**Antibiotic resistance of bacterial strains isolated from houseflies (*Musca domestica*) in Tunisia**

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**ABSTRACT**

**Background:** The houseflies (*Musca domestica*) live in close contact with humans. They are carriers of human pathogenic bacteria in their digestive tracts and on their bodies. These insects have been involved as vectors of different human pathogens or multidrug resistant bacteria, such as *Enterobacteriaceae*, *Staphylococcus aureus*, and *Pseudomonas* spp*.* This study aimedto assess the prevalence of antibiotic-resistant Gram-negative bacteria in flies collected from laying hen, a market, and houses in Tunisia.

**Material and methods:** One hundred houseflies were collected between September and December 2019 from three different locations: a laying hen farm, a market, and houses. Sixty-one isolates, comprising 23 *Escherichia coli,* 31 *Klebsiella pneumoniae* and 7 *Pseudomonas aeruginosa* were obtained. The antimicrobial sensitivity was determined by the disk diffusion method using twenty-one antibiotics discs, and the ESBL-producing isolates were screened by the double-disc diffusion test. β-lactamases genes, associated resistance genes, and integrons were studied by PCR.

**Results:** Most of the bacterial isolates 96.7% (59/61) were collected from the houses and the market. The ESBL producing isolates were 14.8% (9/61), seven *K. pneumoniae* isolates, and two *E. coli* isolates. The highest rate of ESBL-producing strains was observed in houses (7/22; 31.8%), followed by the market (2/43; 4.7%). Resistance to the most used antibiotics was higher in ESBL-producers than non-ESBL-producers. The multi-drug resistant bacteria was detected in 19/61 (31.2%). The following resistance genes were identified among the 3rd generation cephalosporins-resistant (cefotaxime and/or ceftazidime) isolates; *bla*CTX-M-G-1 (76.7%, 23/30), *bla*SHV-1 (43.3%, 13/30), *bla*TEM-1 (36.7%, 11/30), *bla*IMP (16.7%, 5/30), *bla*OXA-48 (10%, 3/30) and *bla*NDM (3.3%, 1/30). Quinolones resistance genes; *qnrs*, *aac(6′)-Ib-cr,* *qnrB* and *qnrA* were found in 11, 11, 7 and 5 isolates, respectively. Tetracycline genes (*tet*) and sulfonamide resistance genes (*sul*) were identified in seventeen and eleven, respectively. The integron 1 (*intI1*) was detected in fifteen (50%) isolates, *qacED1-sul1* genes were identified in ten intI1-positive isolates. The class 2 integron was detected in three isolates.

**Conclusion:** Houseflies collected from houses and markets may be implicated in the spread of multi-drug resistant bacteria that constitute a considerable threat for human public health. ESBLs in the flies reflect the contamination status of the environment and can be used as indicators for contamination.