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Acinetobacter baumannii

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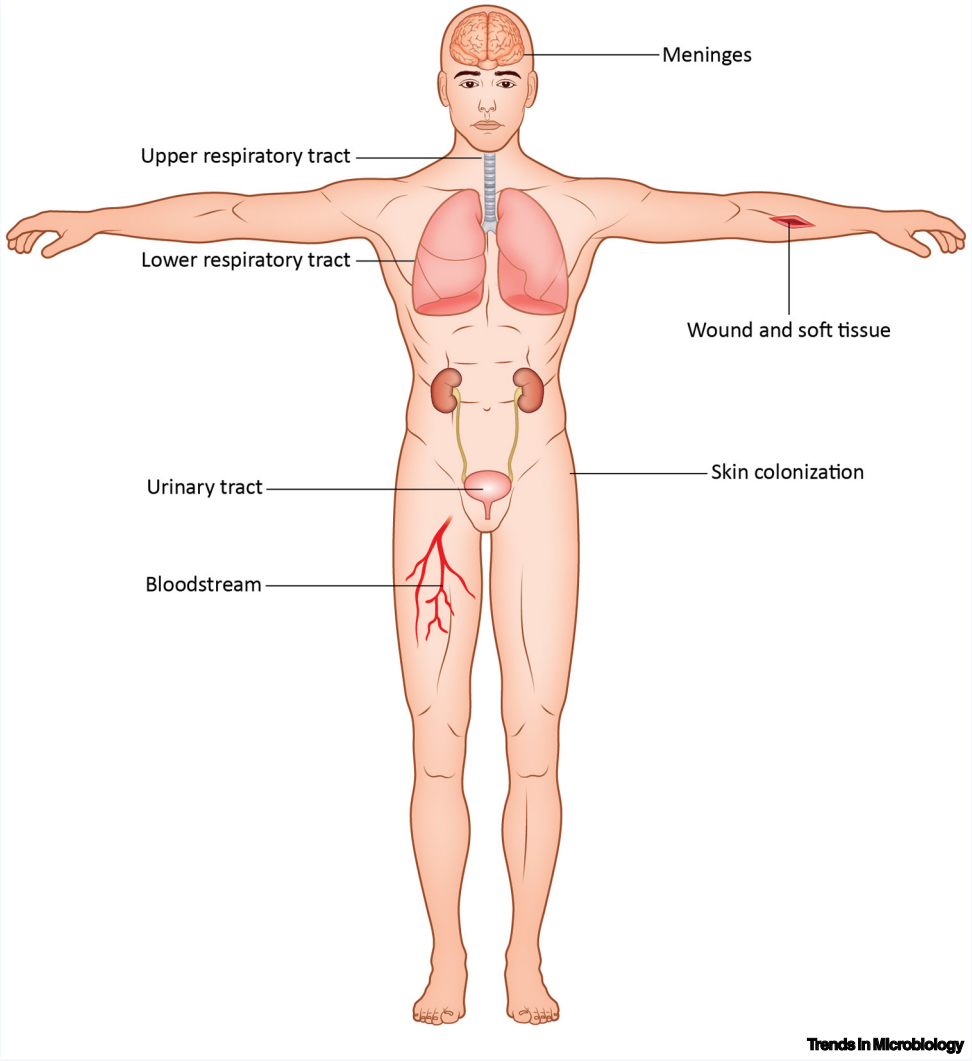

Acinetobacter baumannii is a ubiquitous, Gram-negative, nonflagellated coccobacillus bacterium commonly isolated from the environment. In human medicine, this opportunistic pathogen is responsible for hospital- and community-acquired infections. Resistance to last-resort antibiotics, such as colistin, tigecycline, and carbapenems, earns this bacterium a place among the most problematic nosocomial ESKAPE pathogens, being classified as a bacterium for which research and development of new antibiotics is critically needed by the World Health Organization (WHO) and as an urgent threat to public health by the Centers for Disease Control and Prevention (CDC). Its ability to form biofilms and resist desiccation and disinfectants is additionally alarming as these characteristics allow *A. baumannii* to thrive within hospital settings. The antibiotic resistance, the environmental persistence, along with the absence of identified host-damaging toxins in its genome, suggest that the virulence potential of *A. baumannii* is based on a 'persist and resist' strategy wherein these bacteria also resist complement-mediated killing and oxidative stress. At the genetic level, due to a plastic genome, we observe a high heterogeneity amongst isolates, adding complexity to the study of *A. baumannii* as an entity. Therefore, *A. baumannii* represents a modern and worldwide challenge which requires constant surveillance by the public health community.

KEY FACTS:

Isolation of extensively resistant and pan-drug-resistant strains ranked as 'high priority' by the WHO (global priority list of antibiotic-resistant bacteria to guide research, discovery and development of new antibiotics, 2017) and the CDC (antibiotic resistance threats in the USA, 2019).

Belongs to the 'ESKAPE' group of most problematic nosocomial pathogens.

Resistant to desiccation, disinfectant, oxidative stress, and complement-mediated killing.

First described as a fast-growing extracellular bacterium; several strains show a potential for intracellular growth in eukaryotic cells.

High genetic diversity; rapidly evolving bacteria, with some isolates competent for natural transformation.

Lipooligosaccharide instead of classical lipopolysaccharide, with 14 variants identified so far.

At least 128 polysaccharide capsule types identified so far.

Presence of several secretion systems (SSs): T1SS, T2SS, and T6SS, but absence of T3SS and T4SS usually found in Gram-negative pathogens.

