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

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Abstract : Antibiotic resistance is increasing globally and has become a major health challenge. Extended-spectrum beta-lactamase is clinically important because the ESBL gene are mostly plasmid encoded and these plasmids frequently carry genes encoding resistance to other classes of antimicrobials thereby limiting antibiotic options in the treatment of infections caused by these organisms. The specific objectives of this study were to determine the prevalence of ESBLs production in Escherichia coli, to determine the antibiotic susceptibility pattern of ESBLs producing Escherichia coli, to detect TEM, SHV and CTX-M genes and the risk factors to acquisition of ESBL producing Escherichia coli. The protocol of the study was approved by Health Research and Ethics committee of the University of Nigeria Teaching Hospital (UNTH), Enugu. It was a descriptive cross-sectional study that involved all hospitalized patients in UNTH from whose specimens Escherichia coli was isolated during the period of the study. The samples analysed were urine, wound swabs, blood and cerebrospinal fluid. These samples were cultured in 5% sheep Blood agar and MacConkey agar (Oxoid Laboratories, Cambridge UK) and incubated at 35-370C for 24 hours. Escherichia coli was identified with standard biochemical tests and confirmed using API 20E auxanogram (bioMerieux, Marcy 1'Etoile, France). 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 ESBL Epsilometer test strips (Liofilchem srl, Italy). The ESBL bla genes were detected with polymerase chain reaction, after extraction of DNA with plasmid mini-prep kit (Jena Bioscience, Jena, Germany). Data analysis was with appropriate descriptive and inferential statistics. One hundred and six isolates (53.00%) out of the 200 were from urine, followed by isolates from different swabs specimens 53(26.50%) and the least number of the isolates 4(2.00) were from blood (P value = 0.096). Seventy (35.00%) out of the 200 isolates, 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 (P value = 0.13). Sixty-eight (97.14%) of the isolates were susceptible to imipenem while all of the isolates were resistant to ampicillin, chloramphenicol and tetracycline. From the 70 positive isolates the ESBL genes detected with polymerase chain reaction 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%). There was no gene detected in 4(5.71%) of the isolates. 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. In conclusion, 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, research and infection control in the hospital.

Keywords : antimicrobial, Escherichia coli, extended spectrum beta lactamase, resistance
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