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Sommario/riassunto	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 Enterococcus faecium (VRE), methicillin- and vancomycin-resistant Staphylococcus aureus (MRSA and VRSA), extended spectrum -lactamase (ESBL) or carbapenem-resistant Klebsiella pneumoniae, carbapenem-resistant Acinetobacter baumannii, carbapenem-resistant Pseudomonas aeruginosa and extended spectrum -lactamase (ESBL) or carbapenem-resistant Enterobacter 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

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.