

Salmonella Quantification (SalQuant®) with Hygiena's BAX® System for Beef Carcass Swabs

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BAX® System Q7

BAX® System X5

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INTRODUCTION:

The microbiological hygiene of cattle at slaughter is an important requirement to properly assess contamination risks for meat entering the ground beef supply. Many interventions are used on the harvest floor to help reduce and eliminate harmful organisms from beef commodities. The effectiveness of these interventions as well as sanitary procedures are commonly measured by the amount of indicator organisms detected. Several research studies have shown that the presence of indicator organisms such as coliforms, *E. coli* and aerobic counts are positively correlated to pathogens (1). Typically, pathogens are only tested for prevalence, which doesn't allow the resultant transfer rates to be well understood.

The use of quantitative methods can provide more valuable data and insight on managing these pathogens in targeted reduction efforts.

PURPOSE:

The purpose of this study was to develop and verify the BAX® System Real-Time PCR assay for *Salmonella* quantification (SalQuant®) in beef carcass swabs.

REGISTERED TRADEMARKS:

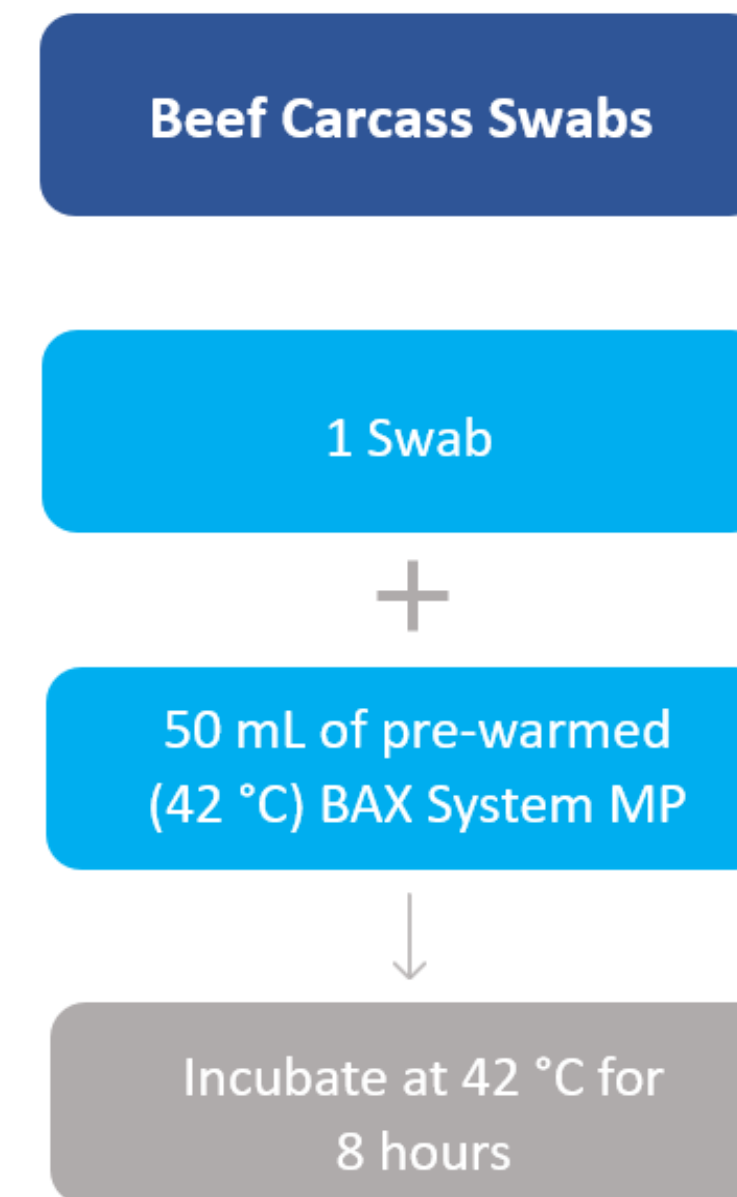
BAX® is a registered trademark of Hygiena for its line of equipment, reagents and software used to analyze samples for microbial contamination. SalQuant® is a registered trademark of Hygiena.

METHODS:

Sample Preparation

Beef carcass swabs were collected by an industry partner and artificially inoculated with a cold-stressed culture of *Salmonella* to create 15 samples total (3 replicate samples per inoculation level), ranging from 1.0 to 4.0 Log CFU/swab. Swabs were enriched in pre-warmed (42 °C) BAX MP media and incubated for 8 hours.

At the same time, a 3-tube x 5-dilution MPN was conducted for each inoculation level following the USDA FSIS Appendix 2.05.



