WHONET Epidemiology Report- Animal Health

World Health Organization

WHO Test Laboratory

August 24, 2022

Table of contents

1. Data volume

Documenting the volume of testing performed by a laboratory is useful for monitoring changes in sampling practices over time and for comparing the workloads between laboratories. One may also identify time periods where data entry is incomplete, and many laboratories experienced a significant decrease in bacteriological testing in April 2020 with the arrival of COVID-19.

Some laboratories enter all bacteriological results into WHONET, whereas other only enter the results for positive samples. Some laboratories enter the results from other laboratory sections, including mycology, parasitology, and virology.

The below table and figure present the number of isolate records and the number of animals over time.

Laboratory	Number of isolates	Number of patients	Isolates per patient	Unknown	2000
TST	400	400	1	37	363

Table 1: The number of isolates and animals by laboratory over time. For each time period, the numbers indicate the number of animal records, including negative results.

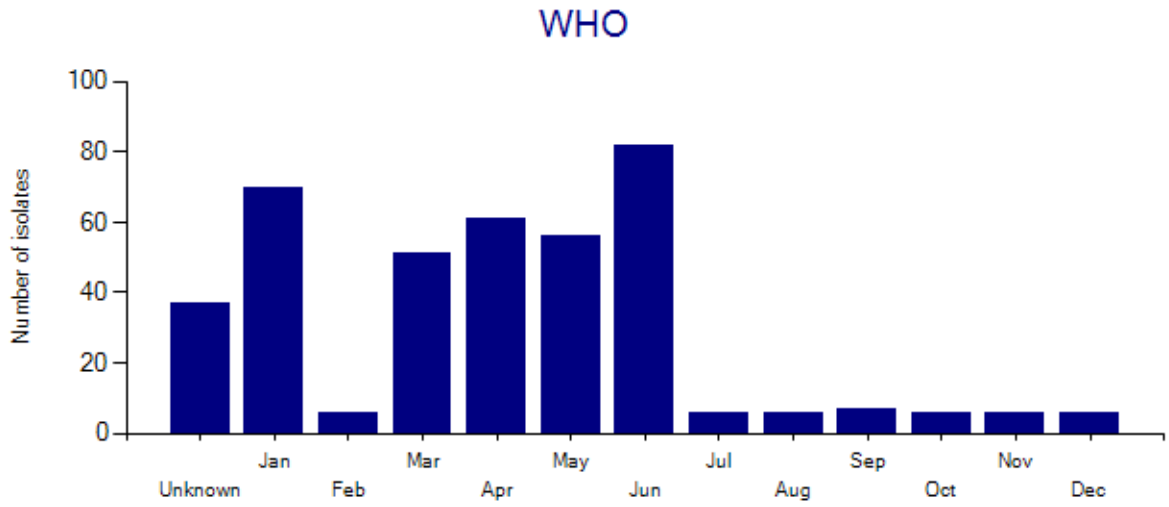

Figure 1: The distribution of isolates over time, including negative results.

The table includes the average number of isolate records per animal. This metric quantifies how often animals have multiple samples taken over time. In low-resource settings, this number is typically between 1.1 and 1.5 isolates per animal. A lower number may indicate that there are few animals with multiple samples, but it may also suggest that there are no meaningful identification numbers that can be used to track animals over time. A higher number may suggest one of two problems: 1) identification numbers are reused for different animals over time; or 2) there may be a problem in the data export from a laboratory information system or in the BacLink configuration.

2. Animal and sample details

2.1 Animal demographics

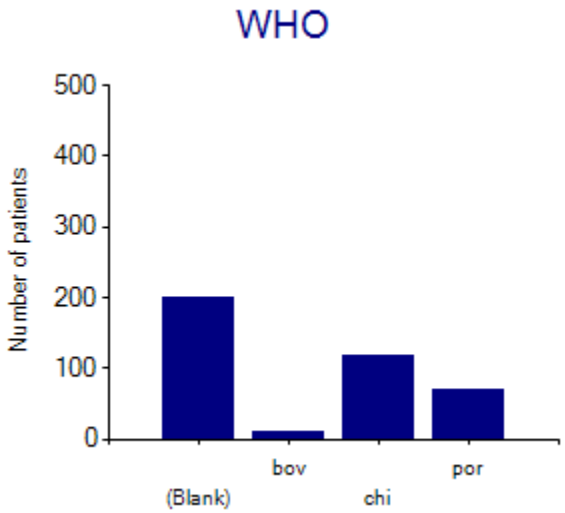

Figure 2: Animal species by country

The distribution of animals by sex and age group is displayed in the below figures.

