Bulletin UASVM Animal Science and Biotechnologies 70(1)/2013, 175-180
Print ISSN 1843-5262; Electronic ISSN 1843-536X

# The Contamination Level of the Poultry Carcasses During the Slaughtering Flow

**Marius M. CIOBANU[1)], Roxana LAZĂR[1)], Alina N. POSTOLACHE[2)], Casiana A. APETROAEI (PETRESCU)[1)], Nicoleta GĂINĂ (DIACONU)[1)], Paul C. BOIŞTEANU[1)]**

[1)]University of Agricultural Sciences and Veterinary Medicine, Faculty of Animal Science, 3 M. Sadoveanu Alley, 700490 Iaşi, Romania; mar.ciobanu@yahoo.com
[2)]SCDCB Research and Development, Dancu, Iasi, Romania; narcisa.postolache@gmail.com

**Abstract.** During the past years, both production and consumption of poultry meat has known an ascending path worldwide. This led to an intensive production simultaneous with a growing number of agricultural farms. In this context, germ contamination may be influenced by several technological factors during the slaughtering process. The aim of the present study is to evaluate the impact of some poultry slaughtering stages such as bleeding, depluming, evisceration, washing, cooling, packing –on the carcasses germ flora. The experiment took place in a slaughtering house situated in Iasi County, Romania. The evaluation was accomplished by the following microbiological parameters: total number of germs (TNG), *Coliformi fecali*, *Enterobacteriaceae*, *Escherichia coli*.

The samples were gathered for five months from a total number of 180 "Ross 308" poultry carcasses, which were randomly chosen during the slaughtering. The biological material comes from the poultry growing specialized farms.

As for the evolutional point of view, the largest germ charge on the carcasses surface was noticed just after the deplumation and evisceration. These are the stages when the microorganism contamination occurs intensively. The highest mean values for every parameter we studied are: TNG– 7.12±0.13 $\log_{10}$ ufc/g; *Coliformi fecali*–5.48±0.14 $\log_{10}$ ufc/g, *Enterobacteriaceae*–5.59±0.09 $\log_{10}$ ufc/g at evisceration stage, *Escherichia coli*–4.80±0.11 $\log_{10}$ ufc/g at depluming stage.

Statistically there were significant differences ($P<0.001$) between the calculated mean values for every microbiological parameter during each stage of the slaughtering process. This study brings valuable information regarding the microflora dynamics during the slaughtering process.

**Keywords:** bacterial microflora, poultry carcasses, contamination

## INTRODUCTION

In the last years, both production and consumption of poultry meat was on an ascendant curve at world level, this thing leading to intensification of production, at the same time with expansively of number and size of agricultural exploitations (Abu-Rwaida *et al.*, 1994; McNamara, 1997; Keener *et al.*, 2004).

Global level of total number of germs at fresh processed carcasses is influenced by the moment of feeding withdrawal before slaughtering (Bilgili, 1988; Izat *et al.*, 1989), excretion (Cox and Pavic, 2010), transport (McNab *et al.*, 1993), outside air temperature (Renwick *et al.*, 1993), processing stages during slaughtering (Mead *et al.*, 1993) and by the hygiene practices inside slaughtering house (Mead, 1989).

In 1989 Mead presented the main reasons for slaughtering contamination, with direct implications on difficulties regarding micro-organisms control during processing: high rate of production, which maintain birds in a close space, with a relative high density; existence of some limits in processing equipments designs, including those ones utilized for scalding and

feather-plucking and evisceration; difficulties for an adequate washing of abdominal cavity after evisceration, when carcass is a whole and exist the tendency of bacteria clamping in feathers crevices and follicles (Thomas and McMeekin, 1980; Mead, 1989). The current study was carried out to determine the effects of processing procedures on microbial quality of carcasses during different processing stages and to help local industry to improve quality and safety of poultry products.

## MATERIALS AND METHODS

Samples were gathered from a total number of 180 poultry carcasses (*Ross 308*) during 5 successive visits, experimental batch on which microbiological gathering and samples analyses were applied being formed by 6 carcasses (two carcasses at one hour, two hours, respectively three hours from the beginning of slaughtering process), randomized selected from technological flow from six different points, as follows: just after bleeding, after evisceration, after washing of eviscerated carcasses, after feather - plucking, after carcass chilling and after packaging.

From selected carcasses were collected skin samples of ~10 g from cervical area with a sterile scissors, in sterile plastic bags (special bags for Stomacher) and stored from gathering till laboratory. Samples were processed for examination after 3 hours from gathering.

