RESEARCH ARTICLE

Previously titled: Prevalence and diversity of Salmonella isolated from layer farms in central Ecuador

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Abstract

Background: Given the considerable role played by Salmonella in the incidence of food contamination, around the world, surveillance of this infection is prioritized by both food producers and health care authorities. Data remains insufficient concerning the prevalence of Salmonella in poultry systems in Ecuador and in Latin America in general.

Methods: In this study, we evaluated the presence and diversity of Salmonella serovars in samples taken from 21 layer farms and backyard layers in central Ecuador during August-November 2017. Salmonella was isolated following standardized methods (ISO 6579) and the serovar determination was carried out by PCR.

Results: A significant presence of Salmonella was detected in the 21 farms evaluated, with a frequency of 76% (95% confidence interval (CI): 53-92) in environmental surfaces, 33% (95%CI: 15-57) in pooled cloacal swabs from layer hens, 33% (95% CI: 13–59) on feed samples, and 10% (95%CI: 1-30) in backyard layer feces from traditional local markets. The dominant serovars detected were S. Infantis and S. Typhimurium.

Conclusions: This study forms a basis for further surveillance of Salmonella serovars in layer farms in central Ecuador.

Keywords
Salmonella, Layer Poultry, Ecuador, Serovars.
Corresponding author: William Calero-Cáceres (wr.calero@uta.edu.ec)

Author roles: Salazar GA: Formal Analysis, Investigation, Writing – Original Draft Preparation; Guerrero-López R: Conceptualization, Supervision, Validation; Lalaleo L: Formal Analysis, Investigation, Writing – Review & Editing; Avilés-Esquivel D: Methodology, Validation; Vinueza-Burgos C: Formal Analysis, Methodology, Writing – Original Draft Preparation; Calero-Cáceres W: Conceptualization, Formal Analysis, Funding Acquisition, Investigation, Methodology, Supervision, Writing – Original Draft Preparation, Writing – Review & Editing

Competing interests: No competing interests were disclosed.

Grant information: This study was supported by the Dirección de Investigación y Desarrollo DIDE-Universidad Técnica de Ambato (Project Grant information: 1568-CU-P-2017).

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How to cite this article: Salazar GA, Guerrero-López R, Lalaleo L et al. Presence and diversity of Salmonella isolated from layer farms in central Ecuador [version 2; peer review: 2 approved] F1000Research 2019, 8:235 (https://doi.org/10.12688/f1000research.18233.2)

First published: 28 Feb 2019, 8:235 (https://doi.org/10.12688/f1000research.18233.1)
Introduction

The genus *Salmonella* is considered a leading cause of foodborne illnesses around the world (WHO, 2017). These bacteria are among the most significant agents of food and water poisoning in the United States and Europe (Bäumler et al., 2000; Callejón et al., 2015; Varma et al., 2005). Globally, it is estimated that 93.8 million cases of *Salmonella*-related gastroenteritis occur annually, resulting in 155,000 deaths (Majowicz et al., 2010). In Ecuador, typhoid, together with paratyphoid fever, causes around 1,500 hospitalizations per year, while non-typhoidal salmonellosis leads to more than 2,000 hospitalizations over the same period. These infections have accounted for approximately 25% of total reported gastrointestinal illnesses in recent years (MSP, 2018). *Salmonella* represents a complex and diverse genus, but only a small number of serovars are involved in human infections (Issenhuth-Jeanjean et al., 2014; Thiennimitr et al., 2012).

*Salmonella* detection and the investigation of foodborne outbreaks is of maximum importance to public health, which has resulted in the establishment of epidemiological surveillance programs in many developed countries (EFSA, 2013). These measures provide information about endemic *Salmonella* serovar patterns, outbreaks, temporal trends and the monitoring of control actions (CDC, 2018). The principal reservoir of *S. enterica* is the intestinal tract of livestock, representing one of the main sources of infection for humans (Antunes et al., 2016). Despite this epidemiological and economic importance, in South America there is a paucity of information concerning *Salmonella* in poultry systems (Alexandre et al., 2000; Donado-Godoy et al., 2012). Research conducted in 2016 pertaining to broiler chicken farming in Ecuador indicated the presence of *Salmonella* serotypes *S. Infantis*, *S. Enteritidis* and *S. Corvallis* (Vinuesa-Burgos et al., 2016). However, among layer hens, no information about the prevalence or diversity of *Salmonella* has been reported in this country nowadays. The purpose of this study was to estimate the presence and diversity of *Salmonella* bacteria present in 21 layer farms in central Ecuador.

