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Bundesinstitut für Impfstoffe und biomedizinische Arzneimittel
Federal Institute for Vaccines and Biomedicines

COMBINE
Part of IMI AMR Accelerator

COMBINE Preclinical Bacterial Repository

Bacterial Identification

Bacterial Strain	DSMZ ID	Historical ID
Pseudomonas aeruginosa	DSM 50071	ATCC 10145

The bacterial species has been confirmed by 16S rDNA gene sequencing.

Bacterial Isolation

Country	Institution	Date	Source
Unknown	Unknown	Unknown	Unknown

Antimicrobial resistance

Meropenem	Levofloxacin
Not resistant	Not resistant

In vitro antimicrobial resistance has been determined following EUCAST guidelines.

Intended use

The COMBINE[1] Preclinical Bacterial Strain Repository contains Gram-negative bacterial strains shown to be reproducibly virulent in the COMBINE murine pneumonia models. The COMBINE protocol was developed together with stakeholders from academia, industry and regulatory experts to standardise and refine antimicrobial efficacy models. Key information were published in a summary report (Arrazuria et al., 2022)[2].

In Vivo Virulence

In vivo virulence was assessed in CD-1 mice rendered neutropenic by intraperitoneal administration of 150 mg/kg and 100 mg/kg cyclophosphamide on days -4 and -1 pre infection, respectively. Following intranasal inoculated with approximately 1-2x10^8 CFU, strains were considered virulent when the following criteria were met:

- Baseline bacterial burden of 6-7 $\log_{10}$ CFU/lung 2 h post infection;
- At least 1 $\log_{10}$ increase in CFU/lung relative to baseline at the humane or experimental endpoint (≤26 h);
- Endpoint being reached between 12 h and 26 h post infection.

In vivo virulence has been confirmed in two independent laboratories following the COMBINE protocol.

Acquisition

Strains of the COMBINE Preclinical Bacterial Repository are made available via the German Collection of Microorganisms and Cell Cultures (DSMZ).
https://www.dsmz.de/collection/catalogue/details/culture/DSM-50071

Contact

Inquiries may be addressed to IMI-COMBINE@pei.de.

[1] https://amr-accelerator.eu/project/combine/

[2] Arrazuria *et al.*, Front Microbiol, 2022, doi 10.3389/fmicb.2022.988725