



Tackling antibiotic
resistance together

Standardization of the murine pneumonia model

Rakel Arrazuria - Paul Ehrlich Institut (German Federal Institute for Vaccines and Biomedicines)

On behalf of the AMR Accelerator and COMBINE Consortium



Federal Institute for Vaccines
and Biomedicines


AMR Accelerator: Public-Private collaboration with the shared goal of progressing the development of new medicines to treat or prevent resistant bacterial infections (www.amr-accelerator.eu)

Who are we?




98 Participants	489 M€ Budget	9 Projects	15 Programmes in the Portfolio
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TUBERCULOSIS & NTM



Accelerating scientific discoveries and advancing the R&D pipeline of new and innovative agents to treat TB and NTM lung disease.

GRAM-NEGATIVES



Advancing the R&D pipeline of new and innovative agents to address AMR in Gram-negative bacteria.

CAPABILITY BUILDING



Accelerating and validating scientific discoveries in AMR. Coordinating and supporting projects across the AMR Accelerator.



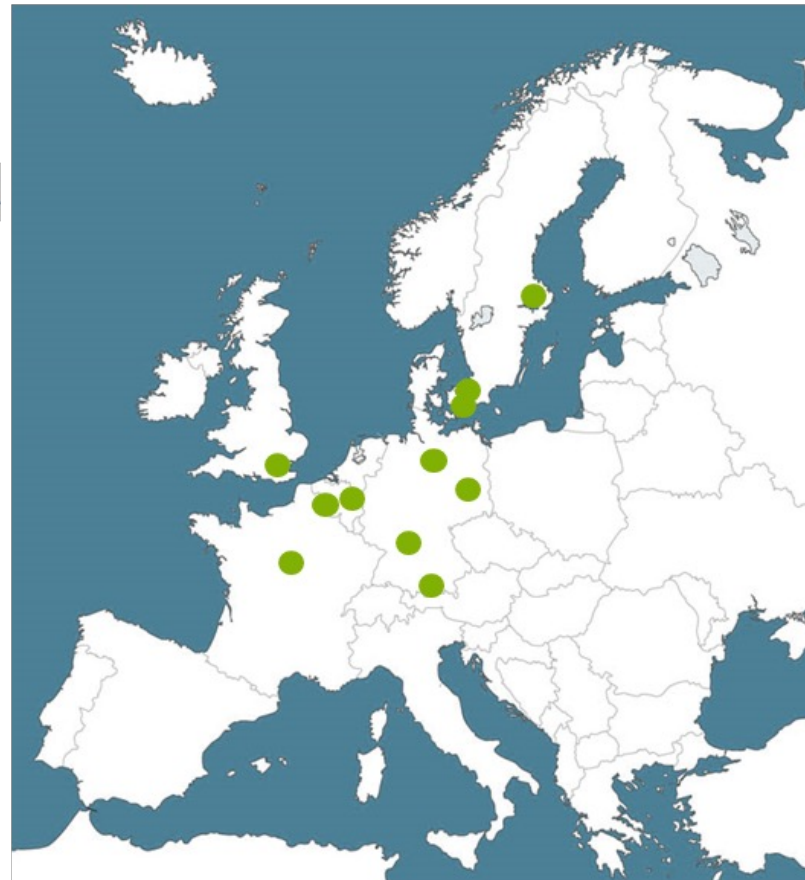
Part of IMI AMR Accelerator

- WP1: Coordination and support
- WP2: IT infrastructure and Data Management.
- WP3: Communication and Networking
- WP4: Clinical Trial Design
- WP5: Animal models**



Collaboration for prevention and treatment of MDR bacterial infections (COMBINE)

➤ 6 year project from Nov 2019 – Nov 2025



Universities, research organisations, public bodies, non-profit groups:

- Uppsala University (UU) Sweden **Coordinator**
- Paul-Ehrlich-Institut (PEI) Germany
- Fraunhofer Gesellschaft (FRAUNHOFER) Germany
- Statens Serum Institut (SSI) Denmark
- BEAM Alliance (BA) France