- Sex: Male - 50%, Female - 50%
- Median age group: Male = 1-4, Female = 1-4

The age distribution will reflect the animal population served by the laboratory.

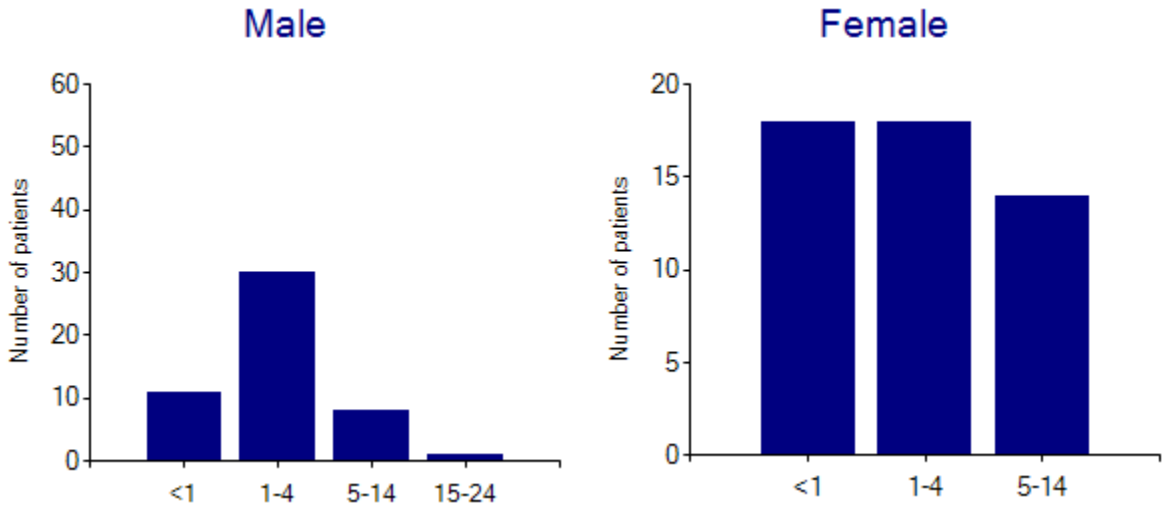

Figure 3: Distribution of the number of animals by sex and age group

2.2 Location details

The distributions of animals by top ten "location" and "location type" are displayed below. The location generally refers to the specific location where samples are collected, such as "Neurology", "Diabetes clinic", or the name of a town, farm, restaurant, or environmental site.

Location type is a category of location such as "inpatient", "outpatient", "farm", "restaurant", or "river". The use of standard WHONET codes is recommended to facilitate comparison of results between laboratories, but this is not required.

Location	Number of isolates	(%)	Number of patients	Isolates per patient
hosp1	61	15.2	61	1
slaugh	40	10	40	1
hosp2	39	9.8	39	1
Upstre	37	9.2	37	1
Downst	36	9	36	1
Wet ma	26	6.5	26	1
farm1	24	6	24	1
mark2	20	5	20	1
rest3	19	4.8	19	1
vet1	19	4.8	19	1

Table 2: The distribution of isolates and animals by location. The location codes are those used by the laboratory to identify the specimen collection site.

Location type	Number of isolates	(%)	Number of patients	Isolates per patient
(Blank)	200	50	200	1
sto	54	13.5	54	1
far	41	10.2	41	1
sla	40	10	40	1
mar	39	9.8	39	1
vet	19	4.8	19	1
res	7	1.8	7	1

Table 3: The distribution of isolates and animals by location type. The user of standard WHONET location types is recommended to facilitate comparisons with other laboratories, but is not required.