To obtain the serial dilutions were respected the requests of ISO 6887-1 for determination of following microbial parameters: *total number of mesophyll aerobic germs*, *faecal coliforms*, *Enterobacteriaceae* and *Escherichia coli*.

Total number of *mesophyll aerobic germs* was determined in according with the demands of ISO 4833 standard. *Enterobacteriaceae* were determined in according with the demands of standard ISO 21528, being used VRBGA (*Violet Red Bile Glucose Agar*) environment with incubation at 37°C for 24 hours. *Enterobacteriaceae* were confirmed by testing the capacity of producing oxidase and to ferment glucose. *Coliforms* were determined respecting standard ISO 4832, using VRBA (*Violet Red Bile Agar*) environment with incubation at 30°C for 24 hours. *Escherichia coli* were determined by using Levine (*EMB -Eosine Methylene Blue Agar*) environment with incubation at 37°C for 24 hours, followed by confirmation of characteristic colonies (darker with a metallic green gloss) by following tests: indole, Voges-Proskauer, methyl red, utilization of titrate.

Data resulted were processed with the application Microsoft Excel. So, was realized a database with corresponding variation series, each series being encoded in according with the specific of studied information. For testing, the statistical significant differences between the averages of studied characters were used ANOVA Single Factor algorithm and Tukey test.

## RESULTS AND DISCUSSIONS

Broiler chickens get in the slaughtering houses, generally, with a high bacteria contamination degree, especially with the pathogenic ones for humans, such as coli form bacteria (Mead *et al.*, 1993; Abu-Rwaida *et al.*, 1994; Geornaras *et al.*, 1997). In *Table 1* are presented the means ($log_{10}$ ufc/g) for total number of microorganisms (*TNG, faecal coliforms, Enterobacteriaceae, Escherichia coli*), which characterized the gathered samples from the level of cervical area derma of poultry carcasses from different points of conveyer line. In evolution, the greatest bacterial load on surface of examined surfaces was enlightened, usually, just after feather plucking or evisceration, these being the stages in which microbial contaminations had a very high manifestation.

Tab. 1

Evolution of poultry carcass microflora ($\overline{X} \pm s_{\bar{x}}$) during slaughtering flow

| Specification | *TNG* * | | *Faecal coliform* * | | *Enterobacteriaceae* * | | *Escherichia coli* * | |
|---|---|---|---|---|---|---|---|---|
| | $\overline{X} \pm s_{\bar{x}}$ | V% | $\overline{X} \pm s_{\bar{x}}$ | V% | $\overline{X} \pm s_{\bar{x}}$ | V% | $\overline{X} \pm s_{\bar{x}}$ | V% |
| Bleeding | 5.15 ± 0.25 | 11.04 | 3.68 ± 0.13 | 8.04 | 4.52 ± 0.21 | 10.21 | 3.23 ±0.09 | 6.49 |
| Feather-plucking | 6.79 ±0.16 | 5.42 | 4.97 ±0.09 | 4.03 | 5.29 ±0.17 | 7.29 | 4.80 ±0.11 | 4.92 |
| Evisceration | 7.12 ±0.13 | 4.24 | 5.48 ±0.14 | 5.88 | 5.59 ±0.09 | 3.73 | 4.66 ±0.15 | 7.31 |
| Washing | 5.05 ±0.11 | 5.09 | 3.55 ±0.09 | 5.82 | 4.28 ±0.14 | 7.28 | 3.33 ±0.15 | 9.76 |
| Chiling | 5.17±0.16 | 6.86 | 3.85 ±0.07 | 4.26 | 3.86 ±0.09 | 5.17 | 3.58 ±0.09 | 5.77 |
| Packaging | 5.24 ± 0.14 | 5.87 | 3.62 ±0.12 | 7.42 | 4.34 ±0.10 | 5.25 | 2.61 ±0.13 | 11.50 |

INTERPRETATION OF DIFFERENCES

**FISHER test:** $\hat{F} = 31.657$; $F_{0.001}(5.174) = 5.976$; $\hat{F} \square F_{0.001}$ ◎ ***

**TUKEY test:** $w_{5\%} = 0.682$; $w_{1\%} = 0.792$

| - | B | FP | E | W | Ch | P |
|---|---|---|---|---|---|---|
| P | ns | ad | ad | ns | ns | 0 |
| Ch | ns | ad | ad | ns | 0 | - |
| W | ns | ad | ad | 0 | - | - |
| E | ad | ns | 0 | - | - | - |
| FP | ad | 0 | - | - | - | - |
| B | 0 | - | - | - | - | - |