Small and medium-sized enterprises (SMEs) and mid-sized companies (<€500 m turnover):

- Asclepia (AC) Belgium
- GRIT42 (G42) Denmark
- BIOCOM (BC) Germany

EFPIA companies:

- GlaxoSmithKline (GSK) United Kingdom **Project Lead**
- Evotec (EVT) Germany
- Janssen (JNJ) Belgium

<https://amr-accelerator.eu/project/combine>

WP5: Animal Models & PK/PD

Improve animal infection model reproducibility and translation to clinical efficacy

Problem:

- Animal infection models are excellent tools, yet translational gaps remain
- Methods used for study conduct & analyses impact results
- Lack of standardization hinders interpretation & comparison

Our ambitious goals:

- Develop a standardized animal infection model
- Benchmark standard model using relevant control compounds
- Establish *in vivo* reference strain bank supported by data from the model
- Provide framework for PK/PD analysis & mathematical modelling
- Improve understanding of preclinical-to-clinical translation

Generate & Validate a standardized infection model

- Select appropriate model and parameters to standardize
- Generate efficacy data for control antibiotics using candidate strains

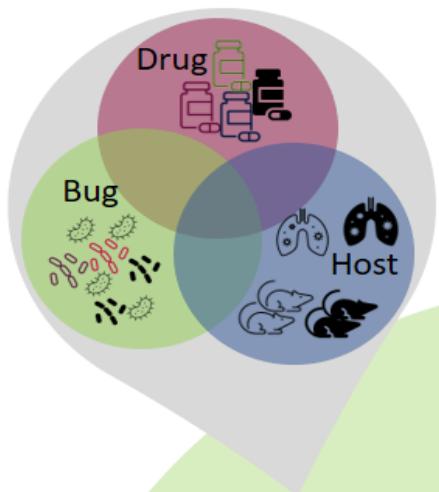
Establish Reference Strain Bank

- Identify strains that can be made available to the AMR community
- Select candidate strains that perform well in a standard model across labs