Methods

**Samples**

Samples were collected between August–November 2017 from different layer farms in central Ecuador (Tungurahua and Cotopaxi provinces), which accounts for around 60% of egg production in the country. A total of 21 farms (>1,000 birds) in Latacunga, Cevallos, Quero and Ambato (all Ecuador) were sampled, based on their willingness to provide verbal consent for this study (verbal consent was obtained over written consent owing to the farmers’ reluctance to sign their names, as they perceived this could be used to identify them). Further details for each site can be found in Dataset 1 (Calaro-Cáceres, 2019a)). One laying hen house per farm was selected. The following samples were collected in each house: 21 pooled cloacal swabs (10 cloacal swabs per pool); 21 manure drag swabs (environmental swabs, 1 per business); 21 caecum content samples (1 layer per farm). To evaluate the potential risk from contaminated feed, 18 composite samples were taken from farmyards (18 of the 21 farms consented verbally to having these samples taken). Additionally, 21 fecal samples from backyard layers were sampled in traditional local markets. All samples were transported in an icebox at 3–5°C within 2 hours of collection for bacterial isolation. The experiment was performed under supervision of the ethical committee of the Faculty of Agricultural Sciences, Universidad Técnica de Ambato.

**Detection of Salmonella**

*Salmonella* was isolated following standardized methods (ISO 6579) (ISO, 2017). The samples were pre-enriched in buffered peptone water (Oxoid, Basingstoke, England) and then incubated at 37±1°C for 18 h ± 2 h. Next, Rappaport Vassiliadis Soy Broth (RVS Broth) (Merck Millipore, Darmstadt, Germany) was used a selective medium, being inoculated with the pre-enriched culture and incubated at 41.5±1°C for 24±3 h. One loopful of the selective enrichment medium was streaked onto xylose lysine deoxycholate agar (XLD agar) (Becton Dickinson GmbH, Heidelberg, Germany) and incubated at 37±1°C for 24±3 h. Presumptive *Salmonella* isolates (identified as red/yellow colonies with a black center) were purified in Mac Conkey agar (Merck, Darmstadt, Germany) and incubated at 37±1°C for 24 h. Isolates were Gram stained and the following biochemical tests were performed for confirmation the genus *Salmonella*: a catalase test using 30% hydrogen peroxide (Merck Millipore, Darmstadt, Germany); triple sugar iron agar test (TSI) (Becton Dickinson GmbH, Heidelberg, Germany), Simmons citrate agar test (Merck, Darmstadt, Germany), Christensen urea agar test (Britania Lab., Buenos Aires, Argentina), and indole reaction using tryptone water (Merck, Darmstadt, Germany) and Kovac’s reagent (Sigma Aldrich, St. Louis, USA). One isolate per positive sample was selected and cryopreserved using overnight growth in LB broth (Sigma Aldrich, St. Louis, USA) supplemented with 30% glycerol (Merck Millipore, Darmstadt, Germany) and maintained at -80°C until analysis.

**Serovar determination by PCR**

PCR assays were performed to identify the genes under specific conditions (Table 1). One virulence gene related with fimbrial cluster (*hcfC*) was evaluated as target of *S. enterica* specie (Zhu et al., 2015). For serovars and biotypes: A modification methylase gene that are specific of *S. Infantis* (M.SinI) (Ranjbar et al., 2017). 23S rRNA gene associated to S. Typhi
(sty) (Pui et al., 2011). A flagellin gene that show specificity to S. Typhimurium (fliC) (Pui et al., 2011). Gallinarum biotypes were identified by steB fimbral and rhs locus (Zhu et al., 2015). Specific DNA difference fragment (SdfI) served as target to distinguish S. Enteritidis from other serovars (Agron et al., 2001). And a putative membrane protein (gly) to identify S. Kentucky (Zhu et al., 2015). DNA was extracted from overnight cultures in Casein-Peptone Soymeal-Peptone Broth (Merck, Darmstadt, Germany) as described by Muniesa et al. (2004). Approximately =50 ng reaction resulting from the thermal shock of bacterial suspensions (>10^7 UFC/ml) diluted in sterile ddH2O was used as template for the PCR reactions. Amplifications were carried out as follows: initial denaturation at 95°C for 1 min; 35 cycles of 95°C for 30 s, annealing temperature at 72°C for 1 min; and a final elongation step at 72°C for 7 min. The following reference Salmonella strains were used as positive controls for the six serovars under investigation: S. Enteritidis UNIETAR 1, S. Gallinarum b. Gallinarum NCTC 13346, S. Gallinarum b. Pullorum ATCC 19945®, S. Typhi ATCC® 19430, S. Typhimurium ATCC® 26930 and S. Infantis UNIETAR 3CT7.

