

The use of bootstrapping in sample size analysis for the determination of an antimicrobial resistance profile of *E.coli* in broiler chickens

Davy Persoons ¹, Kaatje Bollaerts ² and Jeroen Dewulf ¹

¹Department of obstetrics, reproduction and herd health, veterinary epidemiology unit, Faculty of Veterinary medicine, Ghent University, Merelbeke, Belgium ² Interuniversity Institute for Biostatistics and statistical Bioinformatics, University Hasselt and Catholic University Leuven, Belgium

INTRODUCTION

One of the major issues that arise when trying to determine the optimal sample size for the determination of antimicrobial resistance profiles at herd level is that no single overall prevalence is available but only a number of different expected prevalences.

The objective of this study was to develop a methodology which makes it possible to interpret, challenge and optimize sample size when setting up an antimicrobial resistance profile of *E.coli* in broilers at flock level.

MATERIALS AND METHODS

Five broiler flocks were sampled. In each flock one cloacal swab was taken from 100 randomly selected chickens. *E.coli* was isolated and tested for antimicrobial susceptibility according to a standardized method. The effect of varying sample size on the accuracy of the prevalence estimation of resistance against 14 different antimicrobials was determined by using a bootstrapping methodology. Economic efficiency was determined by a cost effectiveness analysis of the sample size. Both the fixed and variable costs connected to the different sample sizes were taken into account.



RESULTS & DISCUSSION



Figure 1. Prevalence of antimicrobial resistance and corresponding bootstrap confidence intervals for different herd level sample sizes (1 colony per sample).



Figure 3. Cost effectiveness of a sample size for estimations within a 0.1, 0.2 or 0.3 confidence interval width.

Figure 2. proportion of prevalences estimated within a 0.1, 0.2 or 0.3 95% confidence interval width for different sample sizes.

Results showed that a substantial amount of between animal variation in antimicrobial resistance exists (Figure 1), highlighting the importance of an accurate sample size. The proportion of prevalences within a herd profile that can be estimated with sufficient precision (Figure 2) was determined as a way to globalize the results for the whole range of antimicrobials tested. This proportion allows us to predict or check the accuracy of a given sample size. Because of the financial constraints research often has to deal with, sample size was submitted to a cost-effectiveness analysis (Figure 3). An optimal sample size should provide a good compromise between the epidemiological and economical concerns. A good sample size in this case would be 27 (indicated by the arrows on figures 2 and 3). This is the most cost-effective sample size that will allow estimating 70% of the prevalences within a 0.3 confidence interval.

CONCLUSION

Using the proposed bootstrapping method to determine the effect of sample size on the proportion of prevalences that are estimated within a certain confidence interval and the according cost-effectiveness allows to optimize sampling protocols for antimicrobial resistance profile determination in a reliable and informed manner, avoiding the spill of research time and money.

ACKNOWLEDGEMENTS

This work was supported by a grant of the Federal Public Service of Health, Food Chain Safety and Environment (Grant number RT-06/3-ABRISK).