

Assessing the potential transmission of major Salmonella serotypes from chicken feed to humans in Belgium based on the national monitoring program (2010-2017)

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Abstract

Vertical and horizontal transmissions of Salmonella spp. along the food chain (FC) have been reported to play an important role in the contamination of foodstuffs and of humans. This study aims first to clarify to what extent some selected major Salmonella serotypes are represented along the chicken FC and potentially transmitted from feed to humans. Then to discuss if the sampling results of the Belgian National Salmonella monitoring program may be considered as proxy to predict possible dominant serotypes and trends in humans. By using results of this programme, this study tried to highlight statistically significant differences in yearly prevalences between broilers exit status and other matrices (e.g. feed, other chicken categories, foodstuffs). Then to show up statistically significant changes from year to year prevalences in broilers exit status and to look if these changes can also be observed in the other matrices. Results have showed significant differences in yearly prevalences. They also pinpointed that the prevalence for the same serotypes could significantly vary from year to year in broilers exit status but this variation was inconsistently observed in the other matrices. These observations do not support the assumption of significant vertical and horizontal bacterial transmission along the chicken FC. Results in the national program cannot be considered as proxy. Determining the contribution of contaminated animal feed to human illness is challenging as the interplay of many factors makes it difficult. Coupling the actual programme with network analysis, source attribution and genome sequencing would be a way to explore deeper the spread of Salmonella serotypes along the FC. Belgium has put efforts to decrease Salmonella Enteritidis and Salmonella Typhimurium prevalence along the FC, but attention should be also paid to other pathogens that could fill the vacant niche left as Salmonella infantis which prevalence has been increasing in some matrices.

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