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Epidemiology of subclinical salmonellosis in wild birds from NE Spain

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The epidemiology of subclinical salmonellosis in wild birds in a region of high Salmonella prevalence in pigs was studied. Three hundred and seventy nine fecal samples from 921 birds captured in 31 locations near pig premises and 431 (581 birds) from birds from 10 natural settings far from pig farms were analyzed for the presence of Salmonella spp. Positive samples were serotyped and antimicrobial resistance (AR) test performed. Phage typing and PFGE on isolates of S. Typhimurium were carried out. The prevalence of Salmonella positive samples was 1.85% (95%CI=0.93-2.77). A multivariable logistic regression, with observations clustered by site of capture, was used to determine major factors associated to prevalence of salmonellosis. Prevalence was positively associated with samples collected from birds in the proximity of a pig operation (OR=16.5; 95%CI=5.17, 52.65), and from non-migratory (or short distance migration) birds (OR=7.6; 95%CI=1.20, 48.04); and negatively related to mostly-granivorous birds (OR=0.4; 95%CI=0.15, 1.13). Typhimurium was the most prevalent serotype and 4 different XbaI PFGE patterns were detected that matched with the 4 phage types identified (U310, U311, DT164, DT56). The prevalence of multi-drug resistance was low (20%). In 3 farms a high degree of homogeneity among isolates from different birds was observed. These findings suggested that pig farms would facilitate the transmission of this infection among wild birds. The degree of bird congregation may have much to do on the infection transmission as phenotypic and genotypic relatedness among isolates from different birds were observed only in farms where abundant birds were seen.



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