2.3 Sample details

As displayed in the below figure, WHONET specimen types can be grouped into eight broad categories: Blood, Genital, Respiratory, Soft tissue and body fluids, Stool, Urine, Other, and Unknown.

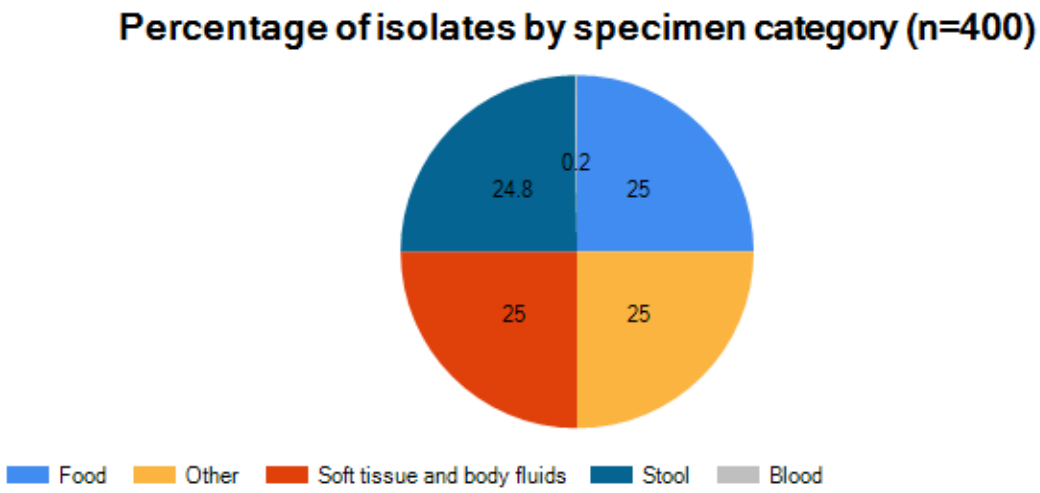

Figure 4: The figure shows the number of isolates stratified by specimen category.

3. Organism statistics

3.1 Organism frequencies

The most common use of WHONET is for bacterial results. However, WHONET can be used to manage results from other pathogens. The below table summarizes results according to organism type.

Organism type	Number of isolates	(%)	Number of patients	Isolates per patient
Aerobic Gram-negative bacteria	400	100	400	1

Table 4: Distribution of results by organism type.

** Negative results: This category includes findings such as "No growth", "No enteric pathogens found", "Normal flora", and "Mixed bacterial species present".*

The below table displays the most frequent results and the average number of isolates per animal. For community pathogens, this average number of isolates per animal is usually low, for example less than 1.2. For hospital pathogens, the average number of isolates per animal is often much higher, especially in intensive care units.

Organism	Code	Number of isolates	(%)	Number of patients	Isolates per patient
Escherichia coli	eco	168	42	168	1
Salmonella sp.	sal	146	36.5	146	1
Campylobacter jejuni	caj	41	10.2	41	1
Campylobacter sp.	cam	41	10.2	41	1
Campylobacter coli	cco	3	0.8	3	1
Escherichia coli, enteropathogenic (EPEC)	eep	1	0.2	1	1

Table 5: The distribution of the most common organism results.

The below table summarizes WHONET's alerts for "important species". Such pathogens are typically of public health importance because of their potential for outbreaks. They are often included in national disease control programs.

Organisms	Number of isolates	Priority
Salmonella sp.	146	Medium priority
Campylobacter coli	3	Medium priority
Campylobacter jejuni ss. jejuni	41	Medium priority

Table 6: Public health alerts - important species

3.2 Organism frequencies by specimen categories

The below figures display the most frequent results by specimen category. The most common pathogens are listed below by category.

