



Study of resistant bacteria at live poultry sales points in the governorate of Sousse

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Background

Antibiotic resistance is a major global health concern impacting humans, animals, and the environment. In broiler chickens, misuse of antibiotics promotes the emergence of resistant bacteria that can persist and spread along the production chain.

This study investigates the dissemination of ESBL-producing *E. coli* in live chickens in Tunisia, highlighting their potential role as reservoirs for antimicrobial resistance.

Materials and Methods

A total of 79 cloacal swabs were collected from 11 sales points across three regions in Sousse, Tunisia. Samples were enriched, incubated, and cultured on cefotaxime-supplemented MacConkey agar to isolate resistant strains. Positive isolates underwent identification, antibiotic susceptibility testing, and PCR for phylogenetic grouping and MLVA to assess clonal relationships. One clone per profile was selected for whole-genome sequencing.

Results

Among the 79 samples, 24 ESBL-producing *E. coli* resistant to cefotaxime and 12 to ertapenem were identified, mainly from regions 1 and 3. Phylogenetic analysis revealed four phylogroups (A, B1, B2, D), and MLVA distinguished nine clones. Whole-genome sequencing of nine representative isolates identified ST10, ST359, and ST770. ST10 and ST770 co-occurred at sales point 4 (region 1), while ST770 was also found in region 3. Most sequenced strains carried the *bla*_{CTX-M-55} gene, with one isolate harboring *bla*_{CTX-M-1}. Further analysis of genetic contexts is ongoing.

