Schmallenberg virus (SBV): Predicting within-herd seroprevalence using bulk milk ELISA results

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Conclusions

Bulk milk (BM)-ELISA results are highly predictive of within-herd SBV seroprevalence

Herds with negative BM-ELISA results can have SBV seropositive animals in the herd

Introduction

Schmallenberg virus (SBV) causes ruminant abortions and congenital malformations, and mild clinical signs in adult dairy cattle (milk drop, fever, diarrhoea).

Objectives

- ✓ Determine the ability of bulk milk (BM)-ELISA results to predict within-herd SBV seroprevalence (Herd SP)
- ✓ Explain the variation in prediction limits of the BM-ELISA results using the distribution of individual animal blood ELISA results

Materials and Methods

Blood and bulk milk samples

- ✓ 4,019 individual lactating cow blood samples and 24 bulk milk samples collected from 26 Irish dairy farms were tested for SBV-specific antibodies (ID Screen® ELISA testing kits). Results were expressed as sample-to-positive percentage (S/P%) ratios.

Statistics

- ✓ Herd SP results were regressed on BM-ELISA results using general linear regression models
- ✓ Empirical distribution function (EDF) curves, which plot the distribution of individual animal blood ELISA results in each herd, were compared pairwise across herds (n=325 paired herd comparisons) using the Kolmorogov-Smirnov (KSa) statistical test.

EDF-curves were compared in herds with similar

1. BM-ELISA antibody titres (S/P% difference ≤5%)
2. Herd SP (SP% difference ≤5%)
3. Mean-herd serum antibody titres (S/P% difference ≤5%)

Results

Animal-level and within-herd seroprevalence

- Animal-level SP = 83%; Herd SP range: 10.7-100%
- 24 herds were BM-ELISA positive (Herd SP range: 30-100%); 2 herds were BM-ELISA negative (Herd SP 10.7% and 16%)

Prediction of within-herd seroprevalence from BM-ELISA (Fig.1)

- BM-ELISA results were moderately predictive of Herd SP (R^2 = 0.832)