Improve Preclinical-to-Clinical Translation

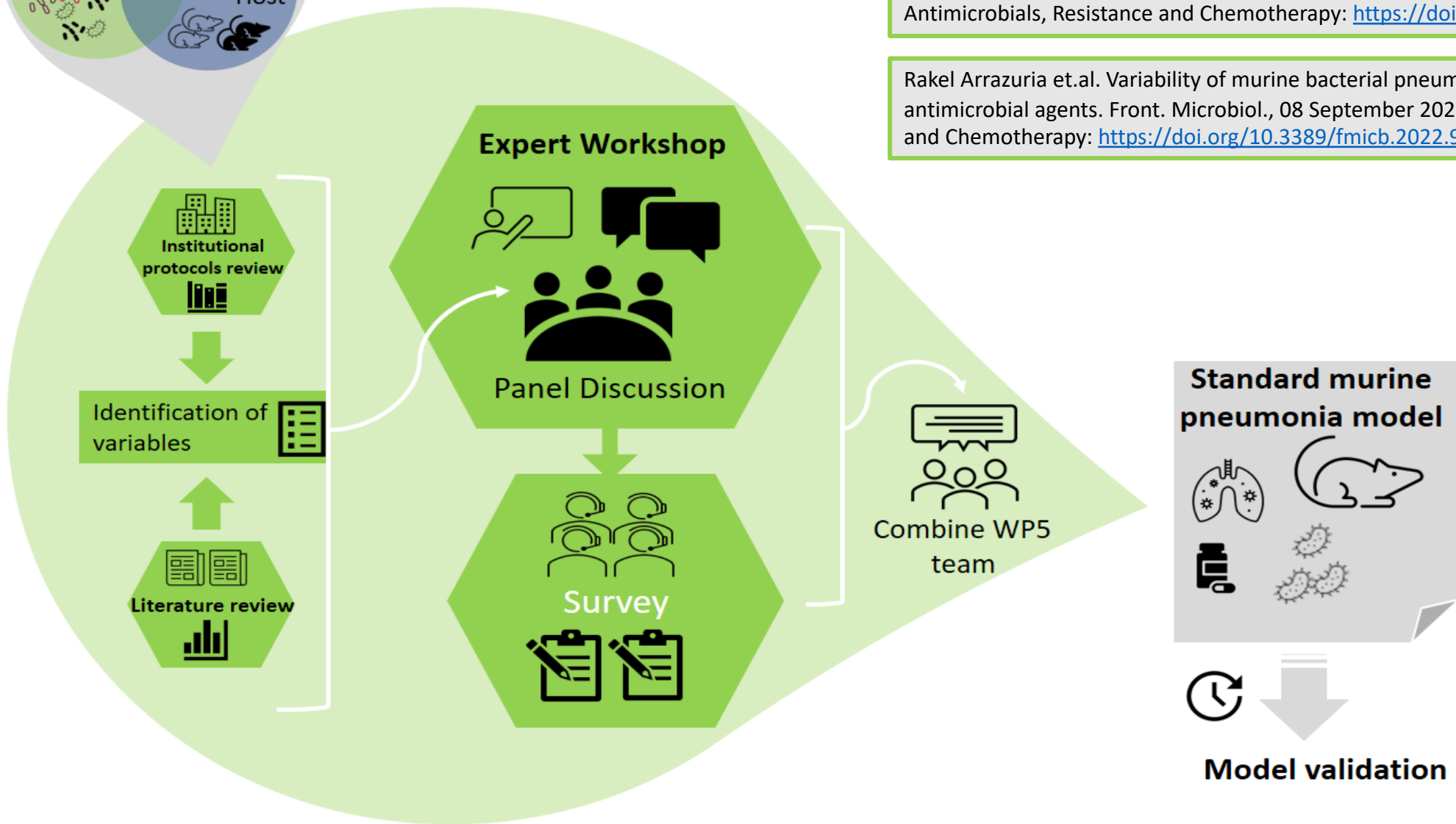
- Demonstrate how to best interpret and use the data for PK/PD modeling
- Evaluate how response in our standard model translates to the clinic

Standardization Process



Rakel Arrazuria et.al. Expert Workshop Summary:
Advancing towards a standardized murine model to evaluate treatments for AMR lung infections. Front. Microbiol., 08 September 2022 Sec. Antimicrobials, Resistance and Chemotherapy: <https://doi.org/10.3389/fmicb.2022.988725>

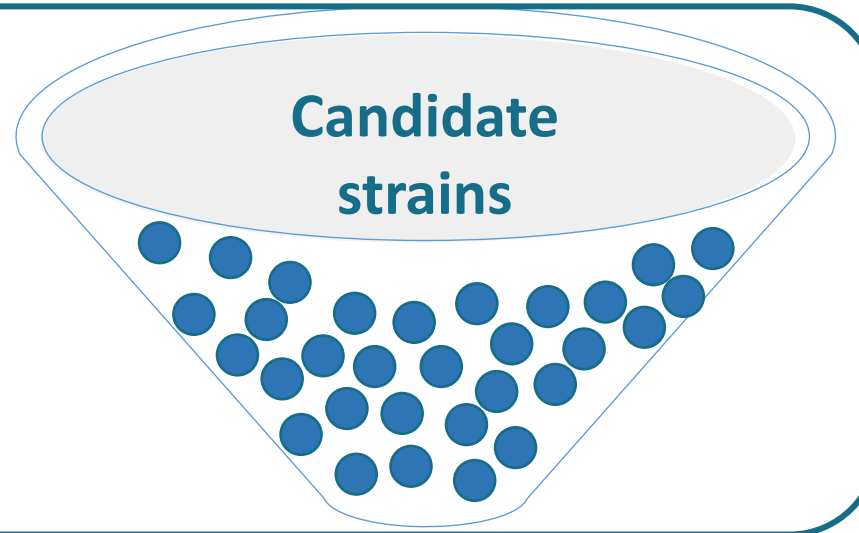
Rakel Arrazuria et.al. Variability of murine bacterial pneumonia models used to evaluate antimicrobial agents. Front. Microbiol., 08 September 2022 Sec. Antimicrobials, Resistance and Chemotherapy: <https://doi.org/10.3389/fmicb.2022.988728>