The reaction mixture contained: 12.5 µl of DreamTaq Green PCR Master Mix (Thermo Fisher Scientific, Massachusetts, USA), 0.5 µl of each primer (30 µM stock), 9 µl of nuclease-free water (Thermo Fisher Scientific, Massachusetts, USA), and 2.5 µl of crude DNA were used. PCRs were performed with an Applied Biosystems SimplyAmp Thermal Cycler (Thermo Fisher Scientific, Massachusetts, USA). A total of 10 µl of each PCR product were analyzed by agarose gel electrophoresis and stained using Sybr® Safe DNA Gel Stain (Invitrogen, Carlsbad, USA).

Table 1. Oligonucleotides used in this study.

<table>
<thead>
<tr>
<th>Organism</th>
<th>Name and direction</th>
<th>5’ to 3’ sequence</th>
<th>Gene</th>
<th>Annealing temperature (°C)</th>
<th>Amplicon size (bp)</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td>Enteritidis</td>
<td>sdf-F</td>
<td>TGT GTT TTA TTA GAT GCA AAG C G</td>
<td>sdf locus</td>
<td>56</td>
<td>293</td>
<td>(Agron et al., 2001)</td>
</tr>
<tr>
<td>Enteritidis</td>
<td>sdf-R</td>
<td>CGT TCT TGT GGT ACT TCA GAT GAC</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Enterica</td>
<td>bcfC-F</td>
<td>GGG TGG GCG GAA AAC TAC TTT</td>
<td>bcfC</td>
<td>56</td>
<td>993</td>
<td>(Zhu et al., 2015)</td>
</tr>
<tr>
<td>Enterica</td>
<td>bcfC-R</td>
<td>CGG CAC GGC GGA ATA GAG CAC</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Infantis</td>
<td>M. SinF</td>
<td>CAC AAT GAA CGT GGT GAA GGA</td>
<td>M.Sin I</td>
<td>56</td>
<td>184</td>
<td>(Ranjbar et al., 2017)</td>
</tr>
<tr>
<td>Infantis</td>
<td>M. SinR</td>
<td>TGA ACT ACG TTC GCT GCT CTG</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Gallinarum biotype Gallinarum</td>
<td>steB-F</td>
<td>TGT CGA CTG GGA CCC GCC CGC CCG C</td>
<td>steB</td>
<td>56</td>
<td>636</td>
<td>(Pugliese et al., 2011)</td>
</tr>
<tr>
<td>Gallinarum biotype Gallinarum</td>
<td>steB-R</td>
<td>CCA TCT TGT AGC GCA CCA T</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Gallinarum biotype Pullorum</td>
<td>rhs-F</td>
<td>TCG TTT ACG GCA TTA AAC AAG TTA</td>
<td>rhs locus</td>
<td>56</td>
<td>402</td>
<td>(Zhu et al., 2015)</td>
</tr>
<tr>
<td>Gallinarum biotype Pullorum</td>
<td>rhs-R</td>
<td>CAA ACC CAG AGC CAA TCT TAT CT</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Typhi</td>
<td>sty-1</td>
<td>TGC CGG AAA CGA ATC T</td>
<td>23S rRNA</td>
<td>53</td>
<td>300</td>
<td>(Zhu et al., 1996)</td>
</tr>
<tr>
<td>Typhi</td>
<td>sty-2</td>
<td>GGT TGT CAT GCC AAT GCA CT</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Typhimurium</td>
<td>Fli15</td>
<td>CGG TGT TGC CCA GGT TGG TAA T</td>
<td>fliC gene</td>
<td>53</td>
<td>620</td>
<td>(Pui et al., 2011)</td>
</tr>
<tr>
<td>Typhimurium</td>
<td>Typ04</td>
<td>ACT GGT AAA GAA AAC TAC T</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Results
Assessing the presence of Salmonella
Overall, 31 out of 34 isolates which showed phenotypic characteristics in accordance with Salmonella were confirmed by PCR as S. enterica (Table 2). Of the 21 farms, 16 (76%, 95%CI: 53-92) showed the presence of Salmonella on environmental surfaces, and Salmonella bacteria were isolated in 7 pooled cloacal swabs (33%, 95%CI: 15–57) and in 6 of 18 composite feed samples (33%, 95%CI: 13–59). Feces from backyard layers showed the presence of Salmonella in 2 of 21 samples (10%, 95%CI: 1–30). Dataset 1 shows the location of each sample and the presence or absence of Salmonella (Calero-Cáceres, 2019a).