**FISHER test:** $\hat{F} = 54.245$; $F_{0.001}(5.174) = 5.976$; $\hat{F} \square F_{0.001}$ ◎ ***

**TUKEY test:** $w_{5\%} = 0.456$; $w_{1\%} = 0.530$

| - | B | FP | E | W | Ch | P |
|---|---|---|---|---|---|---|
| P | ns | ad | ad | ns. | ns. | 0 |
| Ch | ns | ad | ad | ns. | 0 | - |
| W | ns | ad | ad | 0 | - | - |
| E | ad | ac | 0 | - | - | - |
| FP | ad | 0 | - | - | - | - |
| B | 0 | - | - | - | - | - |

**FISHER test:** $\hat{F} = 22.024$; $F_{0.001}(5.174) = 5.976$; $\hat{F} \square F_{0.001}$ ◎ ***

**TUKEY test:** $w_{5\%} = 0.575$; $w_{1\%} = 0.668$

| - | B | FP | E | W | Ch | P |
|---|---|---|---|---|---|---|
| P | ns | ad | ad | ns | ns | 0 |
| Ch | ac | ad | ad | ns | 0 | - |
| W | ns | ad | ad | 0 | - | - |
| E | ad | ns | 0 | - | - | - |
| FP | ad | 0 | - | - | - | - |
| B | 0 | - | - | - | - | - |

**FISHER test:** $\hat{F} = 48.567$; $F_{0.001}(5.174) = 5.976$; $\hat{F} \square F_{0.001}$ ◎ ***

**TUKEY test:** $w_{5\%} = 0.530$; $w_{1\%} = 0.584$

| - | B | FP | E | W | Ch | P |
|---|---|---|---|---|---|---|
| P | ad | ad | ad | ad | ad | 0 |
| Ch | ns | ad | ad | ns | 0 | - |
| W | ns | ad | ad | 0 | - | - |
| E | ad | ns. | 0 | - | - | - |
| FP | ad | 0 | - | - | - | - |
| B | 0 | - | - | - | - | - |

***** = $\log_{10}$ ufc/g; **TNG** = total number of mesophyl aerobic germs; **P** = packing; **Ch** = chilling; **W** = washing; **E** = evisceration; **FP** = feather-plucking; **B** = bleeding;
ns. = insignificant differences; ac = distinct significant differences; ad = very significant differences

Tab. 2

Evolution of poultry carcass microflora ($\bar{x} \pm s_{\bar{x}}$) during some slaughtering stages function of time from slaughtering process starting

| Specification | **Microbiologic parameter** | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | *NTG* ***** | | | *Faecal coliforms* ***** | | | *Enterobacteriaceae* ***** | | | *Escherichia coli****** | | |
| | **1 h** | **2 h** | **3 h** | **1 h** | **2 h** | **3 h** | **1 h** | **2 h** | **3 h** | **1 h** | **2 h** | **3 h** |
| *Bleeding* | 4.91±0,10[a] | 5.43±0,21[d] | 6.15±0,14[d] | 3.37±0,24 | 3.43±0,24 | 3.86±0,08 | 4.13±0,22 | 4.50±0,29 | 4.99±0,27 | 3.14±0.11 | 3.28±0.20 | 3.55±0.17 |
| *Feather - plucking* | 6.94±0.08 | 7.03±0.31 | 7.12±0.30 | 4.68±0.28 | 5.05±0.32 | 5.41±0.27 | 5.06±0.39 | 5.52±0.43 | 5.71±0.35 | 4.42±0.38 | 4.51±0.41 | 4.85±0.49 |
| *Evisceration* | 7.16±0.34 | 7.31±0.33 | 7.44±0.22 | 5.39±0.42 | 5.47±0.43 | 5.54±0.37 | 5.41±0.25 | 5.68±0.31 | 5.92±0.38 | 4.67±0.28 | 4.72±0.31 | 4.97±0.41 |
| *Washing* | 4.21±0.30 | 4.43±0.35 | 4.76±0.37 | 3.57±0.43 | 3.66±0.54 | 3.97±0.54 | 4.25±0.38 | 4.28±0.31 | 4.34±0.40 | 3.49±0.53 | 3.61±0.39 | 3.72±0.29 |
| *Chilling* | 5.27±0.35 | 5.49±0.27 | 5.56±0.31 | 3.76±0.28 | 3.81±0.26 | 3.99±0.20 | 3.59±0.37 | 3.71±0.35 | 3.94±0.34 | 3.34±0.37 | 3.49±0.38 | 3.64±0.41 |

***** = $\log_{10}$ ufc / g; **NTG** = total number of mesophyl aerobic germs; **1 h** = one hour from processing starting; **2 h** = two hours from processing starting;
**3 h** = three hours from processing starting;
Difference signification between bacteria number function of processing time (in comparison with first batch – 1 h)
[ad] = very significant differences - P<0.001.

