

## Chapter 10

# Herbal Bioactives: An Escape to ESKAPE Pathogens

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### ABSTRACT

*Infection is caused in the human body due to the invasion of pathogenic microbes, their multiplication, and production of toxins. The ESKAPE pathogen comprises a group of six bacterial pathogens, namely Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa, and Enterobacter spp. These pathogens are associated with the emerging cases of antimicrobial resistance to commonly used antibiotics such as penicillin, vancomycin, etc. Most of these pathogens are multidrug resistant, which is among the major threats to human health at present. The developing resistance to existing antibiotics imposes a burden on modern science to exercise the mechanism behind this and also the identification of novel targets to combat antimicrobial resistance. This chapter describes briefly about the mechanism of development of antimicrobial resistance and some herbal medications that can be used to combat the same. It also describes some of the traditional preventives that can be practiced to deal with infections.*

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## **INTRODUCTION**

Nosocomial infections are caused by a variety of microbes, including viruses, fungi, bacteria, and many other agents. These infectious pathogens can be born inside the host, i.e., endogenous or may be transferred from an external source, i.e., exogenous. There are increasing incidences of antibiotic resistance in such pathogens leading to a significant burden on the healthcare system and affecting the mortality and morbidity rates. There is a group of six bacterial pathogens, called the ESKAPE pathogens, which comprises of *Enterococcus faecium*, *Streptococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Enterobacter* spp. These bacterial pathogens are grouped differently by the Infectious Disease Society of America due to emerging cases of antibiotic resistance among them or simply because of their ability to escape the effect of antibiotics (WHO, 2017). This emerging resistance mechanism in these species poses a great threat to life on earth and on the other hand, demands a novel and active approach to target the bacterial infections.

MDR infections are among the top three causes of threat to public health. In the year 2017, the World Health Organization (WHO) developed a global pathogen priority list (PPL), for the antibiotic-resistant bacteria to stimulate research and healthcare initiatives. The bacterial strains from ESKAPE pathogens top the list of PPL. The global PPL has divided bacterial pathogens into three priority tiers based on their abundance, emergence, and significance as critical, high, and medium (Rice, 2010). The bacteria in the ESKAPE pathogens list are among the critical and high tier. Carbapenem-resistant *A. baumannii* and *P. aeruginosa* along with extended spectrum  $\beta$ -lactamases (ESBL) or carbapenem-resistant *K. pneumoniae* and *Enterobacter* spp. are listed in the critical priority list of pathogens, whereas vancomycin resistant *E. faecium* (VRE) and vancomycin and methicillin-resistant *S. aureus* (VRSA and MRSA) are in the list of high priority group. So, it needs special attention to compensate for the elevating mortality and morbidity rates (Llaca-Diaz, 2012). A survey of clinical samples from South Africa, over five years from the year 2011 to 2015, resulted in 64,502 ESKAPE pathogens. *S. aureus* was found to be the most abundant pathogen summing up to 38% of all the samples followed by *K. pneumoniae*, which accounted for 22.2% of the total isolates, from respiratory samples. However, *S. aureus* was still the most isolated species from all other samples as well (Ramsay, 2018).

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