Specimen category	Most common organism (%)
Blood	Salmonella sp. - (100%)
Food	Salmonella sp. - (56%)
Other	Escherichia coli - (100%)
Soft tissue and body fluids	Salmonella sp. - (32%)
Stool	Salmonella sp. - (58%)

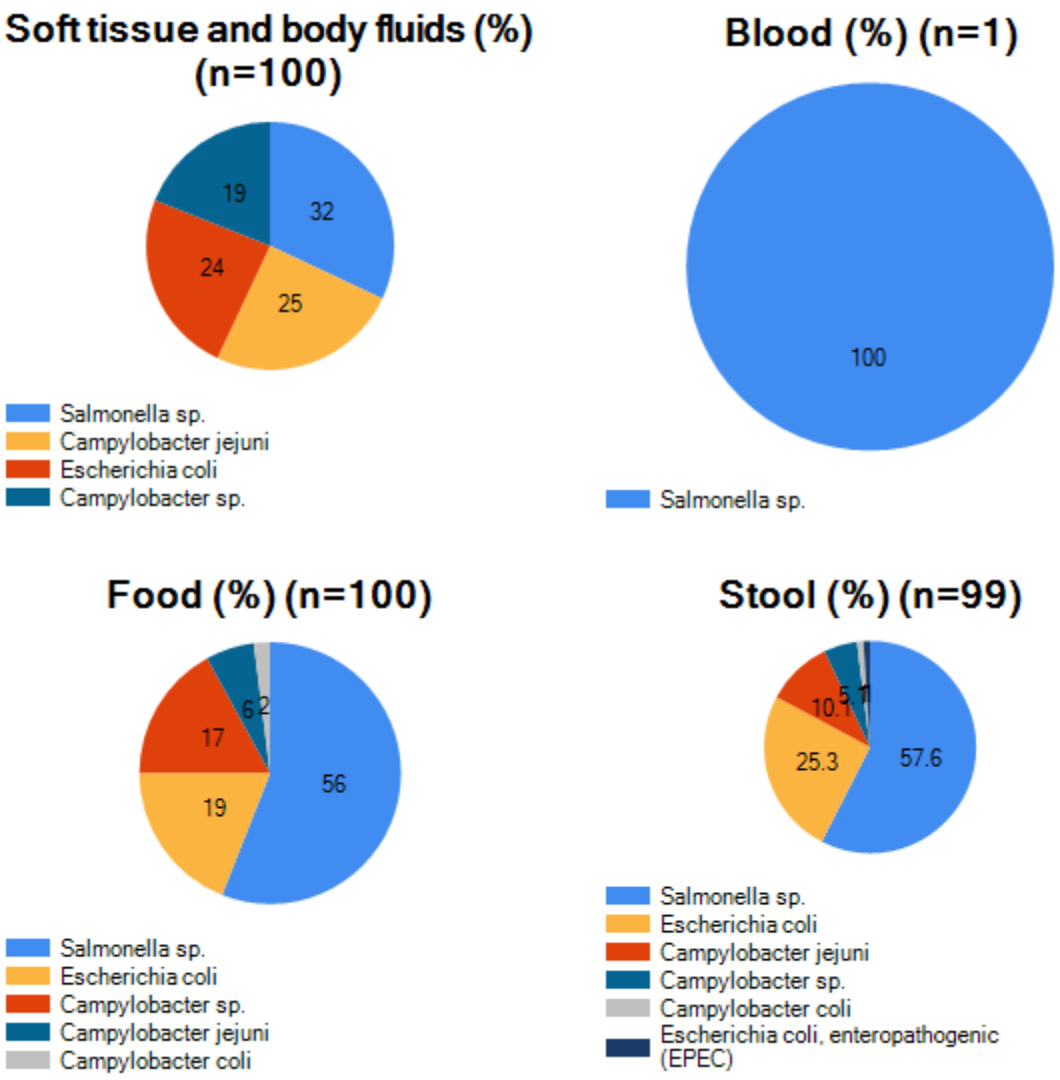

Figure 5: Most common organisms by specimen category. Numbers represent the percentage of isolates.

3.3 Organism trends

It is valuable to study changes in organism isolation over time. Organism frequencies depend on several factors.

The frequency of organisms seen in a microbiology laboratory may change over time for different reasons.

- Microbial factors
    - Long-term changes in organism epidemiology related to organism dissemination, virulence factors, and disease prevention measures such as vaccination and improved sanitation
    - Short-term changes suggestive of disease outbreaks. Statistical algorithms for automated outbreak detection are described in a separate section.
- Non-microbial factors

- Healthcare services provided and animal populations
- Sampling practices
- Laboratory capacity and practices for organism identification

A simple way to look for long-term changes is with simple linear regression of organism counts over time, as shown in the below table.