Determining presence of serovars
Regarding to the presence of individual serovars (Figure 1), the highest occurrence was of S. Infantis, detected in 58% (18/31) of isolates, followed by S. Typhimurium, present in 32% of samples (10/31) (Supplementary Figure 1 (Calero-Cáceres, 2019c)). The serovar of 10% of Salmonella isolates (3/31) were unable to be serotyped by the panel of tests. In poultry feed samples, S. Infantis was present in 100% (6/6), while in S. enterica isolated from manure drag swabs, S. Infantis was detected in 50% (8/16) and S. Typhimurium in 50% (8/16). In backyard poultry fescs from local markets, S. Infantis was detected in 100% of positive samples (2/2). The most heterogeneous diversity of Salmonella serotypes was observed in pooled cloacal swabs, with 2 S. Infantis, 2 S. Typhimurium and 3 S. enterica consisting of serovars not covered within the panel. Dataset 1 lists the identity of the serovar taken from each sampling location (Calero-Cáceres, 2019a). Dataset 2 shows PCR gels for confirmation of Salmonella serovars (Calero-Cáceres, 2019b).
Table 2. *Salmonella*-positive samples in relation to evaluated matrices.

<table>
<thead>
<tr>
<th>Location</th>
<th>Sample</th>
<th>Matrix</th>
<th>Samples, n</th>
<th>Positive samples, n (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Farms</td>
<td>Feed</td>
<td>Composite feed</td>
<td>18</td>
<td>6 (33%)</td>
</tr>
<tr>
<td></td>
<td>Environment</td>
<td>Environmental swabs</td>
<td>21</td>
<td>16 (76%)</td>
</tr>
<tr>
<td></td>
<td>Animal</td>
<td>Laying hen cloacal swab (composite)</td>
<td>21</td>
<td>7 (33%)</td>
</tr>
<tr>
<td>Local markets</td>
<td>Environment</td>
<td>Backyard poultry feces</td>
<td>21</td>
<td>2 (10%)</td>
</tr>
</tbody>
</table>

Figure 1. Distribution of *Salmonella* serovars according to the evaluated matrices.

Discussion

The overall results showed a significant presence of *Salmonella* in layer farms in the central Ecuador region, one of the main sources of egg production in the country, with a detection of at least one sample positive per farm in the 76% of the evaluated sites. This result is similar to that reported in Colombia (65%) (Donado-Godoy et al., 2012), and considerably higher than the presence of *Salmonella* in broiler chicken farms in northern Ecuador (15.9%) (Vinueza-Burgos et al., 2016).

The notable presence of *Salmonella* in poultry feed suggests that this may constitute a potential reservoir of this bacteria for poultry systems in the evaluated region, and consequently, a potential route of infection and colonization of poultry and subsequent entry into the food chain (Fink-Gremmels, 2012; Jones, 2011). In recent research conducted in an integrated poultry farm in Ecuador, 4.1% (8/194) of samples were positive for *Salmonella*, particularly in animal-based feed (Villagómez Estrada et al., 2017). Therefore, the accurate detection of this pathogen in feed is necessary in order to identify the critical points of contamination (facilities, raw materials, transport, storage, producers), that one may apply effective measures to reduce the risk of transmission.

The finding of only *S. Infantis* in poultry feed may be attributed to the high level of persistence of this serovar over time in poultry feed, which in turn results in its considerable presence in Ecuadorian broiler chicken (Andino et al., 2014; Vinueza-Burgos et al., 2016). Although the origin of this serovar in feed it is not well defined, studies have pointed to cross-contamination with feces, persistent contamination of storage bins and surfaces, and poor ingredient selection as main causes of feed contamination with *Salmonella* (Davies & Wray, 1997; Huss et al., 2018; Laban et al., 2014). Genomic tools, such as multilocus sequence typing, BOX-PCR, (GTG)5-PCR or whole-genome sequencing may help to identify the origin of feed contamination in a larger study.

