut microbiota population possibly result in the transfer of gut bacteria to the mesenteric lymph system, causing immune reactions and the release of inflammatory cytokines, which eventually results in activation of cord (CNS) and vagus nerves.

These reactions negatively affect gut-brain axes. Recent studies have shown that coronary plaque bacteria are vulnerable to inflammation, in contrast to their ancestral gut bacteria (3). This can be involved in ischemic heart attacks and cardiovascular diseases (CVD), such as atherosclerosis and hypertension. Although microbiota brings numerous advantages to their hosts, some microfloral members are carcinogenic due to their ability to invade tissues and activate oncogenes. In general, it is estimated that up to 90% of all human diseases, ranging from routine to systematic and severe diseases, are associated with microbiota (4). Examples of these diseases include various types of cancers (e.g., colorectal cancer (CRC)), CVDs, asthma, types 1 and 2 diabetes, autoimmune neurodegenerative diseases (Alzheimer's and Parkinson's diseases), rheumatoid arthritis (RA), multiple sclerosis (MS), cystic fibrosis (CF), Amyotrophic lateral sclerosis (ALS), fibromyalgia, irritable bowel syndrome (IBD), metabolic syndromes, especially obesity, and psycho-behavioral diseases such as phobia, stress, depression, and autism. In addition to the problematic transfer of microflora bacterial cells to other organs, gene transfer between members of the normal microflora and pathogens is strongly suggested (5). For example, enterococci play keys an important role in the transfer of antibacterial resistance determinants (and possibly other virulence genes) within the members of intestinal microflora, probably via bacteriophage transduction (6). This results in the rapid progression of antimicrobial resistance, which does not sound good at all! In conclusion, most bacteria seem to include both positive and negative roles in nature, contrary to our previous thoughts.

Therefore, the common belief that bacteria are just black or white should be reconsidered.

Footnotes

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References

1. Metcalf CJE, Koskella B. Protective microbiomes can limit the evolution of host pathogen defense. *Evol Lett.* 2019;**3**(5):534-43. doi: [10.1002/evl3.140](https://doi.org/10.1002/evl3.140). [PubMed: [31636945](https://pubmed.ncbi.nlm.nih.gov/31636945/)]. [PubMed Central: [PMC6791398](https://pubmed.ncbi.nlm.nih.gov/PMC6791398/)].
2. Harsch IA, Konturek PC. The Role of Gut Microbiota in Obesity and Type 2 and Type 1 Diabetes Mellitus: New Insights into "Old" Diseases. *Med Sci (Basel).* 2018;**6**(2). doi: [10.3390/medsci6020032](https://doi.org/10.3390/medsci6020032). [PubMed: [29673211](https://pubmed.ncbi.nlm.nih.gov/29673211/)]. [PubMed Central: [PMC6024804](https://pubmed.ncbi.nlm.nih.gov/PMC6024804/)].
3. Pothineni NVK, Subramany S, Kuriakose K, Shirazi LF, Romeo F, Shah PK, et al. Infections, atherosclerosis, and coronary heart disease. *Eur Heart J.* 2017;**38**(43):3195-201. doi: [10.1093/eurheartj/ehx362](https://doi.org/10.1093/eurheartj/ehx362). [PubMed: [29020241](https://pubmed.ncbi.nlm.nih.gov/29020241/)].
4. Wang B, Yao M, Lv L, Ling Z, Li L. The Human Microbiota in Health and Disease. *Engineering.* 2017;**3**(1):71-82. doi: [10.1016/j.eng.2017.01.008](https://doi.org/10.1016/j.eng.2017.01.008).
5. Džidić S, Šušković J, Kos B. Antibiotic resistance mechanisms in bacteria: biochemical and genetic aspects. *Food Technology & Biotechnology.* 2008;**46**(1).
6. Mazaheri Nezhad Fard R, Barton MD, Heuzenroeder MW. Bacteriophage-mediated transduction of antibiotic resistance in enterococci. *Lett Appl Microbiol.* 2011;**52**(6):559-64. doi: [10.1111/j.1472-765X.2011.03043.x](https://doi.org/10.1111/j.1472-765X.2011.03043.x). [PubMed: [21395627](https://pubmed.ncbi.nlm.nih.gov/21395627/)].