Dear editor,

I have read the article TM Shamaila, K Ndashe, C Kasase, M Mubanga, L Moonga, J Mwansa, BM Hang’ombe (2018) invA gen and antibiotic susceptibility of Salmonella spp. isolated from commercially processed broiler carcasses in Lusaka District, Zambia. Health Press Zambia Bull. 2018;2(6); pp 6-12. I would like to comment on the choices of approach and methods implemented in the project. In my view, these have rendered results that may lead to misinterpretations and unnecessary alarm in the media and among consumers.

As a first observation, swabbing of carcasses is not the usual choice method for detection and identification of Salmonella in meat samples. In processing plants, swabbing is used for estimating success of disinfection procedures on surfaces (e.g. cutting tables, workers’ hands). Swabs are tested for S. aureus, Total Coliforms and E. coli, but not Salmonella [1]. The results are quantitative and expressed in CFU/surface area. Salmonella detection in food products is a qualitative method, in which the two possible results are “detected” or “unable to detect Salmonella” in a given mass of sample. Samples are normally taken from skin (neck, for example) and meat cuts, before and after going through the chiller [2], for more representative quantification of contamination throughout the process. The samples undergo an enrichment process, followed by successive inoculations in selective media, ending with confirmation of suspicious isolates and serotyping. The work on which the authors based their choice of swabbing the cloaca and visceral surfaces (sic) [3], reports washing of whole carcasses in buffered peptone water as a sampling method, not swabbing. Carcass washing was done because Northcutt et al. [3] evaluated the level of contamination on the carcass surface, but it is not usually implemented.

Secondly, the advantage of being able to use molecular procedures is to perform a test of high specificity at an earlier stage (e.g. from an enrichment broth), and faster than obtaining isolates in selective media and ulterior serotyping. Running PCR and microbiological studies simultaneously is not a sensible practice, unless in specific cases, such as the validation of the PCR method. If that was the objective of the work, then it was not clearly stated.

Finally, and most importantly, although the authors reported having serotyped the isolates identified as Salmonella spp., they did not mention the serovars to which the isolates belonged. Instead, they used the presence of the invA gen as a marker for Salmonella spp. The problem with this approach is that the invA gen is common to all members of the genus Salmonella [4], however some serovars of Salmonella found in chicken carcasses are very specific for chickens and do not represent a risk for human population (for example, Salmonella enterica subsp. Enterica serovar gallinarum).

In other words, this approach may have overestimated the actual risk to humans on those samples. If it is compulsory to follow the molecular diagnostic path, then a gen more specific to serovars of human interest should be targeted, as for example the fliC gen for Salmonella enterica subsp. enterica serovar typhimurium [4]. Figure 1 (modified from [5]) resumes this idea - whilst the PCR for gen invA helps to discriminate at the top of the hierarchy between Salmonella and other non-Salmonella genera, procedures to indicate risks to human health should be targeting genes at the serovar level (bottom of the diagram).

Sincerely

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Figure 1. Classification of members of the genus *Salmonella* (after [5]). The gene invA is common to all members of the genus, even the serovars adapted to chickens. Detection of serovars pathogenic to humans by PCR may require more specific genes, such as fliC for *Salmonella enterica* subsp. *enterica* serovar typhimurium [4].