Drag swabs revealed the presence of two different serovars in the sampled poultry farms: Infantis and Typhimurium. These
non-typhoidal *S. enterica* serovars are commonly associated with poultry systems and are linked to outbreaks of foodborne illness (Anderson *et al.*, 2016; Pui *et al.*, 2011). Serovars vary in their persistence over time and geographic distribution around the world (Hendriksen *et al.*, 2011), making further studies desirable in order to evaluate the variations in serovar persistence in the locations sampled in this research.

In backyard layer feces sampled at local markets, *S. Infantis* alone was detected (2/2), but further evaluation of *Salmonella* serovars in backyard flocks is recommended in order to improve surveillance of this potential source of salmonellosis (Behravesh *et al.*, 2014). In pooled cloacal swabs, the serovars detected were *Infantis* (2/7), *Typhimurium* (2/7) and unidentified serovars (3/7). *Infantis* and *Typhimurium* serovars are commonly detected in poultry around the world (Foley & Lynne, 2008; Foley *et al.*, 2011). Complementary analysis by serotyping the unclassified serovars is necessary in order to identify *Salmonella* bacteria not covered by the panel.

Data remains insufficient concerning the prevalence of *Salmonella* in poultry systems in Ecuador and in Latin America in general. The coordination of similar future studies may provide a starting point for surveillance of zoonotic bacteria within a defined public health area, leading to an improvement in policies and safe practices in the food industry. Such studies may reduce the risk of infection and establish protocols for corrective measures to be implemented in key upstream points of the chain as indicated by the data.

At the same time, the intervention of public health authorities may be required in order to ensure the participation of a fully representative range of poultry businesses in future research. This study depended on the voluntary consent of farm owners to providing samples, which may have led to selection bias. In order to establish a thorough program of surveillance, all potential sources of *Salmonella* infection in the region need to be made accessible to researchers.

These findings show a significant presence of *Salmonella* in layer farms in the central zone of Ecuador. The predominant serovars are *S. Infantis* and *S. Typhimurium*, typified by PCR. The principal source of infection could be related with poultry feed. From a public health perspective, it is necessary to establish adequate surveillance of *Salmonella*, including protocols covering biosecurity practices, antibiotic usage and random sampling programs.

### Data availability

#### Underlying data

Figsshare: Dataset 1. Origin, biochemical tests, PCR results and serovar of *Salmonella* isolates. [https://doi.org/10.6084/m9.figshare.7726163.v2](https://doi.org/10.6084/m9.figshare.7726163.v2) (Calero-Cáceres, 2019a)

Figsshare: Dataset 2. PCR results of *bcfC*, *fliC* and *M.SinI* genes. [https://doi.org/10.6084/m9.figshare.7726217.v2](https://doi.org/10.6084/m9.figshare.7726217.v2) (Calero-Cáceres, 2019b)

#### Extended data

Figsshare: Supplementary figure 1. Multiplex PCR amplification of serovar-specific genes. a) *bcfC* and *mSinI* fragments (*S. Infantis*), b) *bcfC* and *fliC* fragments (*S. Typhimurium*).

[https://doi.org/10.6084/m9.figshare.7732934.v1](https://doi.org/10.6084/m9.figshare.7732934.v1) (Calero-Cáceres, 2019c)

Data are available under the terms of the Creative Commons Zero “No rights reserved” data waiver (CC0 1.0 Public domain dedication).

### Grant information

This study was supported by the Dirección de Investigación y Desarrollo DIDE-Universidad Técnica de Ambato (Project 1568-CU-P-2017).

The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

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Open Peer Review

Current Peer Review Status: ✔ ✔

Version 2

Reviewer Report 17 April 2019

https://doi.org/10.5256/f1000research.20651.r46971

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Tania Gaviria Cantín
Departamento de Ciencias Naturales, Exactas y Estadística. Facultad de Ciencias Básicas, Universidad de Santiago de Cali, Cali, Colombia

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Molecular microbiology, bacterial genetics, molecular biology, genetic engineering

I have read this submission. I believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Reviewer Report 09 April 2019

https://doi.org/10.5256/f1000research.20651.r46970

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Eloy Gonzalez-Gustavson
Laboratory of Virus Contaminants of Water and Food, Section of Microbiology, Virology and Biotechnology, Department of Genetics, Microbiology and Statistics, Faculty of Biology, University of Barcelona, Barcelona, Spain

I agree with the changes.

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Epidemiology, biostatistics, environmental microbiology, parasitology
I have read this submission. I believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Eloy Gonzalez-Gustavson

Laboratory of Virus Contaminants of Water and Food, Section of Microbiology, Virology and Biotechnology, Department of Genetics, Microbiology and Statistics, Faculty of Biology, University of Barcelona, Barcelona, Spain

The scientific names in the manuscript need to be reviewed.

