GERMAN FEDERAL INSTITUTE
FOR RISK ASSESSMENT

15 YEARS
Science in the
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Bundesinstitut für Risikobewertung

"Selected outcomes of the research consortia RESET and MedVet-Staph on specific questions related to antimicrobial resistance“

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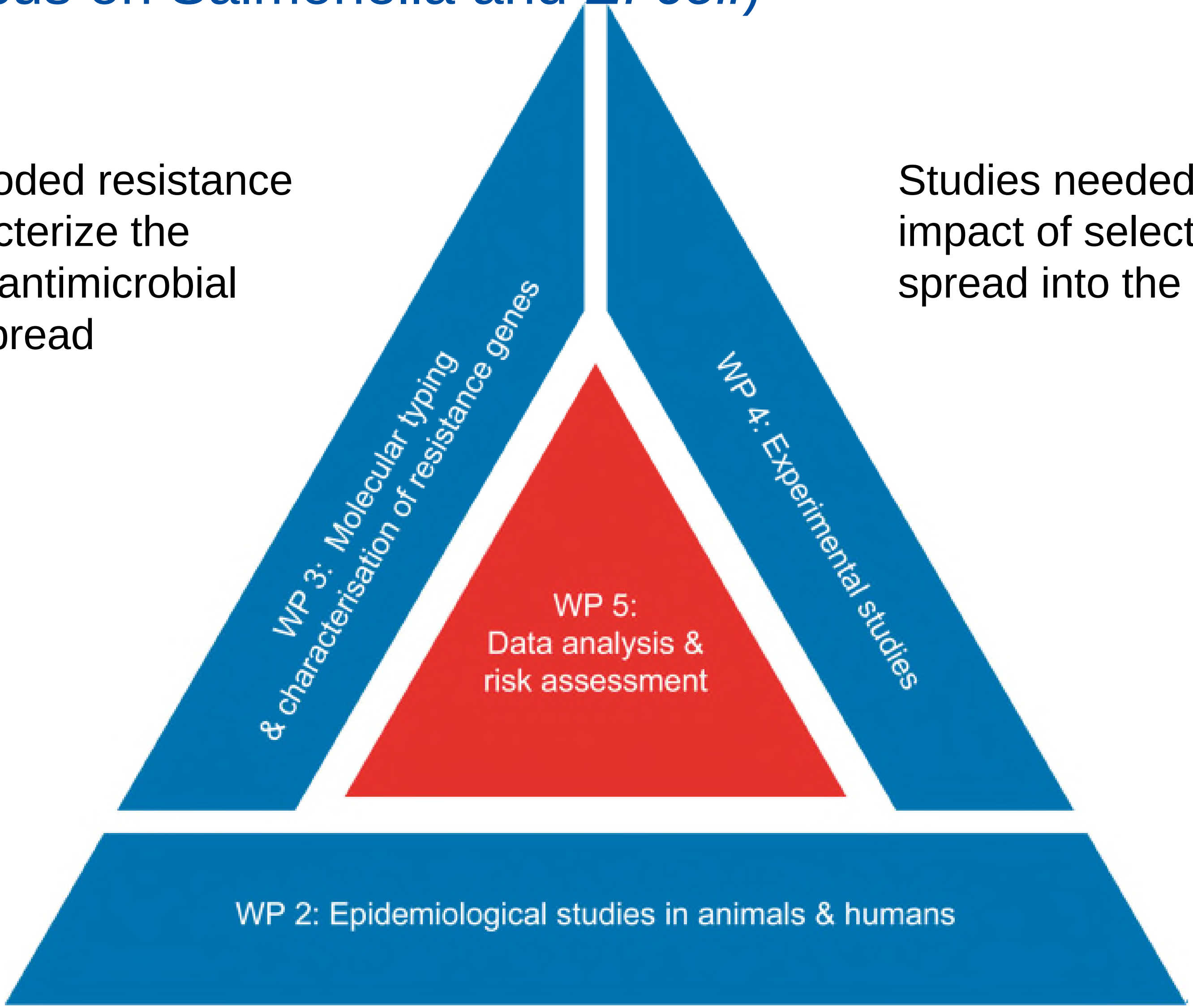
Extended-spectrum beta-lactamase (ESBL), AmpC beta-lactamase producing Enterobacteriaceae (with a focus on Salmonella and *E. coli*)

Plasmid encoded resistance genes characterize the dynamics of antimicrobial resistance spread