Figure 1. Sampling design

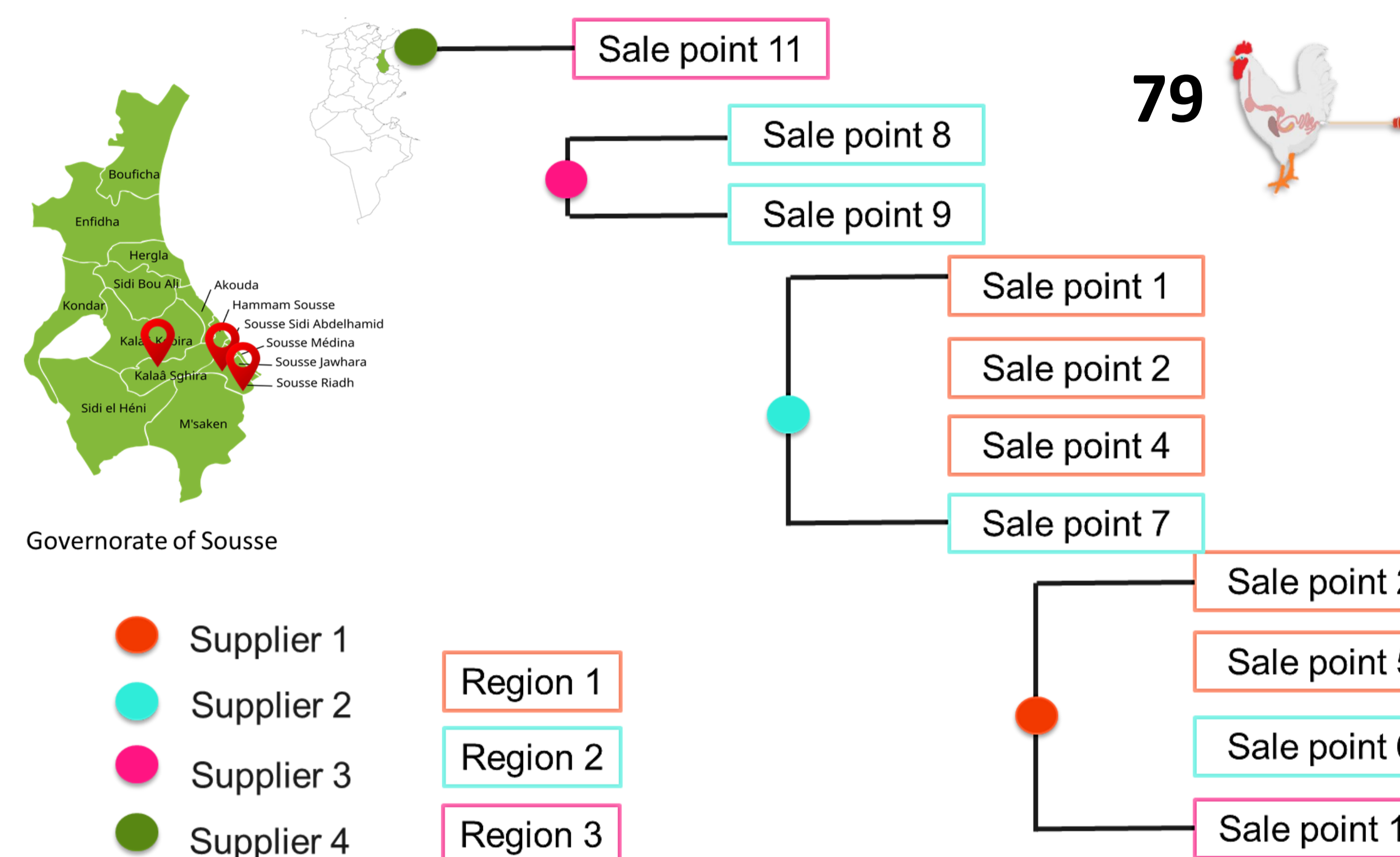


Figure 2. Isolation of resistant strains and determination of phylogroups

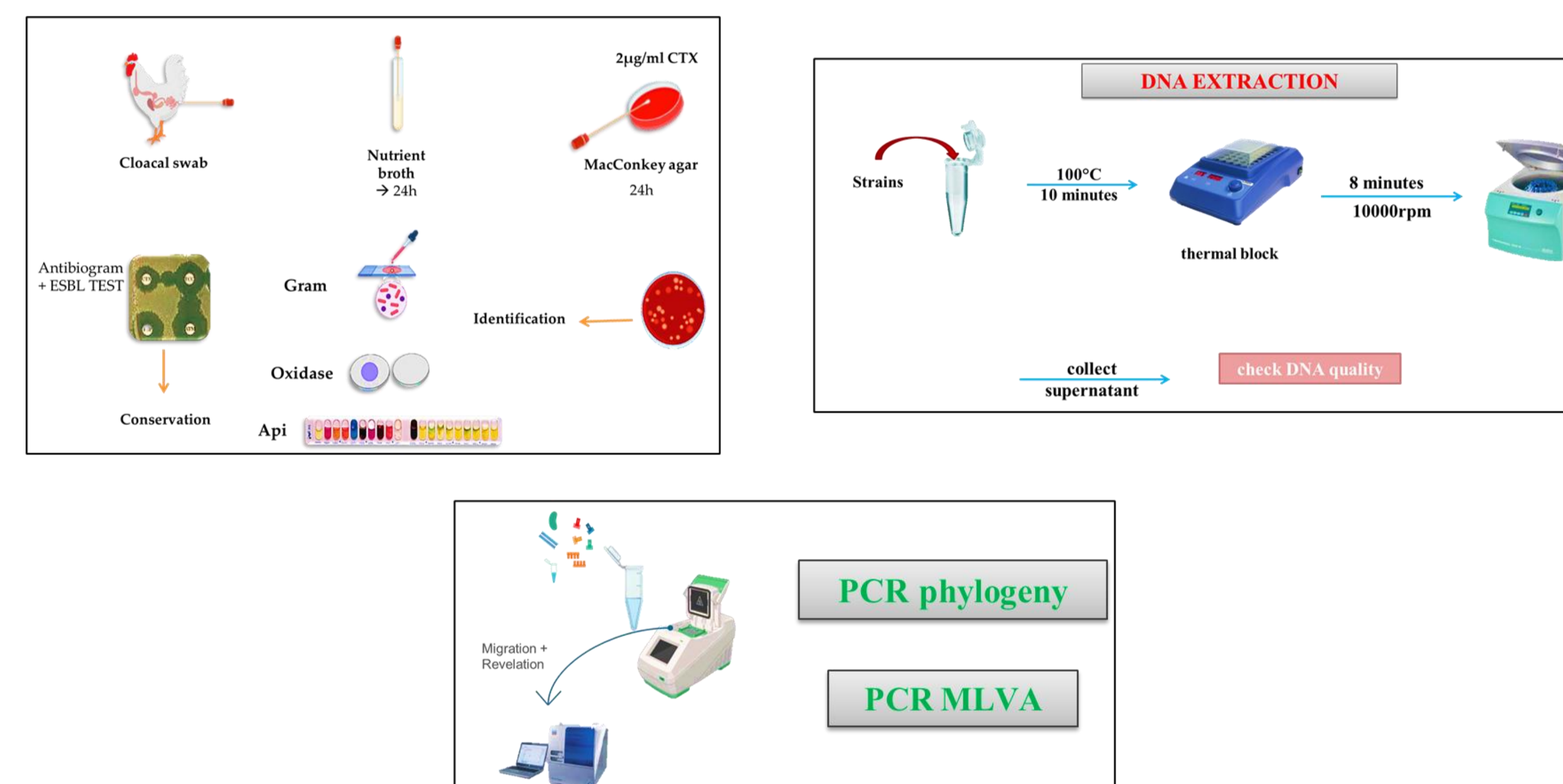
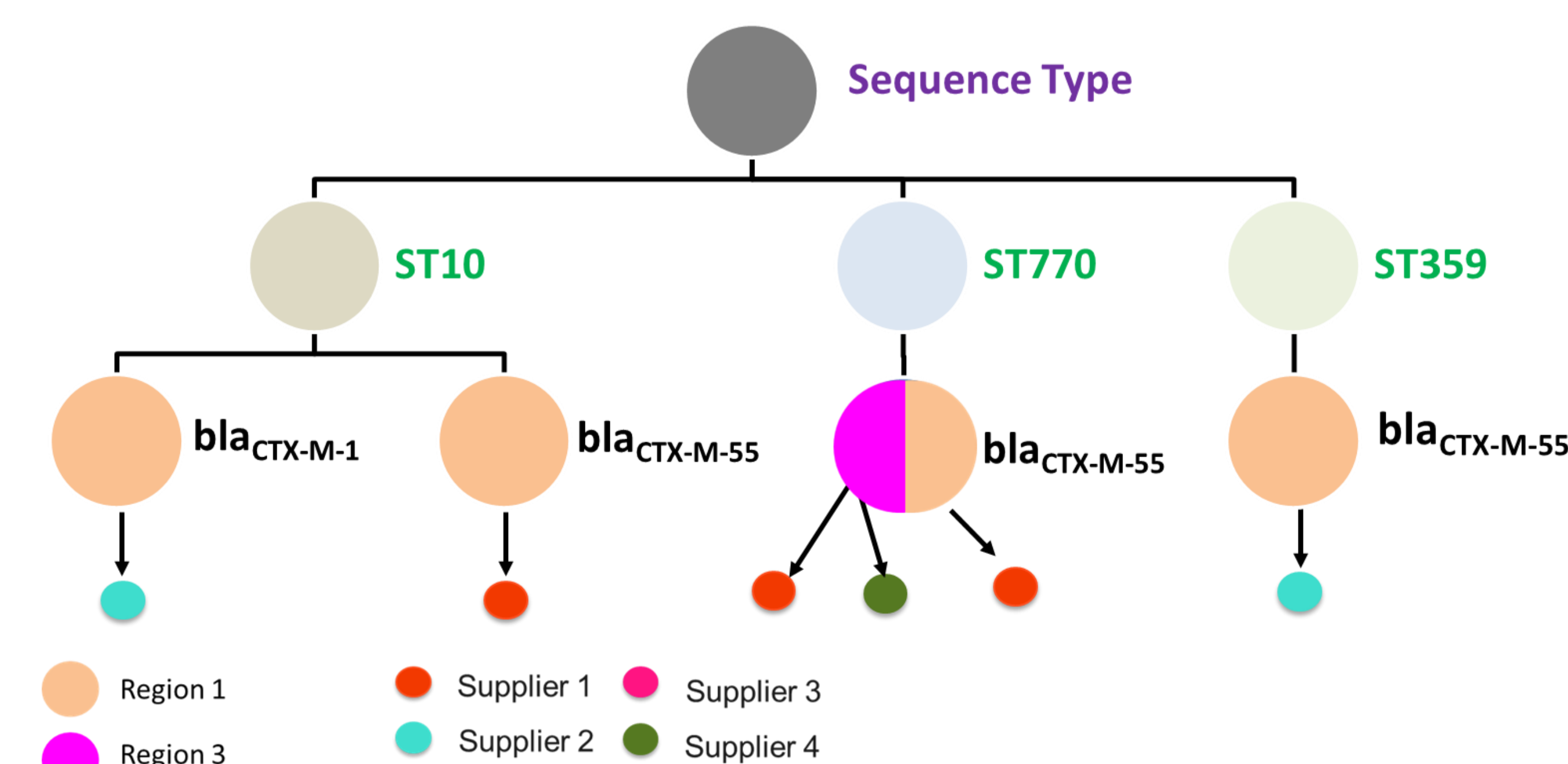


