

# Genomic Surveillance of Antimicrobial Resistance: One Health Approach

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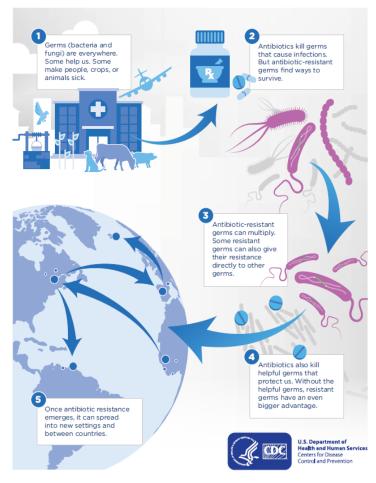








#### **How Antibiotic Resistance Spreads**



- Antimicrobial Resistance (AMR) is a pressing global health issue, rendering common antibiotics ineffective against widespread bacterial infections
- The 2022 Global Antimicrobial Resistance and Use Surveillance System (GLASS) report highlighted median reported rates in 76 countries of 42% for third-generation cephalosporin-resistant *E. coli* and 35% for methicillin-resistant *Staphylococcus aureus*, which are major concerns



**RESEARCH ARTICLE** 

Excess mortality attributable to antimicrobialresistant bacterial bloodstream infection at a tertiary-care hospital in Indonesia .."We used routine databases of the microbiology laboratory and hospital admission at Dr. Wahidin Sudirohusodo Hospital, a tertiary-care hospital in South Sulawesi from 2015 to 2018. Of 77,752 hospitalized patients, 8,341 (10.7%) had at least one blood culture taken.."

Pathogens	Total	Community origin	Hospital origin	P value
Escherichia coli				
3 <sup>rd</sup> generation cephalosporin-resistant	78% (81/104)	50% (6/12)	82% (75/92)	0.01
3 <sup>rd</sup> generation cephalosporin-resistant plus carbapenem resistant	4% (4/104)	0% (0/12)	4% (4/92)	0.46
Klebsiella pneumonia				
3 <sup>rd</sup> generation cephalosporin-resistant	56% (96/171)	56% (18/32)	56% (78/139)	0.99
3 <sup>rd</sup> generation cephalosporin-resistant plus carbapenem resistant	25% (43/171)	25% (8/32)	25% (35/139)	0.98
Staphylococcus aureus				
Methicillin-resistant	51% (124/245)	61% (30/49)	48% (94/196)	0.10
Acinetobacter spp.				
Carbapenem-resistant	48% (82/171)	13% (1/8)	50% (81/163)	0.04
Pseudomonas aeruginosa				
Carbapenem-resistant	19% (13/68)	33% (2/6)	18% (11/62)	0.35



Original Article

Nasopharyngeal carriage rate, serotype distribution, and antimicrobial susceptibility profile of *Streptococcus pneumoniae* isolated from children under five years old in Kotabaru, South Kalimantan, Indonesia

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**Table 3** Antibiotic profile for 34 multidrug resistant *S. pneumoniae* isolates from children under five years old in Kotabaru, South Kalimantan, Indonesia.

Antibiotics	Sussceptible	Intermediate	Resistant	Range MICs	
	n(%)	n(%)	n(%)		
Penicillin <sup>a</sup>	19 (56)	9 (26)	6 (18)	0.12 - >4	
Amoxicilin/Clavulanic Acid 2:1	13 (38)	10 (29)	11 (32)	≤2/1−8/4	
Cefepime <sup>a</sup>	18 (53)	16 (47)	0 (0)	≤0.5–2	
Cefotaxime <sup>a</sup>	23 (68)	11 (32)	0 (0)	≤0.12−2	
Ceftriaxone <sup>a</sup>	20 (59)	13 (38)	1 (3)	≤0.12 - >2	
Cefuroxime	5 (15)	0 (0)	29 (85)	≤0.5 - >4	
Moxifloxacin	34 (100)	0 (0)	0 (0)	≤1	
Levofloxacin	28 (82)	0 (0)	6 (18)	1–2	
Meropenem	5 (15)	18 (53)	11 (32)	≤0.25−1	
Ertapenem	33 (97)	1 (3)	0 (0)	≤0.5−2	
Vancomycin	34 (100)	0 (0)	0 (0)	≤0.5−1	
Azithromycin	5 (15)	0 (0)	29 (85)	≤0.25 - >2	
Erythromycin	5 (15)	0 (0)	29 (85)	≤0.25 - >2	
Tetracycline	3 (9)	0 (0)	31 (91)	≤1 - >8	
Trimethoprim/Sulfamethoxazole	0 (0)	4 (12)	30 (88)	1/19 - >4/76	
Linezolid	34 (100)	0 (0)	0 (0)	0.5-1	
Clindamycin	19 (56)	0 (0)	15 (44)	≤0.12 - >1	
Chloramphenicol	33 (97)	0 (0)	1 (3)	2–16	

