A model for determining optimal sampling protocols targeting detection of new disease introduction into expected negative animal populations

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INTRODUCTION

For animal production sites (especially those of very high value, such as genetic production and breeding/reproduction sites), that are expected to be and remain negative for a particular disease agent, an appropriate detection plan for new introduction of undesired disease agents must include both continuous clinical observation and well designed diagnostic sampling/testing protocols. Whereas basic sample size determination methods for disease detection from single samplings are generally understood, the factors that contribute to appropriatly sized and timed sampling are less well understood and frequently poorly applied in the design and execution of protocols. A stochastic model was developed to improve sampling protocol development targeting detection of new disease introduction into expected negative animal populations.

MATERIALS AND METHODS

An algorithm described by Rothman and Greenland (1998)[1] was modified and incorporated into a tool built to stochastically model onset of detection of new disease agent introduction in expected negative animal populations. An animal isolation scenario was modeled where a new cohort of 500 replacement females are moved into an empty site every 60 days, where no live animals exit to a downstream site during the first 30 days and animals are moved from the isolation to the downstream site as needed over the second 30 days of the overall 60 day period, after which the isolation site is emptied and sanitized in preparation for the next incoming group of replacement females. Model scenarios were compared by varying positive animals at entry (1 or 5 index case animals), contact probability (30%, 50% or 70%), transfer probability (30% or 70%), detection onset lag (2 or 3 days) and detection duration (14 or 21 days). Detection probability curves were generated across a 60 day period for each scenario at sample sizes of 15, 30, 45 and 60. For the sample sizes evaluated, the cohort day at which greater than or equal to 90%, 95% and 99% of model runs were detected as positive was used as the criteria for comparing scenarios.

RESULTS

Table 1 contains results for three different levels of contact probability (Cp) for both 1 index positive animal and 5 index positive animals.

For two scenarios comparing 5 or 1 index positives (both with 30%/70% contact/transfer probabilities and 2/14 day detection onset/duration) at a sample size of 30, the 95% detection threshold specification was achieved at the 15th and 23rd cohort day, respectively.

Table 1: Replacement animal isolation day at which the modeled detection rate equals or exceeds the Detection Rate Specification

Sample Size	Detection Rate Specification	Index = 1hd Cp = 30% Tp = 70% Onset = 2d Dur = 14d	Index = 1 Cp = 50% Tp = 70% Onset = 2d Dur = 14d	Index = 1 Cp = 70% Tp = 70% Onset = 2d Dur = 14d	Index = 5hd Cp = 30% Tp = 70% Onset = 2d Dur = 14d	Index = 5 Cp = 50% Tp = 70% Onset = 2d Dur = 14d	Index = 5 Cp = 70% Tp = 70% Onset = 2d Dur = 14d
15	90%	26	17	13	18	11	9
	95%	27	18	14	19	12	10
	99%	29	20	15	20	13	12
30	90%	22	15	11	14	9	7
	95%	23	16	12	15	10	8
	99%	26	17	13	17	12	9
45	90%	20	13	10	11	8	6
	95%	21	14	11	12	9	7
	99%	23	15	12	14	10	8
60	90%	18	12	9	9	7	6
	95%	19	13	10	11	8	6
	99%	21	14	11	13	9	7

An animal housing layout that reduces contact probability and/or infectious agents that have a relatively low transfer probability would tend to reduce the rate of transmission. In a replacement animal isolation facility where expected negative animals are held temporarily prior to entering an expected negative breeding herd, a facility design that maximizes contact probability would be most desirable to facilitate a greater opportunity for detection of exposure and transmission of disease agents intended to keep out of a negative breeding herd population. It follows then, that the importance of maximizing animal-to-animal contact increases as the animal isolation period decreases and/or the transmission rate (transfer probability) of a targeted infectious agent decreases.

Notably, where there is a single index positive case at isolation entry and the contact probability (Cp) is relatively low (30%), a 30 day strict isolation period does not allow enough time to collect-ship samples, do the testing and obtain the results prior to the scheduled first movements of animals out of the isolation. This issue is only exacerbated if unexpected positive results occur that require retesting and possible resampling-testing.

CONCLUSION

This stochastic sampling protocol model can be used to derive more informed and appropriate detection sampling protocols for the detection of new disease agent introduction into expected negative animal populations, as well as generate tables to be used as references for disease detection sampling that take into account the dynamics of exposure and transmission in animal cohorts.

REFERENCES

1. Rothman KJ, Greenland S. Concepts of Infectious Disease Epidemiology. Modern Epidemiology, Second Edition (1998) Lippincott and Raven, Philadelphia, PA; pp529 – 554