Organism	Q1-00	Q2-00	Slope
Campylobacter jejuni ss. jejuni	17	24	7.0
Campylobacter sp.	12	29	17.0
Salmonella sp.	47	99	52.0

Table 7: Organisms with statistically significant increases in organism frequency over time using simple linear regression. p<0.05 - The slope indicates that estimated change in the number of animals by quarter.

Organism	Q1-00	Q2-00	Slope
Escherichia coli	49	45	-4.0

Table 8: Organisms with statistically significant decreases in organism frequency over time using simple linear regression. p<0.05 - The slope indicates that estimated change in the number of animals by quarter.

4. Antimicrobial statistics

4.1 Gram-positive and Gram-negative antibiograms

Appendix A contains the cumulative antimicrobial susceptibility test statistics for Gram-positive and Gram-negative bacteria, typically known as an "antibiogram". The number of isolates tested is greater than or equal to 20. The official recommendation from the CLSI M39 document and others is at least 30 isolates, but a limit of 20 is still useful, especially in a low-resource setting with smaller data volumes and for organisms of clinical importance.

Policymakers must be very aware of problems in laboratory test quality and different types of bias due to animal presentation, sampling practices, and laboratory test practices. Routine microbiology laboratory data typically underestimates the incidence of microbial disease but overestimates the proportion of resistance.

4.2 Isolate alerts - Important resistance

The below table summarizes WHONET's high- and medium-priority "important resistance" alerts. The findings should be confirmed to ensure that there is no error in the organism identification or in the antimicrobial susceptibility test.

WHO has defined a "Global Priority List of Antimicrobial Resistant Bacteria". These are summarized in a separate section.

Organisms	Alert	Number of isolates	Priority
Enterobacteriaceae	Carbapenems = Non-susceptible	1	High priority
Salmonella sp.	Cephalosporin III = Non-susceptible	23	High priority
Salmonella sp.	Fluoroquinolones = Non-susceptible	90	High priority
Salmonella sp.	Nalidixic acid = Non-susceptible	48	High priority
Enterobacteriaceae	Amikacin = Non-susceptible	2	Medium priority
Enterobacteriaceae	ESBL-producing Enterobacteriaceae	101	Medium priority
Enterobacteriaceae	Possible ESBL-producing Enterobacteriaceae	141	Medium priority

Table 9: Public health alerts - important resistance

4.3 Multidrug resistance: ECDC definitions of MDR/XDR/PDR

In a 2012 publication, the European Centre for Disease Prevention and Control (ECDC) proposed definitions for common bacterial pathogens resistant to multiple antimicrobials. MDR/XDR/PDR results are summarized in the below table.

- MDR Multidrug resistance
- XDR Extensive drug resistance
- PDR Pan-drug resistance

Organism	Number of isolates	MDR	Possible XDR	Possible PDR
Staphylococcus aureus	86	25 (29%)	10 (12%)	4 (5%)
Enterococcus faecalis	1			
Escherichia coli	168	141 (84%)	119 (71%)	21 (13%)
Klebsiella pneumoniae	23			
Pseudomonas aeruginosa	32	2 (6%)	2 (6%)	
Acinetobacter sp.	8	1 (13%)		

Table 10: MDR, XDR, PDR summary

4.4 Multidrug resistance: Resistance profiles

One of the most valuable, but least utilized, analyses in WHONET is "resistance profiles" for studying multidrug resistance. The study of multidrug resistance has several applications:

- Phenotypic strain tracking facilitates the monitoring of distinct microbial subpopulations, greatly improving the recognition of 1) new strains; and 2) hospital and community outbreaks. Clusters identified by phenotypic tracking could be investigated by molecular typing to confirm clonality.
- The study of cross-resistance is useful in the development of treatment guidelines, including: 1) the determination of recommended "first-line" and "second-line" treatment options; and 2) estimating the value of combination therapy on local pathogens.
- Predicting resistance mechanisms based on the results from antimicrobials within a specific antimicrobial class or subclass or related classes.
- Exploring potential errors in laboratory test practices, for example the finding of isolates of Escherichia coli susceptible to ampicillin but resistant to imipenem is unlikely, and may be due to a testing error, for example with imipenem disks that have lost their disk potency.

