

1. Record Nr.	UNINA9910566473203321
Titolo	Antimicrobial Resistance and Virulence - 2nd Volume
Pubbl/distr/stampa	Basel, : MDPI - Multidisciplinary Digital Publishing Institute, 2022
ISBN	9783036539072
Descrizione fisica	1 online resource (156 p.)
Soggetti	Biology, life sciences Microbiology (non-medical) Research & information: general
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Sommario/riassunto	<p>The worldwide dissemination of antimicrobial-resistant bacteria, particularly those resistant to last-resource antibiotics, is a common problem to which no immediate solution is foreseen. In 2017, the World Health Organization (WHO) published a list of antimicrobial-resistant "priority pathogens", which include a group of microorganisms with high-level resistance to multiple drugs, named ESKAPE pathogens, comprising vancomycin-resistant <i>Enterococcus faecium</i> (VRE), methicillin- and vancomycin-resistant <i>Staphylococcus aureus</i> (MRSA and VRSA), extended spectrum -lactamase (ESBL) or carbapenem-resistant <i>Klebsiella pneumoniae</i>, carbapenem-resistant <i>Acinetobacter baumannii</i>, carbapenem-resistant <i>Pseudomonas aeruginosa</i> and extended spectrum -lactamase (ESBL) or carbapenem-resistant <i>Enterobacter</i> spp. These bacteria also have the ability to produce several virulence factors, which have a major influence on the outcomes of infectious diseases. Bacterial resistance and virulence are interrelated, since antibiotics pressure may influence bacterial virulence gene expression and, consequently, infection pathogenesis. Additionally, some virulence factors contribute to an increased resistance ability, as observed in biofilm-producing strains. The surveillance of important resistant and virulent clones and associated mobile genetic elements is essential to decision making in terms of</p>

mitigation measures to be applied for the prevention of such infections in both human and veterinary medicine, being also relevant to address the role of natural environments as important components of the dissemination cycle of these strains.

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