The high level of microbial load in this area of slaughter unit is a consequence of the functional particularities of feather-plucking equipments, but also due to some temporary hygiene lacks. At the opposite pole were placed the obtained results after carcass washing, consequently with evisceration. The larger variation interval of obtained means during whole slaughtering flow was calculated for *E. coli* (2.19 ufc/g).

Statistical interpretation of differences between obtained means for each microbial parameter corresponding to each processing stage revealed the existence of very significant differences between batches ($P<0.001$), through Tukey test being establish the significance level between the formed pairs.

Comparison of the results function of processed carcasses number revealed an increasing of microorganisms' number on the carcasses' surface concomitantly with increasing number of processed carcasses. The results are shown in *Table 2*. Microbial load for *TNG* observed at three hours from beginning of slaughtering process was higher, with around 0.72 $\log_{10}$ ufc/g in comparison with the values obtained after one hour from process start.

## CONCLUSION

Washing stage was the most efficient stage considering the decreasing of total number of studied microorganisms, chilling of carcasses and packaging -leading to step-by-step increasing. One possible explication could be the negative influence of air loading from warehouses or technological water loading used for chilling the carcasses by spraying. Considering these conditions, future research should be necessary for a proper establishment of causes or for confirmation, at the same time with the application of selective processing measures during poultry slaughtering.

*Acknowledgments.* This research was financed by grants from POSDRU/ CPP107/DMI1.5/S/77222 of the *University of Applied Life Sciences and Environment, Iaşi, Romania*. The biological material for this experiment was assured by S.C. Fermador S.A. Războieni.

## REFERENCES

1. Abu-Rwaida, A.S., Sawaya W.N., Dashti B.H., Murad M., Al-Othman H.A. (1994). Microbiological quality of broilers during processing in a modern commercial slaughterhouse in Kuwait, J. Food Prot., vol. 57, 887–892.

2. Bilgili, S.G. (1988). Effect of feed and water withdrawal on shear strength of broiler gastrointestinal tract, Poultry Science, vol. 67, 845–847.

3. Cox, J.M., Pavic A. (2010). Advances in enteropathogen control in poultry production, J. Appl. Microbiol., vol. 108, 745–755.

4. Geornaras, I., A. de Jesus, E. van Zyl, A. van Holy. (1997). Bacterial populations of different sample types from carcasses in the dirty area of a South African poultry abattoir, J. Food Prot., vol. 60, 551–554.

5. Izat, A.L., Colberg M., Driggers C.D., Thomas R.A. (1989). Effect of sampling method and feed withdrawal period on recovery of microorganisms from poultry carcasses, J. Food Prot., vol. 52, 480–483.

6. Keener, K.M., Bashor M.P., Curtis P.A., Sheldon B.W., Kathariou S. (2004). Comprehensive review of Campylobacter and poultry processing, Compr. Rev. Food. Sci. Food Safety, vol. 3, 105–116.

7. Mead, G.C. (1989). Hygiene problems and control of process contamination, In Processing PoultryEd. Elsevier Applied Science, London, UK, 183–221.

8. Mead, G.C., Hudson W.R., Hinton M.H. (1993). Microbiological survey of five poultry processing plants in the UK, Br. Poultry Science, vol. 34, 497–503.
9. McNab, W.B., Renwick S.A., Lowman H.R., Clarke R.C. (1993). Variability of broiler carcass bacterial load at three abattoirs, as measured by a hydrophobic grid membrane filter interpreter, J. Food Prot., vol. 56, 700–705.
10. McNamara, A. M. (1997). Generic HACCP applications in broiler slaughter and processing, Journal of Food Protection, vol. 60, 579–604.
11. Renwick, S.A., McNab W.B., Lowman H.R., Clarke R.C. (1993). Variability and determinants of carcass bacterial load at a poultry abattoir, J. Food Prot., vol. 56, 694–699.
12. Thomas, C.J., McMeekin A.T. (1980). Contamination of broiler carcass skin during commercial processing procedures: An electron microscopic study, Appl. Environ. Microbiol., vol. 40, 133–144.
13. **** I.S.O. 21528 (2004). Microbiologia alimentelor şi nutreţurilor. Metoda orizontală pentru detecţia şi enumerarea Enterobacteriaceelor. Partea 1: Detecţia şi enumerarea prin tehnica MPN cu preîmbogăţire, ASRO, Bucureşti.