

## Challenges in Research and Risk Assessment Field

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## Research and specific data needs

- A global research agenda should complement National and European initiatives, involving all relevant stakeholders
- More clarity on the factors guiding emergence and selection of resistant bacteria is needed
- Quantitative source attribution should be enabled to understand better the impact of different sources (e.g. animal populations) and pathways
- The impact of human use on animal health should be addressed (e.g. spread of carbapenemases)
- The effectiveness for the food chain and the relevance for public health as well as the spread into the environment should be considered



## **Emerging risks**

- Current monitoring system covers known risks in major animal populations, but not each animal population is covered, and those covered can not be monitored continuously
- We have several gaps, most probably we will miss new mechanisms, new risks
- We have detected quite lately very important emerging risks, e.g. MRSA, ESBL
- Shifts in use patterns may trigger the emergence of new resistance types. Will we miss the spread of carbapenemase producing strains in livestock populations?
- What about food of **vegetable** origin (e.g. imported fruits)?
- What about **wildlife** (e.g. migratory birds) as vectors?
- What about **sewage plants** as source for spreading risks?



## Impact of trade and travel

- Antimicrobial usage policies are quite different globally. Trade may have a major impact on the spread of antimicrobial resistance
- **Trade of animals** will increase the risk of introduction bugs into the livestock populations, health certificates does not cover these risks
- **Trade of goods** increases the risk of exposure of human populations, and spreading of resistant bacteria
- Travel of humans is very relevant, as new resistance types (e.g. NDM) have been imported into our countries
- Traceability of goods is insufficient. Transmission pathways can hardly be identified, emerging new resistance mechanisms may spread widely before the true origin has been identified