

Editor's Note

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Most of the bacteria are beneficial or harmless to the mankind and few are deadliest, pathogenic, and elicit immunity. The pathogenic bacteria are capable of causing diseases when enters into the body and their severity varies from species to species and it depends on the concentration and demographics as well. Advanced clinical microbiology deals with the various clinical applications of microbes for the improvement of health. Majorly four types of microorganisms such as bacteria, fungi, parasites, and viruses, and one type of infectious protein called prion responsible for all the existing infectious diseases. Current volume 7 and issue 5 of the journal had published a research article, review article, and perspective article which minutiae the gut microbiome, sepsis, and antibiotic resistance.

The digestion process of human being is incomplete without the gut microbiome; human gut is blessed with a complex ecosystem of microbiota. It is very well understood that the complex integrity of gut microbiota delivers good health; in recent years many efforts are under process to increase the microbial community by supplements such as probiotics. Author Ebinesh et al. [1], had presented perspective article by applying the awareness of new horizon to use the bacteriophages in manipulating the gut microbiota and thus gut health. The key reason to use bacteriophage is due to their property of host specificity. Lytic phages can be used to void the pathogenic bacteria whereas lysogenic phages can be used to tune the genome of host bacteria. In fact, author had narrated the possible obstacles of this novel approach and expecting to make use of bacteriophages to build a healthy gut especially in children.

Mahendra et al. [2] in his research article aims to investigate the bacterial resistance pattern from adult sepsis patient at Dr.

Moewardi General Hospital. The morbidity and mortality associated with sepsis is globally increasing, due to septic shock exerted by virulent pathogens. The pathogenic bacteria were isolated from the blood sample of the patients at Dr. Moewardi General Hospital and subjected to the identification and AST patterns analysis as per the international guidelines. The study concludes that the chief causative agent was gram negative bacteria than gram negative.

Antibiotic resistance is ever since existing worldwide issue, recent days due to many evident factors impacted the patient outcome, researchers and clinicians determined to control the genes which are responsible for the resistance. The objective of author Salah AM's review was to evaluate the published data on the prevalence of antibiotic resistance in *E. coli* and responsible genes from animal origins in Tunisia. The findings of this article point the use of higher level antibiotics to produce increased meat at pig and poultry industries. Outright concern was that high rate of resistance to commonly used antibiotics such as tetracycline, streptomycin, quinolones/fluoroquinolones and trimethoprim/sulfamethoxazole [3].

References

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