In a section on "Antimicrobial susceptibility test practices", a set of "core antimicrobials" for Staphylococcus aureus and Escherichia coli has been proposed based on the data analyzed in this report. The below tables use these core antimicrobials to create resistance profiles. The tables only include isolates that were tested against all core antimicrobials.

Organism	Number of antibiotics	Core antibiotics	Number of isolates tested against all antimicrobials (%)
Staphylococcus aureus	7	Penicillin G, Erythromycin, Clindamycin, Oxacillin, Gentamicin, Trimethoprim/Sulfamethoxazole, Ciprofloxacin	86/86 (100%)
Escherichia coli	9	Cephalothin, Ampicillin, Gentamicin, Trimethoprim/Sulfamethoxazole, Cefotaxime, Imipenem, Cefuroxime, Mezlocillin, Aztreonam	84/168 (50%)

Resistance profile	Number of isolates	%Isolates	Number of patients
PEN	23	26.7	22
PEN ERY	17	19.8	17
(Susceptible)	9	10.5	9
PEN OXA	5	5.8	5
ERY	4	4.7	4
ERY CIP	4	4.7	4
PEN ERY CLI OXA CIP	4	4.7	4
PEN ERY CLI OXA GEN SXT CIP	4	4.7	4
PEN ERY CIP	3	3.5	3
PEN ERY OXA CIP	3	3.5	3

Table 11: Multi-drug resistance profiles for Staphylococcus aureus

Resistance profile	Number of isolates	%Isolates	Number of patients
(Susceptible)	45	53.6	41
CEP AMP MEZ	10	11.9	9
CEP	6	7.1	6
CEP AMP	4	4.8	4
AMP MEZ	3	3.6	3
AMP SXT MEZ	3	3.6	3
CTX	2	2.4	2
CEP AMP CXM	2	2.4	2
CEP AMP CTX CXM	2	2.4	2
SXT	1	1.2	1

Table 12: Multi-drug resistance profiles for Escherichia coli

5. Reporting to the World Health Organization and the United Nations

5.1 WHO Global Priority List of Antibiotic-Resistant Bacteria

Priority	Organism	Antibiotic results	Number (%)
Critical	Acinetobacter spp.	Carbapenem-resistant	-
	Pseudomonas aeruginosa	Carbapenem-resistant	-
	Escherichia coli	Cefotaxime-resistant	115/116 (99%)
	Escherichia coli	Ceftriaxone-resistant	9/67 (13%)
	Escherichia coli	Meropenem-resistant	0/12 (0%)
High	Enterococcus faecium	Vancomycin-resistant	-
	Staphylococcus aureus	Methicillin-resistant (MRSA)	-
	Staphylococcus aureus	Vancomycin-resistant	-
	Staphylococcus aureus	Vancomycin-intermediate	-
	Helicobacter pylori	Clarithromycin-resistant	-
	Campylobacter spp.	Fluoroquinolone-resistant	30/38 (79%)
	Salmonella spp.	Fluoroquinolone-resistant (Ciprofloxacin)	2/146 (1%)
	Neisseria gonorrhoeae	Third generation cephalosporin-resistant	-
	Neisseria gonorrhoeae	Fluoroquinolone-resistant	-
Medium	Streptococcus pneumoniae	Penicillin non-susceptible	-
	Haemophilus influenzae	Ampicillin-resistant	-
	Shigella spp.	Fluoroquinolone-resistant	-

Table 13: WHO Global priority list of antibiotic-resistant bacteria

5.2 WHO GLASS results

The WHO Global Antimicrobial Resistance Surveillance System (GLASS) collects annual data on specific antimicrobials from eight pathogens from four specimen types. Two of the GLASS statistics have been selected as indicators for the United Nations Sustainable Development Goals.

