gentamicin or amoxicillin +/- gentamicin. The majority of patients infected with Salmonella had bacteremia, being septic arthritis also very common; most were treated with fluoroquinolones. Altogether, 17 patients died, and others developed complications.

This study further revealed that a critical step towards successfully treating these patients is to achieve an accurate diagnosis quickly; instituting effective empirical antibiotic therapy is also paramount.

Molecular Detection and Antibiotics Resistance Pattern of Extended-Spectrum Beta-Lactamase Producing Escherichia coli in a Tertiary Hospital in Enugu, Nigeria

I. Nwafia*, M. Ohanu, S. Ebede, U. Ozumba

University Of Nigeria Nsukka, Enugu campus

Background and Purpose: We looked for the extended-spectrum beta-lactamase producing Escherichia coli from clinical specimens in a tertiary hospital in Enugu, Nigeria. This is to enhance antibiotic stewardship in clinical practice.

Methodology: The study protocol was approved by Health Research and Ethics committee of the University of Nigeria Teaching Hospital (UNTH), Enugu. All hospitalized patients in UNTH from whose specimens Escherichia coli was isolated during the period of the study. These samples were cultured in 5% sheep Blood agar and MacConkey and incubated at 35–370C for 24 hours. Escherichia coli was identified with standard biochemical tests and confirmed using API 20E. The antibiotic susceptibility testing was done by disc diffusion method and interpreted according to the Clinical and Laboratory Standard Institute guideline. ESBL production was confirmed using Chromogenic agar. The ESBL bla genes were detected with polymerase chain reaction. Data analysis was with appropriate descriptive and inferential statistics.

Results and Discussions: Out of the 200 isolates, 70 (35.00%) were confirmed positive for ESBL production. Forty-two (60.00%) of the isolates were from female patients while 28(40.00%) were from male patients. Sixty-eight (97.14%) of the isolates were susceptible to imipenem while all of the isolates were resistant to ampicillin, chloramphenicol and tetracycline. The ESBL genes detected were blaCTX-M (n = 26; 37.14%), blaTEM (n = 7; 10.00%), blaSHV (n = 2; 2.86%), blaCTX-M/TEM (n = 7; 10.0%), blaCTX-M/SHV (n = 14; 20.0%) and blaCTX-M/TEM/SHV (n = 10; 14.29%). The most associated risk factors to infections caused by ESBL producing Escherichia coli was previous antibiotics use for the past 3 months followed by admission in the intensive care unit, recent surgery and urinary catheterization.

Conclusions: ESBLs was detected in 4 of every 10 Escherichia coli with the predominant gene detected being CTX-M. This knowledge will enable appropriate measures towards improvement of patient health care, antibiotic stewardship, and infection control in the hospital.

Biometric Fingerprint Identification for Health Workers: A bacteriological Analysis of Sensor Devices

B. Almoosawi*, S. Alwadaei

Salmaniya Medical Complex

Biometric fingerprint identification is expanding both primary care and secondary care facilities. The procedures of fingerprint capturing and reading require physical contact between skin and surface of the hardware devices. The aim of the study was to assess, if there was any bacterial contamination of the fingerprint sensors of biometric devices installed in our hospital.

Materials and Methods: Samples for microbiological examination were taken in sterile cotton swabs from all the biometric finger print devices.

Results: A total of 73 biometric devices were studied for bacterial contamination. Of the samples taken, 4 out of 73 (5.48%) yielded growth of Methicillin- Sensitive Staphylococcus aureus, 1 out of 73 (1.37%) yielded growth of Proteus Mirabilis.

Conclusion: the possibility of transmission of infection via biometric devices, even though minimal does exist and appropriate measures may be taken for prevention.

The impact of water treatment, water reuse and the potential exposure to the risk of antibiotic resistome: the Transmission Antibiotic Resistance from the Environment to Humans

R. Reyed

Srta- City

Sewage treatment plants (WWTPs) and their water reuse are hot spots of antibiotics resistance (AR). The presence in antibiotic-resistant bacteria (ARB) could be the result of overuse and misuse of antibiotics in humans, animal feeding and agriculture, biocides and the incomplete removal of antimicrobials from WWTPs. WWTPs areas ripe for bacteria to shuffle and share their resistance genes. These hot spots of potential resistance transmission included a modern WWTPs and their water reuse in agriculture and food production, If these bacteria happen to come into contact with other microbes that carry resistance genes, those genes can pop over in one step. that such gene-transfer events are generally rare, but they are more likely to occur in these hot spots if the water reuse are hot spots of resistance gene transfer, We speculated that bacteria present in WWTP-where human regularly receive antibiotics- would see even more pressure to share resistance genes. We should concern about such bacteria getting into the food system. This explains why AR is so persistent in the environment. The nonexistence of a important overlap of ARB and antibiotic resistome between the human microbiome and potential environmental sources should not be interpreted as an indication of risk absence. The times of yore decade has eye witnessed a disintegrate of study regarding AR in the environment, mainly in areas under human activities, which they are now recognized. However, a key issue refers to the risk of transmission of resistance to humans, for which a quantitative model is urgently needed. t conclusion is that the risks of spread of AR from the environment to humans must be managed under the precautionary principle, because it may be too late to act if we wait until we have concrete risk values.