# *World Health Organization period prevalence survey on multidrug-resistant microorganisms in health care*

B. Allegranzi[1], N. Damani[1], A. Gayet-Ageron[2], A. Stewardson[3], S. Wallace[4], D. Pittet[2]

[1] WHO Infection Prevention and Control Global Unit, Service Delivery and Safety, Geneva, Switzerland; [2] Infection Control Programme and WHO Collaborating Centre on Patient Safety, University of Geneva Hospitals and and Faculty of Medicine, Geneva, Switzerland; [3] Hand Hygiene Australia and Austin Health, Melbourne, Australia; [4]Southern Health & Social Care Trust, Portadown, UK

## Background

Antimicrobial resistance (AMR) represents a significant threat to human health. To date, there is a paucity of AMR data at the global level. Moreover, developing countries are under-represented in existing reports despite the likely higher AMR burden in such countries when compared to high-income countries.

## Material/methods

We conducted a **laboratory-based global survey on the prevalence of multidrug-resistant organisms (MDROs) in inpatient clinical blood and urinary specimens in a diverse range of healthcare facilities** worldwide, while also evaluating **laboratory microbiology capacity.**

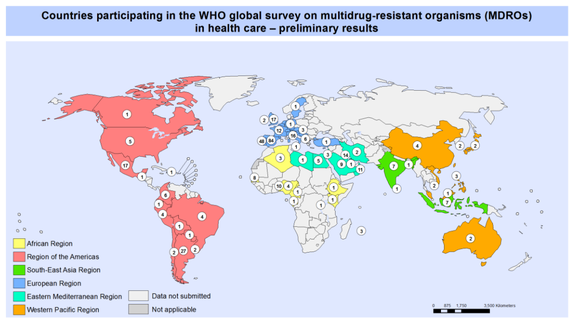
**Summary of methods :**

- **Design:** online survey (1st March-30 June 2014) based on:
  - *routine collection of clinical blood and urine (MSU & CSU) culture specimens*
  - *Only 1st isolate from inpatients during one week*
- **Participants:** health-care settings registered for the WHO SAVE LIVES: Clean Your Hands global campaign and other WHO-associated networks
- **Main targeted resistance patterns:**
  - methicillin-resistant *Staphylococcus aureus* (MRSA)
  - vancomycin-resistant enterococci (VRE)
  - extended-spectrum β-lactamase producing Enterobacteriaceae (ESBL-PE)
  - carbapenem-resistant Enterobacteriaceae (CRE)
  - multi-resistant *Acinetobacter* species (MRAB)

- To evaluate **laboratory microbiology capacity,** we assessed microbiologic **methods used for bacterial identification** and **identification of resistance** (Table).

| **Methods used for bacterial identification** | |
|---|---|
| ***S. aureus*** | **Gram stain AND** confirmation either by *Slide or Tube Coagulase* **OR** Automated **OR** Non-automated methods |
| **Enterococci spp.** | **Gram stain AND** confirmation either by Automated **OR** Non-automated methods |
| **Enterobacteriaceae** | **Gram stain AND** confirmation either by Automated **OR** Non-automated methods |
| **Methods used for identification of resistance** | |
| **Gram stain AND** use of one of the following susceptibility testing methods: **CLSI, or EUCAST, or BSAC or SFM** | |

## Results

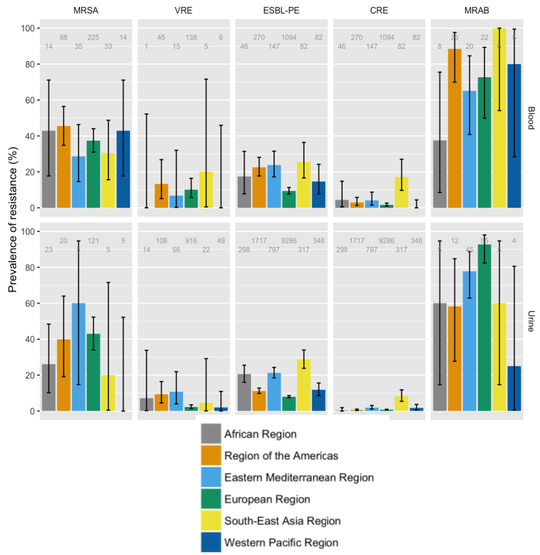



**67 countries**
**420 laboratories**

- **Laboratories with clinical microbiologist: 85.5%.**
- **Laboratories meeting minimum standards for both bacterial identification and identification of resistance:**
  - *Staphylococcus aureus*: 380 (**90.5%**)
  - Enterococci spp: 359 (**85.5%**)
  - *Enterobacteriaceae*: 368 (**87.6%**)

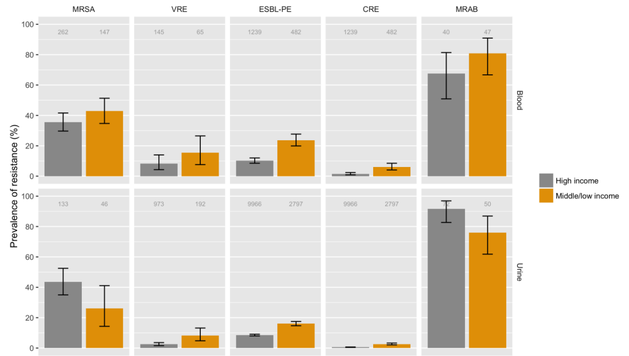
- Capacity was lowest in Africa, particularly for identification of resistance.
- **Enterobacteriaceae** were the most common organisms (1,721 blood and 12,763 urine **strains), and had lowest proportion of MDRO** (Figure 1).
- ***S. aureus*** was the next most frequent organism from blood cultures (n=409), with 38.1% (32.8–42.3) MRSA (Figure 1).

**Figure 1. Prevalence of multidrug resistance**




- MDRO prevalence tended to be higher in low- and middle-income countries.

**Figure 2. Prevalence of multidrug resistance, by World Bank economy**




## Conclusions

This survey demonstrates the feasibility of a global study of MDRO prevalence, and highlights the need for improved laboratory capacity in Africa.

The estimated of prevalence of MDROs among important pathogens in this survey provides a useful addition to the existing evidence, and suggests one possible means for ongoing large scale surveillance. Repeated surveys may be useful to monitor global trends in AMR.

World Health Organization

 Contact: Prof B. Allegranzi, allegranzib@who.int