J Infect Dis Ther 2018, Volume 6
DOI: 10.4172/2332-0877-C2-042

Gut microbiota and Antibiotic resistance

Ivana Haluskova Balter
French society of immunology, France

Bacteria, viruses, parasites and fungi that are resistant to drug cause 700,000 death each year. By 2050 superbugs inured to treatments could cause up to 10 million deaths annually and costs the global economy US$100 trillion. AMR (antimicrobial) resistance is regarded nowadays as a major threat to global public health. The issue is receiving high-level political attention (G7 and G20 in 2017 for first time). The list was drawn up in a bid to guide and promote research and development (R&D) of new antibiotics, as part of WHO's efforts for AMR (27th Feb 2017) Resistance to antibiotics may arise in a population of susceptible bacteria by the accumulation of mutations (e.g. point mutations in DNA gyrase conferring resistance to quinolones) or by the acquisition of resistance genes that protect the cell against antibiotics. Antibiotic resistance genes can cause phenotypic resistance through a variety of mechanisms, including the enzymatic inactivation of the antibiotic, the modification of the antibiotic target and the prevention of the accumulation of lethal intracellular concentrations of the antibiotic through efflux pumps Problem of resistance get worsened due declining number of new antibiotics and limited number of new classes direct research to look for alternatives. Additionally, antibiotics shape the ecology of the gut microbiota in profound ways, causing lasting changes to developing and mature microbiotas. The application of next-generation sequencing has enabled detailed views of the side effects these drugs have on commensal populations during treatment of infections. The human gut thus harbours a complex microbial ecosystem, which consists of hundreds of species, collectively termed the gut microbiota. This interaction between microbiota appears to be bidirectional, namely through signaling from gut-microbiota to brain and from brain to gut-microbiota by means of neural, endocrine, immune, and humoral links. Negative impact on composition and functionality microbiota given existing immune crosstalk including "innate cell immunity training" impact host immune response capacities observed in recent research.Imbalances in the gut microbiota can induce inflammation that is associated also with the pathogenesis of obesity, type 2 diabetes mellitus, and Alzheimer's disease. In conclusion, alternative directions considering strongly their role on host microbiota and immune system modulation should be strongly promoted while tackling issue of antibiotic resistance.

ivankahhaluskova@gmail.com