Phenotypic heterogeneity by 'phase variation' within clonal populations, with virulent opaque and capsulated (VIR-O) and avirulent translucent and less capsulated (AV-T) types identified.

DISEASE FACTS:

Nosocomial, community-acquired, and opportunistic infections.

Broad infection sites [skin and soft tissue, urinary tract, digestive and respiratory tracts, blood, central nervous system (meningitis), etc.].

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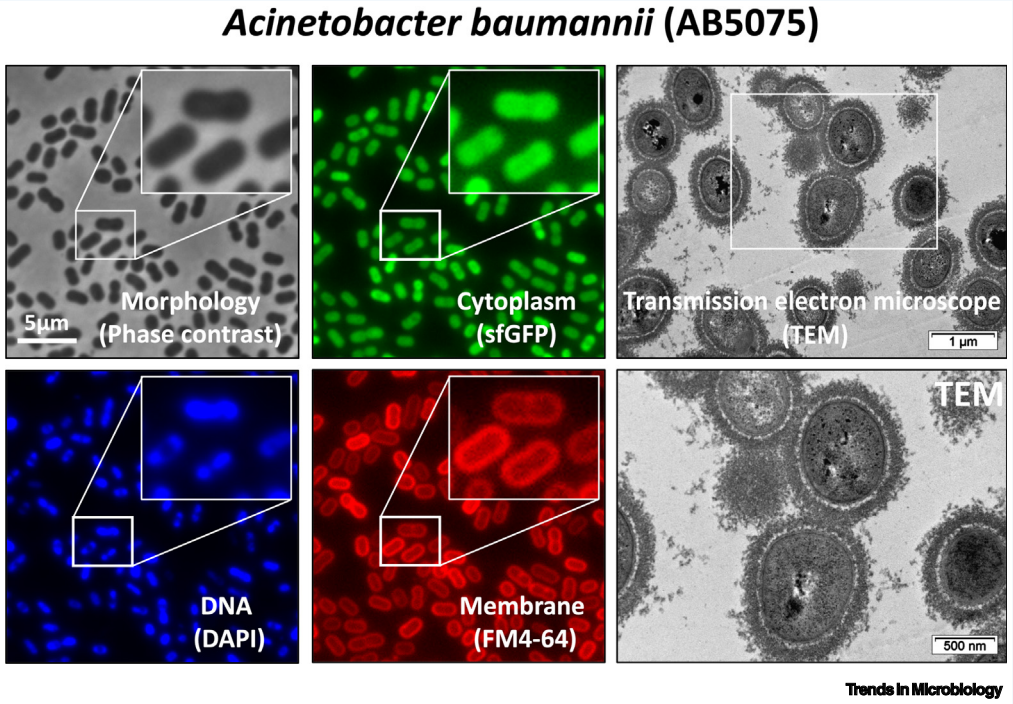

Can thrive in hospital settings, with a peculiar virulence based on a 'persist and resist' strategy.

Infection routes and factors favoring infections: colonization of mechanical devices such as catheters and ventilation equipment, open wounds, major trauma or burns, prolonged hospital stays, and immunocompromisation.

Therapeutic dead end because of last-resort antibiotic resistance.

TAXONOMY AND CLASSIFICATION:
KINGDOM: Bacteria
PHYLUM: Proteobacteria
CLASS: Gammaproteobacteria
ORDER: Pseudomonadales
FAMILY: Moraxellaceae
GENUS: *Acinetobacter*
SPECIES: *Acinetobacter baumannii*

Declaration of interests
No interests were declared.

Literature

1. Sarshar, M. *et al.* (2021) *Acinetobacter baumannii*: an ancient commensal with weapons of a pathogen. *Pathogens* 10, 387
2. De Oliveira, D.M.P. *et al.* (2020) Antimicrobial resistance in ESKAPE pathogens. *Clin. Microbiol. Rev.* 33, e00181-19
3. Wong, D. *et al.* (2017) Clinical and pathophysiological overview of *Acinetobacter* infections: a century of challenges. *Clin. Microbiol. Rev.* 30, 409–447
4. Nowak, J. *et al.* (2017) High incidence of pandrug-resistant *Acinetobacter baumannii* isolates collected from patients with ventilator-associated pneumonia in Greece, Italy and Spain as part of the MagicBullet clinical trial. *J. Antimicrob. Chemother.* 72, 3277–3282
5. Chin, C.Y. *et al.* (2018) A high-frequency phenotypic switch links bacterial virulence and environmental survival in *Acinetobacter baumannii*. *Nat. Microbiol.* 3, 563–569
6. Wyres, K.L. *et al.* (2020) Identification of *Acinetobacter baumannii* loci for capsular polysaccharide (KL) and lipooligosaccharide outer core (OCL) synthesis in genome assemblies using curated reference databases compatible with Kaptive. *Microb. Genom.* 6, e000339
7. Gebhardt, M.J. *et al.* (2015) Joint transcriptional control of virulence and resistance to antibiotic and environmental stress in *Acinetobacter baumannii*. *mBio* 6, e01660-15
8. Gallagher, L.A. *et al.* (2015) Resources for genetic and genomic analysis of emerging pathogen *Acinetobacter baumanii*. *J. Bacteriol.* 197, 2027–2035
9. Harding, C.M. *et al.* (2018) Uncovering the mechanisms of *Acinetobacter baumannii* virulence. *Nat. Rev. Microbiol.* 16, 91–102

https://doi.org/10.1016/j.tim.2021.11.008