Figure 3. Results of whole genome sequencing of nine representative



Discussion

Resistant *E. coli* strains were collected from 11 sales points in Sousse, linked to four poultry distributors. Region 2 had both positive and negative samples, possibly due to varied suppliers or host immune responses. The 24 resistant isolates (carrying bla_{CTX-M-1} or bla_{CTX-M-55}) came from three suppliers and were distributed across three sequence types, indicating potential horizontal gene transfer.

Conclusions

The emergence of resistant bacterial strains carrying resistance genes is largely driven by livestock breeding practices and the misuse of antibiotics, which apply selective pressure favoring their proliferation. These strains often originate at the farm level and persist beyond slaughtering, even surviving high-temperature cooking processes. Resistant bacteria can spread into the environment via manure and wastewater, contaminating soil, crops, and groundwater, or through direct contact with poultry by farmers and handlers. This environmental dissemination increases the risk of transmission to humans, potentially leading to severe and hard-to-treat infections.

Public Health Implications

This study marks an initial step in highlighting the presence of antibiotic-resistant *E. coli* in live chickens intended for human consumption. It has paved the way for further investigations into the prevalence of these resistant strains within the governorate of Sousse. In parallel, alternative therapeutic strategies to replace conventional antibiotics are being explored. Additionally, an awareness day will be organized in September with local poultry farmers, aiming to promote improved breeding practices that minimize the selection and spread of resistant bacteria.

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