6. Summary

Characterization Of *B*-Lactamase Isolated From *Salmonella* Spp. of Different Samples.

Salmonella serovar Typhimurium is a leading cause of foodborne diseases worldwide. Its ability to acquire new antibiotic resistance mechanisms is an increasing therapeutic concern. We report acquisition of the CTX-M-14 ESBL by 6 pediatric isolates of *Salmonella* serovar Typhimurium from Egypt. To our data, this is the first report of CTX-M-producing *Salmonella* in Egypt.

Antibiotic susceptibility and ESBL detection were investigated by CLSI agar dilution methodology. β -lactamase production was investigated by isoelectric focusing (IEF) incorporating clavulanate, cloxacillin, and cefotaxime overlays, CTX-M, OXA, and SHV-specific PCR, sequencing, and conjugation. Strain relatedness was investigated by PFGE.

Two clusters CI and CII were resulted, however the clinical isolates in cluster CI have 85% related by PFGE suggesting they may be subtypes of a common strain, but CI was unrelated to cluster CII. The clinical isolates were highly cefotaxime-resistant, but exhibited only reduced susceptibility to ceftazidime, and were ESBL-positive by the CLSI criteria for *E. coli, Klebsiella*, and *P. mirabilis*. All clinical isolates produced multiple clavulanate-sensitive β -lactamase bands on IEF with pIs of 7.9 and 5.4 (all-clinical isolates), the clinical isolates 68, 79, 93, 108, 115, 126, and 128, showed possibly CTX-M-14 without OXA-1-Like or SHV-12-Like activity. The clinical isolates 92, 96, 99, 100, 102, 111, 120, and 132 showed a resistance pattern possibly OXA-1-Like activity. Eventually, the clinical isolates 59, 65, 76, 78, 94, 95, 113, 119, and 127, showed a resistance pattern possibly SHV-12-Like activity.

The pI 7.9 enzyme was transferrable by conjugation and conferred a CTX-M ESBL phenotype in clinical isolates *Sal*.68, 94, and 111. PCR and sequencing identified the CTX-M gene as CTX-M-14 in clinical isolates *Sal*.68, 94, 111, 113, 119, and 127. In addition, genes for SHV-12 and OXA-1 were also identified by sequencing in clinical isolates number *Sal*.94, 113, 119, 127, and *Sal*.102, 111, 120, 132, respectively.

This report of clinical isolates of *Salmonella* from Egypt producing CTX-M-14 are of epidemiological significance. The successful detection of this ESBL with CLSI methodology suggests that CLSI methodology should be further evaluated for ESBL detection in this genus.