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Infection Control of Spatial Disseminated Multi-Antibiotics Resistant And Phylo-Diverse Staphylococcus Aureus Pathotypes

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Abstract

Focal dissemination of multi-antibiotic resistant (MAR) Staphylococci pathotypes regulated by agr functionalities was investigated and evaluated for infection control. Non-repetitive Staphylococcus aureus strains from soft and skin infections disseminated in several communities were recovered and biotyped, assayed for biofilm and profiled for antibiotic resistance. Strains were further genotyped for spa types, virulence and resistant genes; and mapped for geospatial distribution. Clonal diversity and functional accessory gene regulators (agr) were also evaluated. Staphylococcal infection was not significant with age group ($p>0.05$), but high rate of MSSA (53.0%) and MRSA (1.5%) was observed. Median resistance rates were significantly differ ($p=0.001$) but highest 75 th percentile and media resistance rates were observed in wound infection. Resistance rate of 78.8% at MIC 50 32 μ g/ml and MIC 90 128 μ g/ml to amoxicillin-clavulanate, and more than 40% resistance to ceftazidime, ciprofloxacin, gentamycin, ofloxacin, sulfamethoxazole and tetracycline with MIC 90 and MIC 50 at 32 μ g/ml were observed. More than 0.83 multi-antibiotic resistance index (MARI) were observed among the strains that clustered into separate phylo-group expressing high beta- lactamase and strong biofilm production. Heterogeneous spa types t442 (wound and pus), t657 (wound), t091 (ear) and t657 (ear and wound) revealed high phylo- diversity. Only 4.6% pvl + MSSA-CC1 agr I, pvl + MSSA-CC5 (13.6%) and pvl + MRSA-CC7 agr II (4.6%), expressed enterotoxin; sea, sec, sed, sej, Leukocidins (LukF-PV, lukD, lukE), proteases (aur, slpA sspB, sspE) and resistance genes (fosB, msr (A), bla mph(C),aphA3, sat, fosB, sdrM, Q7A4X2) . Phylogenetic related spa types of livestock origin, specifically bovine milk clustered with detected strains that were prevalent in urban communities with focal dissemination to other nearest suburbs. Clonal dissemination resistant pvl+ MAR MSSA-CC1 and MRSA- CC5 encoding agr were predominant in several peri-urban communities. This require adequate geno-surveillance, population-target antimicrobial stewardship, extensive community health care intervention policy and well-structured infection control programs to prevent further focal dissemination.