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Prevalence of non typhoidal *Salmonella* among HIV patients attending Federal Medical Centre, Ido Ekiti, Nigeria

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Non Typhoidal *Salmonella* (NTS) is an important opportunistic zoonotic pathogen among immunocompromised patients, especially those infected with the Human Immunodeficiency Virus (HIV). This study was therefore carried out to determine the prevalence and antibiotic resistance of NTS among HIV patients in the era of highly active antiretroviral therapy (HAART). A total of 107 stool samples were collected and cultured on bismuth sulfite agar after enrichment in selenite fecal. Bacteriological and biochemical tests were carried out using standard procedure. The CD4+ count was determined using dual-platform flow cytometry. Relevant information was obtained from the patients using a questionnaire. Of 107 patients, 64 were females (60%) and forty-three (40%) were males. Forty-seven (44%) of the patients were in the age group of 21-30 years. Of the patients examined; 42 (39.1%) were businessmen and women while the rate of isolation of NTS was higher among civil and public servants having 33.3%, source of drinking water for 69% of the patients were well water. Seventeen (28.3%) of those who drank from well water yielded positive growth of NTS. Of the 62 (58%) patients on HAART, 32 (52%) had a CD4+ count above 300 cells/µl, three (39.1%) of them yielded positive growth of NTS. Of the 45 patients who were without HAART, 13 (9.4%) had a CD4+ count less than 200 cells/µl, eleven yielded growth. Statistical analysis showed that there was no significant difference between the antibiotic resistance of NTS isolated from HIV patients on HAART and those without antiretroviral therapy. The NTS isolated exhibited 100% resistance to each of penicillin, ofloxacin and ciprofloxacin. Resistance to ceftazidine and gentamycin was 65% and 62% respectively. All the twenty-one NTS isolated from HIV patients in this study exhibited multiple resistances to all antibiotics tested. In conclusion, the high level of multiple antibiotic resistances observed in NTS isolated from HIV patients may likely jeopardize the effectiveness of the treatment of this bacterial infection in them.

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Isolation of *Staphylococcus aureus* with intermediate profile to Vancomycin (VISA) harboring vanB resistance gene from human sources in Jordan

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Staphylococcus aureus is the major bacterial cause of skin, soft tissue and bone infections and one of the commonest causes of healthcare-associated bacteremia. Vancomycin use has used worldwide as a result of empirical therapy against methicillin-resistant *S. aureus* (MRSA) infections. This will create a selective pressure that favors the outgrowth of vancomycin-resistant (VRSA) and vancomycin intermediate *S. aureus* clones (VISA). This study was carried out to evaluate the resistance pattern of *S. aureus* to vancomycin. A total of 1179 samples including 566 (48%) from human and 613 (51.90%) from animals were examined for the presence of S. aureus using standard biochemical tests and PCR amplification of *coa* gene. Their prevalence among human source was: 19.35%, 14% and 8.8% for nasal, nail and skin, respectively. However, animal sources showed: 27.3%, 5.51% and 15.86% for milk, nasal and meat, respectively. Resistance to antibiotics was determined by the disk diffusion method. MRSA strains were tested for vancomycin resistance by minimal inhibitory concentration (MIC) and E-test. Four human isolates (1.87%) have shown to be VISA. The isolates were belongs to the nose (4.76%), nails (3.2%) and clinical samples (1.56%). VISA strains were also resistance to erythromycin, methicillin, TMP and oxacillin. The results were confirmed by PCR amplification of *vanA, vanB, vanC* genes. *VanB* gene was found in all VISA strains. They all exhibited the same PFGE pattern. Though incidence was not so high but this is believed to be the first report of VISA strains containing vanB isolated from a routine nasal and nail carriage.

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