Selection of Isolates

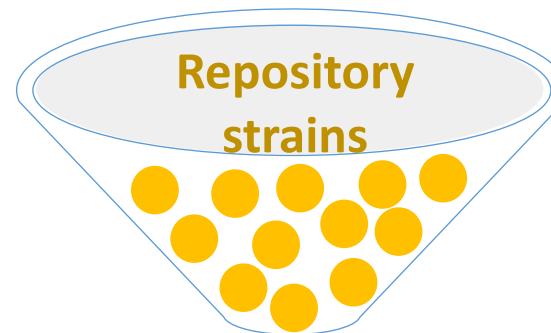
Chosen to test based on:

- Shareability
- Antibiogram
- Contemporary
- Characterization (if available)



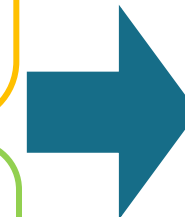
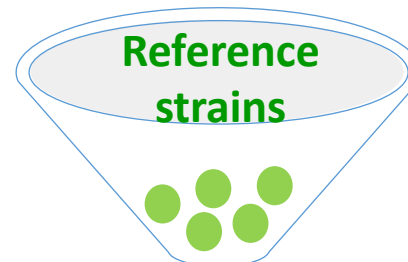
Candidate strains filtered by:

- Virulence
- Standard protocol criteria
- Mortality
- Expected +/- efficacy response



Ref strains chosen for:

- Standard protocol criteria
- PK/PD characterization



Leibniz-Institut
DSMZ-Deutsche Sammlung
von Mikroorganismen
und Zellkulturen GmbH

Work in progress

1. *Validate strains in model*

- To ensure consistent virulence in the model at multiple labs (SSI, PEI, GSK)

2. *Choose reference compounds*

- Examples of different classes (Meropenem and Levofloxacin)
- Reasonable to work with *in vivo*
- Maximize given resources (collaborations)

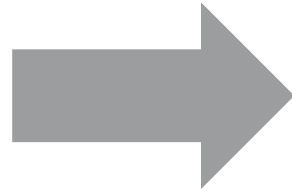
3. *Generate in vivo data*

- PK from infected mice
- PD for ≥ 3 strains of *P. aeruginosa* and *K. pneumoniae*

Our goal in WP5 is to move the AMR community

FROM:

1. Variability in animal models employed for pneumonia
2. Inconsistent strain use
3. Lack of consensus on interpretation
4. Varying application of mathematical modeling
5. Greater translational risk



TO:

1. Standardized & validated pneumonia model
2. (At least some) reference strains
3. More informed interpretation
4. Clear PK/PD modeling framework
5. Greater confidence moving to clinic with new antibacterials

Outreach and collaborations with other organizations

Strains



In vivo studies



- Input and advice on both our general strategy and the chosen parameters in to standardize pneumonia model
- Exchange ideas on study design for validation/benchmarking studies
- Highlight insights and discuss challenges

Would you like to collaborate with COMBINE?



Share **expertise**

*Contact us:
IMI-COMBINE@pei.de*



Support our
data quest

*Share your preclinical and
clinical pneumonia data*



Combine effort
on common
interests

*Conduct validation studies
in your lab
Share isolates for repository*



Acknowledgement

COMBINE WP5 Members

- **Bernhard Kerscher**, Division of Microbiology, Paul-Ehrlich-Institut, Langen, Germany
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All animal experiments were ethically reviewed as per local requirements prior to commencement of work.

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