Specimen type	Organisms
Blood	Staphylococcus aureus, Streptococcus pneumoniae, Escherichia coli, Klebsiella pneumoniae, Acinetobacter spp., Salmonella spp.
Urine	Escherichia coli, Klebsiella pneumoniae
Stool	Salmonella spp., Shigella spp.
Genital	Neisseria gonorrhoeae

The below tables present the statistics for the number of animals with the samples, organisms, and antibiotics requested by the WHO GLASS protocol.

Specimen	Number of patients
BLOOD	1
STOOL	99

Table 14: The number of animals with the specimen types requested by WHO GLASS.

Specimen	Pathogen	Number of patients
BLOOD	SALSPP	1
STOOL	SALSPP	57

Table 15: The number of animals with the specimen types and organisms requested by WHO GLASS.

Specimen	Pathogen	Antibiotic	Number of patients	Number tested	%Resistant	%Intermediate	%Susceptible
STOOL	SALSPP	CIP	57	57		42.1	57.9
STOOL	SALSPP	CRO	57	57	22.8	1.8	75.4
STOOL	SALSPP	J01DD	57	57	22.8	1.8	75.4
STOOL	SALSPP	J01MA	57	57		42.1	57.9

Table 16: The number of animals and antimicrobial statistics for the specimen types, organisms, and antimicrobials requested by WHO GLASS.

5.3 United Nations Sustainable Development Goals

The United Nations has selected two of the above metrics as indicators for the United Nations Sustainable Developments Goals.

SDG 3.d.2: Percentage of bloodstream infection due to methicillin-resistant Staphylococcus aureus (MRSA) and Escherichia coli resistant to 3rd-generation cephalosporin (e.g., ESBL- E. coli) among animals seeking care and whose blood sample is taken and tested.

1. % Methicillin-resistant Staphylococcus aureus in blood (Oxacillin): No results found
2. % Methicillin-resistant Staphylococcus aureus in blood (Cefoxitin): No results found
3. % Third-generation cephalosporin-resistance Escherichia coli in blood: No results found

6. Cluster detection

It is possible to find statistically significant "case clusters" from routine microbiology laboratory data using mathematical algorithms, such as those offered by the free SaTScan software, SaTScan.org. The most valuable use of these approaches is to find possible community and hospital infectious disease outbreaks. However, the data analyst must keep in mind that there are both "outbreak" and "pseudo-outbreak" explanations for statistically significant case clusters.

- True infectious disease outbreak
- Changes in animal identification and sampling practices
- Changes in laboratory testing practices
- Contamination rates of clinical samples
- Deficiencies in laboratory reagents leading to incorrect results
- Variable availability of laboratory reagents leading to variability capabilities
- Variable completeness and practices for data entry

Ultimately, these algorithms cannot make the definitive ascertainment that certain findings represent a true disease outbreak. Rather, the goal is to use laboratory data to identify statistical findings that merit further investigation and possible response by infection control staff for possible hospital breakpoints and public health authorities for possible community outbreaks.

One must also keep in mind that statistical algorithms applied to microbiology laboratory data may not be able to find all outbreaks.

- Many animals involved in an outbreak do not have diagnostic samples taken because they are asymptomatic or have mild symptoms or because there is limited capacity and resources to support sample collection and laboratory testing.
- Small animal numbers and slowly developing clusters may be indistinguishable for baseline random variation.
- The cluster detection algorithm model and algorithm parameters may be poorly optimized for detecting certain types of cluster curves.

6.1 Cluster detection by species

Using "Organism" as the cluster detection variable, the below figures display a number of statistically significant case clusters.

Cluster description	Cluster start date	Cluster end date	p-value - Lowest	Number observed - Total	Total days in cluster
TST - Campylobacter sp.	6/4/2000	3/5/2000	0.00202	22	28
TST - Salmonella sp.	6/6/2000	28/6/2000	0.00101	33	23