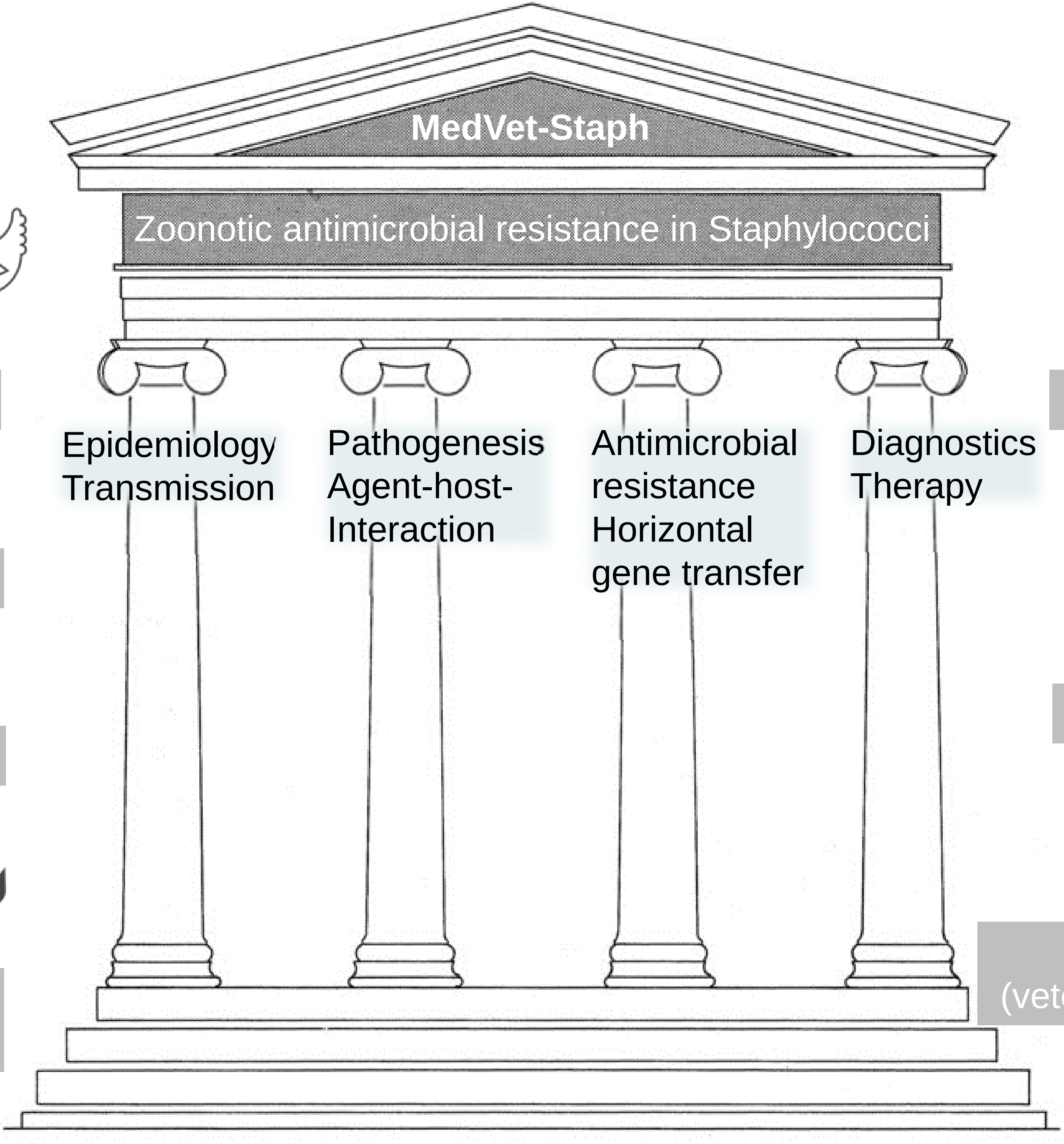
Studies needed to investigate impact of selective pressure and spread into the environment



ESBL/AmpC spread in time, region and between populations

Main results

- ESBL/AmpC- producing *E. coli* are widely spread
  - In livestock populations: 70-100% of farms were positive
  - In humans: 6.3% healthy community; 13% hospital admissions;
- Prevalence of ESBL/AmpC- producing Enterobacteria is increasing
- Infection with ESBL-producing *E.coli* may increase adverse health effects (duration of hospital stay, economic burden, mortality)
- ESBL/AmpC- producing *E. coli* are spread vertically and horizontally in livestock populations
- Selective pressure by antimicrobials in therapeutic and subtherapeutic concentrations is one of the triggers for their spread
- Clonal spread of some sequence types (e.g. ST 410) between animal and human populations could be demonstrated
- Current knowledge indicates a limited contribution of the food chain to colonisation of humans with ESBL-producing *E. coli*



MedVet-Staph

Zoonotic antimicrobial resistance in Staphylococci

Epidemiology
Transmission

Pathogenesis
Agent-host-Interaction

Antimicrobial resistance
Horizontal gene transfer

Diagnostics
Therapy

Livestock

Slaughter

Foodstuff

Companion animals

Farmers, vets

Community

Public health (veterinary & human)

Main results

- Overall *S. aureus* nasal carriage is 41% in the community
- Occupational health risk for farmers and vets, especially when working with pigs. Contact to animals main risk factor
- Household members of this risk population are more frequently (11%) colonised with MRSA than the general population (0,7%)
- Of patients with MRSA CC398, 21 (38%) did not report livestock contact
- MRSA was also detected in wound samples from companion animals
- MRSA are widely spread in livestock and transmitted along the food chain; heterogeneity of types increases along the food chain
- Slaughter process has major impact on contamination rate of carcasses and fresh meat
- Adhesion of *S. aureus* to surfaces in the kitchen environment supports cross-contamination and re-contamination
- Good hygiene practice limits spread of MRSA during food preparation

Thank you for your attention

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