Evaluation of pre-PCR processing approaches for enumeration of Salmonella enterica in naturally contaminated animal feed

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Publication date:
2013

Document Version
Publisher's PDF, also known as Version of record

Citation (APA):
Evaluation of pre-PCR processing approaches for enumeration of *Salmonella enterica* in naturally contaminated animal feed

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**Aim**

To evaluate 3 pre-PCR processing strategies:
1) flotation-qPCR (modified from [1])
2) MPN-PCR (modified from [2])
3) qualitative culture enrichment PCR [2]

for the detection and/or quantification of *Salmonella* in naturally contaminated soy bean meal.

**Introduction**

Animal feed might serve as a reservoir of *Salmonella* contributing to the spread into the food chain. Levels of *Salmonella* in feed samples are low, bacteria are unevenly distributed and stressed and could therefore be hard to recover using standard culture-based methods. Due to this, there is a need for accurate, sensitive, rapid and user-friendly sample preparation methods prior to molecular analyses. Moreover, to facilitate quantitative risk assessment in the feed production chain, there is a need to enumerate *Salmonella* in naturally contaminated feed.

**Methods**

**Figure 1. Overview of the three pre-PCR processing strategies that were investigated. Bags of naturally contaminated soya bean meal (n = 15) were analyzed in parallel with the three methods.**

**Table 1. Comparison of qualitative results with the three methods for the analysis of naturally contaminated soya bean meal samples.**

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<tbody>
<tr>
<td>Flotation-qPCR</td>
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<td>Culture enrichment PCR</td>
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**Results**

Out of the 15 bags analyzed 6, 15 and 9 were positive for *Salmonella* with flotation-qPCR, MPN-PCR and culture enrichment PCR, respectively (Table 1).

Enumeration resulted in values of $1.8 \times 10^2$-7.8$ \times 10^3$ CFU/g (flotation-qPCR) and 0.024 to >5.2 MPN/g (MPN-PCR) (Figure 2).

**Figure 2. Comparison of enumeration results with flotation-qPCR and MPN-PCR for the analysis of naturally contaminated soya bean meal samples.**

**Conclusions**

- The 3 methods provide possibilities to assess the prevalence of *Salmonella* in feed, as well as the numbers of culturable, and non-culturable cells
- Differences in results could be due to non-culturable *Salmonella* and/or a heterogeneous distribution of *Salmonella* in the feed

**References**

1. Löfström et al. (2011) IJFM 145 Suppl 1:S103-109

**Acknowledgements**

This study was financially supported by the EU project BIOTRACER (contract no. 036272) and the Swedish Research Council for Environment, Agricultural Sciences and Spatial Planning (FORMAS).