Table 17: Cluster detection by species

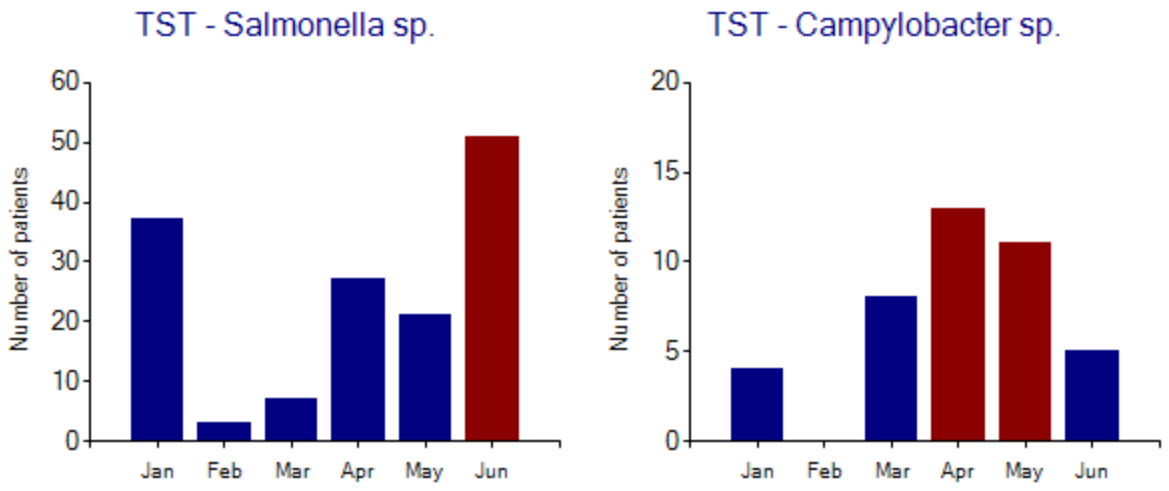

Figure 6: Statistically significant case clusters detected by organism identification (p <= 0.05). The monthly count of animals is presented, and the statistically significant time period detected by SaTScan is indicated in red.

6.2 Cluster detection by resistance profile

The above examples illustrate an approach to cluster detection using the "organism" name. This can be further extended to include cluster detection by geographic location, by hospital ward, by resistance profile, and also be combinations of variables, such as "location + resistance profile". For example, Figure 7 displays statistically significant clusters of phenotypic subpopulations of Escherichia coli defined by the multidrug resistance profile. Each letter represents a particular antimicrobial.

No results found

Table 18: Cluster detection for Staphylococcus aureus detected by resistance profile.

No results found

Figure 7: Statistically significant case clusters of Staphylococcus aureus detected by resistance profile (p <= Not applicable). The weekly count of animals is presented, and the statistically significant time period detected by SaTScan is indicated in red.

No results found

Table 19: Cluster detection for Escherichia coli detected by resistance profile.

No results found

Figure 8: Statistically significant case clusters of Escherichia coli detected by resistance profile (p <= Not applicable). The weekly count of animals is presented, and the statistically significant time period detected by SaTScan is indicated in red.

Appendix A. Antibiograms

No results found

Table 20: Gram-positive antibiogram. %Susceptible, first isolate per animal

No results found

Table 21: Gram-positive antibiotics.

Organism	Number of patients	AMK	AMC	AMP	CTX	CAZ	TIO	CRO	CHL	CIP	ERY	GEN	KAN	NAL	STR	SSS	TCY	SXT
Escherichia coli	167	96	69	11	1	22	72	87	20	42		85	57	8	25	16	12	13
Salmonella sp.	146			77			85	84	79	64		92	92	70	24	53	71	78
Campylobacter jejuni	34									18	100	100					44	

Table 22: Gram-negative antibiogram. %Susceptible, first isolate per animal

Code	Antibiotic	Code	Antibiotic	Code	Antibiotic
AMK	Amikacin	CRO	Ceftriaxone	NAL	Nalidixic acid
AMC	Amoxicillin/Clavulanic acid	CHL	Chloramphenicol	STR	Streptomycin
AMP	Ampicillin	CIP	Ciprofloxacin	SSS	Sulfonamides
CTX	Cefotaxime	ERY	Erythromycin	TCY	Tetracycline
CAZ	Ceftazidime	GEN	Gentamicin	SXT	Trimethoprim/Sulfamethoxazole
TIO	Ceftiofur	KAN	Kanamycin		

Table 23: Gram-negative antibiotics.