The author use incorrectly the terms prevalence and incidence as synonyms.

Incidence is defined as the presence of new cases of an illness over a period of time. The manuscript does not correspond to an incidence study.

I would like to see more information in the manuscript about the design to consider the results as prevalence. I have not found details about the representativeness of the sampling (sample size to get a prevalence) or if they were obtained randomly. If the method does not satisfy the requirement to be considered as prevalence, I recommend replacing the term prevalence by frequency, presence or proportion.

The confidence interval in one case was incorrectly estimated.
"Feces from backyard layers showed the presence of Salmonella in 2 of 21 samples (10%, 95%CI: 0–22)"
This values have to be calculated based on binomial distribution. Actually in the manuscript, the confidence interval was estimated based on normal or t distribution and 0 was included as lower interval.

Is the work clearly and accurately presented and does it cite the current literature?
Partly

Is the study design appropriate and is the work technically sound?
Yes

Are sufficient details of methods and analysis provided to allow replication by others?
Yes

If applicable, is the statistical analysis and its interpretation appropriate?
Partly

Are all the source data underlying the results available to ensure full reproducibility?
Yes

Are the conclusions drawn adequately supported by the results?
Yes

**Competing Interests:** No competing interests were disclosed.

**Reviewer Expertise:** Epidemiology, biostatistics, environmental microbiology, parasitology

I have read this submission. I believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however I have significant reservations, as outlined above.

Reviewer Report 11 March 2019
https://doi.org/10.5256/f1000research.19945.r45084

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Tania Gaviria Cantín
Departamento de Ciencias Naturales, Exactas y Estadística. Facultad de Ciencias Básicas, Universidad de Santiago de Cali, Cali, Colombia

**Title**
I consider that the title is not totally in agreement with the study. This could be modified at “*Salmonella* diversity isolated from ... “ without the word “Prevalence” because the study is not a follow-up of previously reported cases in those same conditions

**Introduction**
In the fourth line you would change the word “poisoning” by contamination
At the end correct one “and” that is in italics
When you say "among the layer hens, no information about prevalence or diversity of *Salmonella* has been reported", you could specify or support if that lack of information is only in Ecuador or at a South American or global level. In the same way, it could important to include some epidemiological data of salmonelosis in Ecuador.

**Methodology**
I think that is not necessary to do DNA extraction to perform PCR, because *Salmonella* an is gram negative bacteria and during the start of the PCR where the temperature rises to 90 °C it is possible to destroy cellular wall and release the DNA. However, it does not affect the results, taking into account that the procedure has been carried out correctly avoiding cross contamination.
On the other hand, in order to reproduce the methodology of this study, the program used for PCR should be indicated. The concentration of primers (30 uM) is the final or initial concentration?
It would be useful to indicate why those particular genes were used as molecular markers for the identification of the species and the serovars.

**Results**

You can ignore the phrase "amplification of the bcfC gene" and leave the table 1 referenced because it is a bit redundant.

Regarding statistical analysis and sample number in representation or not, I prefer not to give many opinions because I'm not qualified enough for that. However, it would be important that the methodology explain in detail how the statistical analysis was performed and the calculation of the incidence.

In order of reference, table 1 of results should be table 2 and vice versa.

Regarding table 1 (positive *Salmonella* samples ...), it could be a little more consistent with what they explain in the methodology because it took me a bit to understand it, taking into account the classification of columns in terms of location, samples, etc.

**Discussion**

I believe that at some point it can be said that the regulations of Ecuador in relation to the health and control of layer farms and local markets and explain how the work is contributing to improve local control, taking into account that this layer farms produce around 60% of egg production in the country.

Is the work clearly and accurately presented and does it cite the current literature?

Yes

Is the study design appropriate and is the work technically sound?

Partly

Are sufficient details of methods and analysis provided to allow replication by others?

Partly

If applicable, is the statistical analysis and its interpretation appropriate?

I cannot comment. A qualified statistician is required.

Are all the source data underlying the results available to ensure full reproducibility?

Partly

Are the conclusions drawn adequately supported by the results?

Yes

**Competing Interests:** No competing interests were disclosed.

**Reviewer Expertise:** Molecular microbiology, bacterial genetics, molecular biology, genetic engineering

I have read this submission. I believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however I have significant reservations, as outlined above.
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