<sup>&</sup>lt;sup>a</sup> Penicillin, ceftriaxone, cefotaxime, and cefepime using CLSI 2019 non-meningitis breakpoints. For penicillin 4  $\mu$ g/mL was intermediate and  $\geq$ 8  $\mu$ g/mL was resistant. While for Cefepime, Cefotaxime, Ceftriaxone, 2  $\mu$ g/mL was intermediate and  $\geq$ 4  $\mu$ g/mL was resistant.



Streptococcus pneumoniae

Penicillinase-stable β-lactams

Staphylococcus aureus

Tetracyclines
Aminoglycosides
Carbapenems
Polymyxins

Acinetobacter spp.

Sulfonamides, trimethoprim Fluoroquinolones Extended-spectrum cephalosporins Carbapenems Polymyxins Penicillins

Escherichia coli

Fluoroquinolones
Extended-spectrum
cephalosporins Carbapenems

Salmonella spp.

Sulfonamides and trimethoprim
Fluoroquinolones
Extended-spectrum cephalosporins
Carbapenems
Polymyxins
Penicillins

Klebsiella pneumoniae

Global Antimicrobial Resistance and Use Surveillance System (GLASS) priority pathogens

Extended-spectrum cephalosporins Macrolides Aminocyclitols Fluoroquinolones Aminoglycosides

Neisseria gonorrhoeae

Triazole antifungals
Amphotericin B
Echinocandin antifungals

Candida spp.\*

Fluoroquinolones
Extended-spectrum cephalosporins
Macrolides

Shigella spp.

Extended-spectrum cephalosporins Aminocyclitols Quinolones Polymyxins

Pseudomonas aeruginosa\*

Annex 2. Global Antimicrobial Resistance and Use Surveillance System priority pathogens and associated antimicrobial resistance



## Whole-Genome Sequencing in Genomic Surveillance

- Disease surveillance and outbreak investigation
- Vaccine Development and Monitoring:

- Identification of Pathogens
- Outbreak Tracing

- Strain Variation
- Vaccine Target Identification

- Antimicrobial Resistance Monitoring:
- Identification of Resistance Genes
- □ Surveillance of Resistance Patterns

- Public Health Response:
- □ Real-Time Monitoring
- Targeted Intervention



## Whole-Genome Sequencing in Genomic Surveillance

- Genomic Epidemiology:
- Population Dynamics
- Contact Tracing
- One Health Approach:
- Interconnectedness: WGS supports one health approach by integrating genomic data from humans, animals, and the environment



Aim of study: To characterize analysis the bacterial pathogens both phenotypic and genomic data from community, health facilities (hospital), food production animal and environment and antimicrobial use (AMU) in hospital, community, veterinary and agricultural.

Topic: Infectious disease and immunology (Health)



## Project timeline:

### 1<sup>st</sup> year :

- Sample collection from different hospitals (WHO priority pathogen isolates such as ESBL, Carbapenem resistant organisms, MRSA, *S. pneumonia*-penicillin resistant, from any clinical specimens)
- Sample collection and isolation of WHO priority pathogen from community
- Data collection of antimicrobial use in hospital is using AMU PPS method adopted from WHO.

### 2<sup>nd</sup> year

- Sample collection and isolation of WHO priority pathogen from animal (chicken), food product (meat, shrimp) and environment (water and sediment)
- History of antimicrobial use in community, animal is using questionnaires.
- Extraction of bacterial DNA from all samples

### 3<sup>rd</sup> year

- Library preparation for whole genome sequencing (WGS)
- Bioinformatic analysis of WGS result, to characterize of AMR bacteria, mechanism of resistance,

transmission of antimicrobial gene (ARG) between human, animal and environment.



## Thank you