



Public Health  
England

# Research gaps – medical needs

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## Understanding the origins of resistance

- Where do clinically-relevant 'R genes' come from ?
  - very poor knowledge even for prevalent types e.g. TEM
  - few exceptions e.g. CTX-M
  - defining better the resistome for last resort agents
- Where does 'escape' to clinically-relevant species occur ?
  - How frequent are escape events ?
- Can we explain the differential success of 'R genes' ?
  - How / where do they associate with integrons / IS / transposons / plasmids ?
  - The dynamics of gene / carrier / host strain combinations
- Can we develop models of clinical impact and cost-effective interventions?



## What happens in the human gut ?

- Better understanding of:
  - 'R gene' transfer in the gut: colonists or during transient passage
  - the ecology of 'high-risk clones' (HiRiCs)
  - how do they compete with each other / normal flora ?
- How are the above affected by antibiotics ?
- Obscure gut microbiota as hosts of clinically-relevant 'R genes'
  - confounders of rapid diagnostics or legitimate targets ?



## What happens in the environment ?

- Better understanding of:
  - ‘R genes’ in clinically-relevant species in the environment
  - antibiotic residues in the environment
  - the ecology of resistance (blooms and extinctions)
  - hospital outflows vs. agricultural run off vs. industrial outflows
  - rivers vs. bathing waters
  - model exposure and assess public health risk
  - would interventions be cost-effective ?



## ...and finally, a blatant advert

- extensive collections of MDR clinical isolates
- independent evaluations of:
  - diagnostics
  - AST platforms
  - developmental antibiotics
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