RESULTS:

Curve Development (Figure 1): Data was assessed using linear regression to compare the cycle threshold (Ct) and known inoculation levels to create a best fit equation. The fit of the line was assessed using R² and Log Root Mean Square Error (RMSE).

- R² of 0.87
- Log RMSE of 0.43
- Enumerable range of 1.0 – 4.0 Log CFU/swab

MPN Comparison (Figure 2): Compared to MPN, SalQuant results demonstrated a more accurate Log CFU/swab estimation at each inoculation level.

SIGNIFICANCE:

The results of this study demonstrate accurate and rapid quantification of *Salmonella* from beef carcass swabs that can provide the industry with more valuable data and insight on managing this organism in beef.

By incorporating a quantitative method, processors can quickly and confidently respond to increasing levels of *Salmonella*. This can lead to improved sanitation measures and antimicrobial interventions to decrease the incidence of pathogens.

FIGURES:

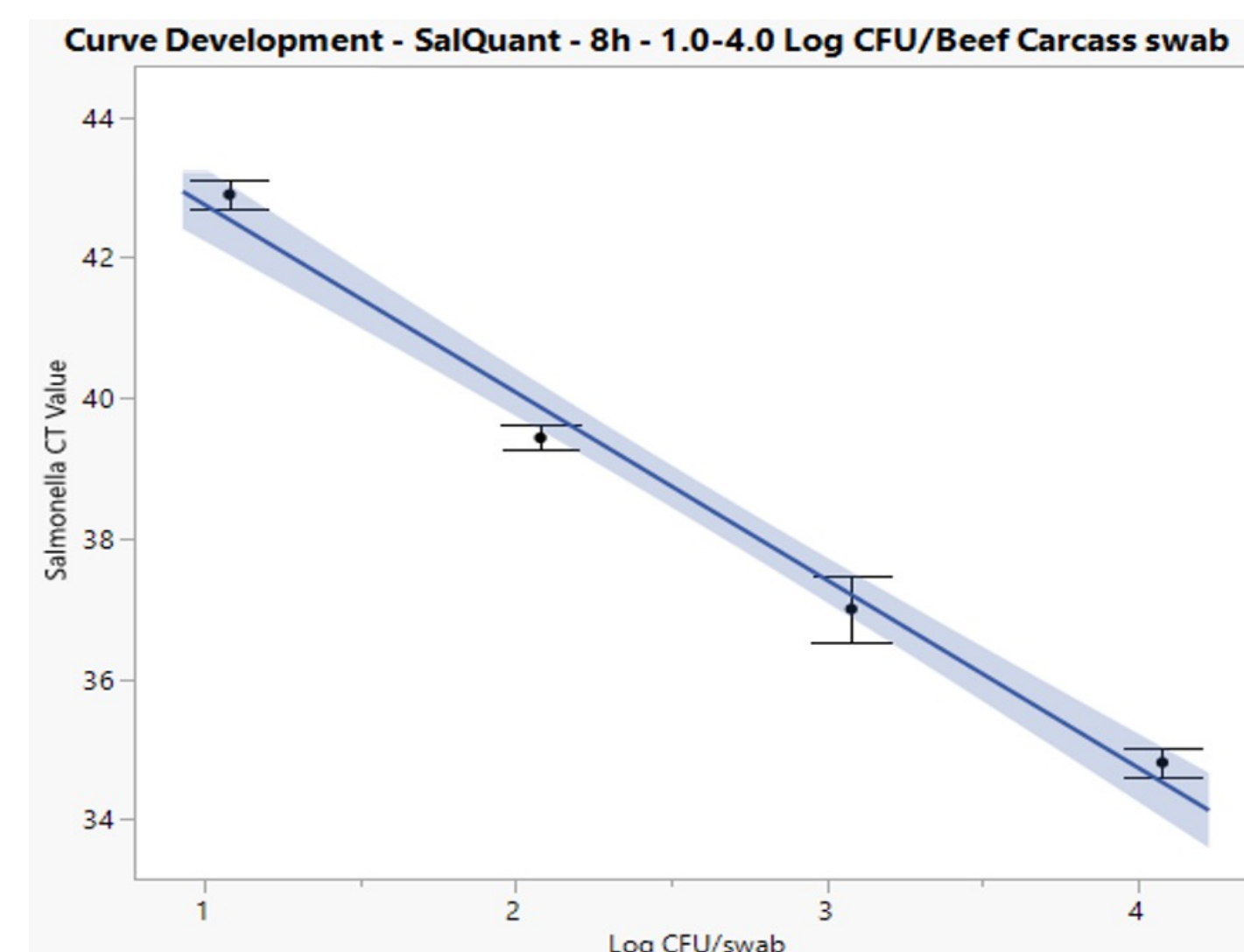
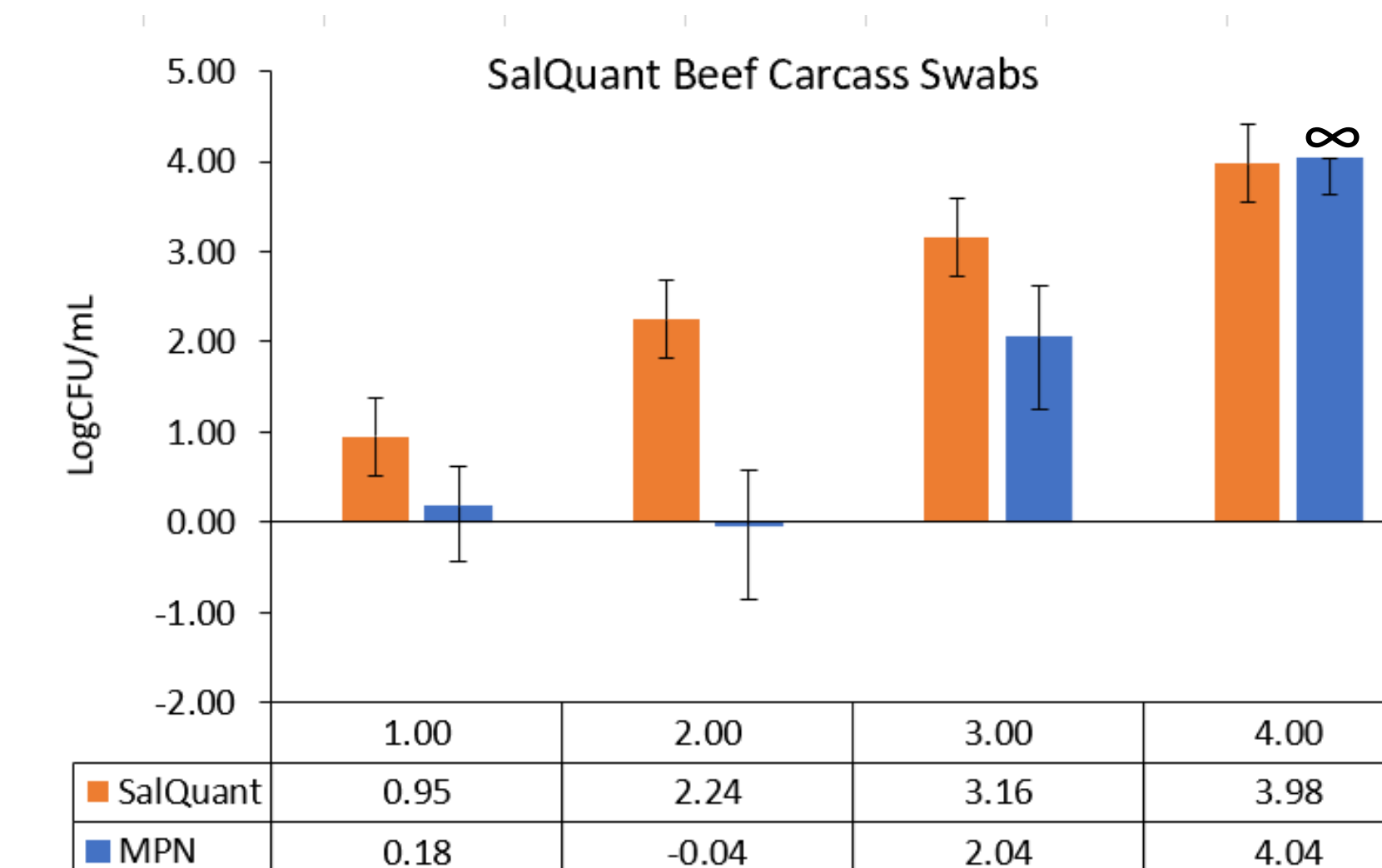


Figure 1 (Left). Mean (*Salmonella* Ct) and *Salmonella* Ct vs. Inoculated Log CFU/Swab

Figure 2 (Right). MPN and SalQuant Comparison



REFERENCES:

1. Brichta-Harhay, D. M., Guerini, M. N., Arthur, T. M., Bosilevac, J. M., Kalchayanand, N., Shackelford, S. D., Wheeler, T. L., and Koohmaraie, M. 2008. *Salmonella* and *Escherichia coli* O157:H7 Contamination on Hides and Carcasses of Cull Cattle Presented for Slaughter in the United States: an Evaluation of Prevalence and Bacterial Loads by Immunomagnetic Separation and Direct Plating Methods. *Applied and Environmental Microbiology*, 74(20), 6289 – 6297.