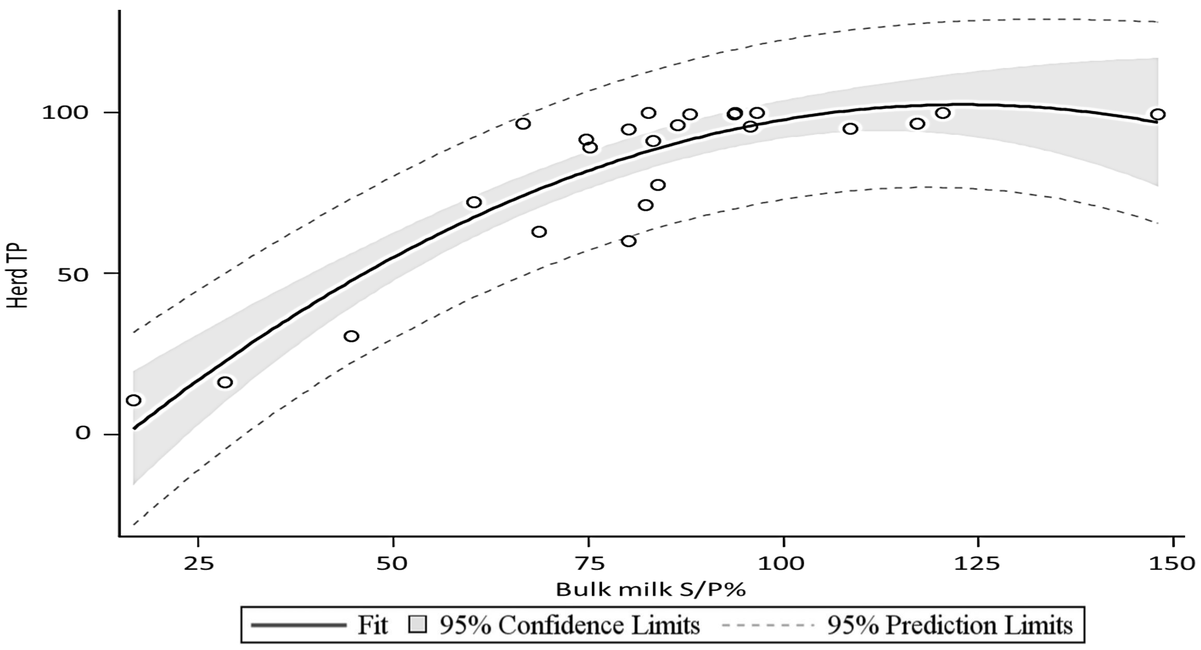

Fig.1 Predicting within-herd seroprevalence from BM-ELISA results

Table 1.
Animal-level antibody distributions and herd-level antibody prevalences

Herd-level antibody prevalences	No. of herds*	No. of paired-herd EDF-curve comparisons	EDF-curve	
			Similar	Different
Similar BM-ELISA S/P% (Fig.2)	18	33	6 (18%)	27 (82%)[1]
Similar Herd SP %	22	115	62 (64%)	53 (46%)[2]
Similar mean-herd S/P%	25	123	73 (53%)	50 (47%)[3]

*number of herds with a result similar to one or more other herds

Animal-level antibody distributions and herd-level antibody prevalences (Table 1)

The distributions of individual animal blood results were significantly different in:

1. 82% of herds with similar BM-ELISA results
2. 46% of herds with similar within-herd seroprevalence
3. 47% of herds with similar mean-herd S/P% results

An example of two herds with identical BM-ELISA but different EDF curves is shown in Fig. 2

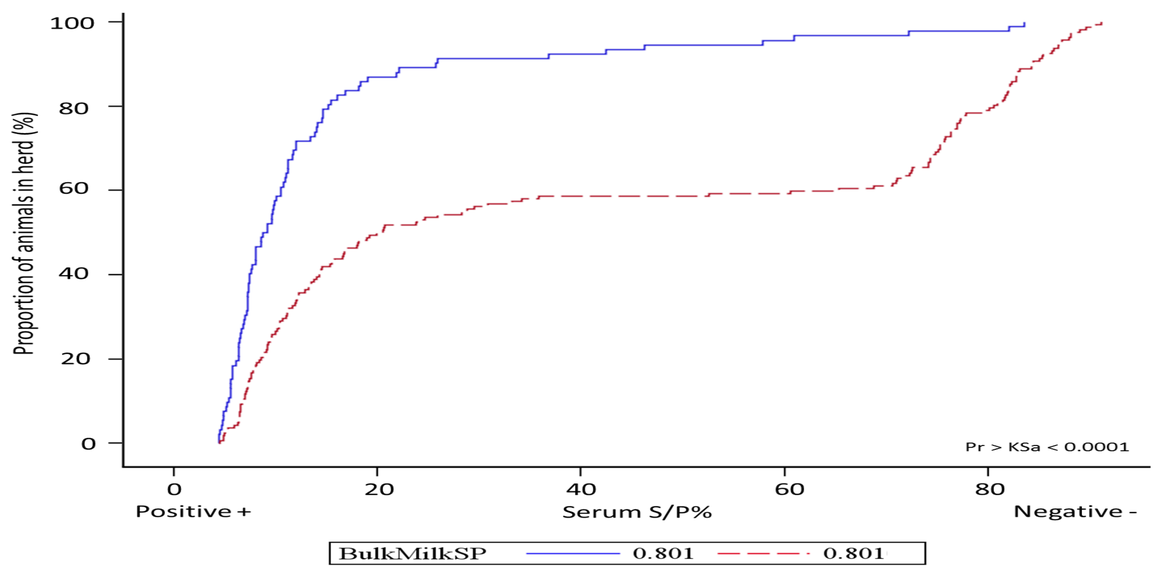

Fig.2 EDF-curve comparison in two herds with identical BM-ELISA results

Discussion

Animal-level and within-herd seroprevalence

- Animal-level SP was high but varied widely across herds in this SBV exposed region
- Herds with a negative BM-ELISA result can have seropositive animals present in the herd

Prediction of within-herd seroprevalence from BM-ELISA

- Predictions were most accurate for BM-ELISA values between 60 and 110 S/P%
- Predictions were less accurate (wide prediction limits) at low and high BM antibody titres

Animal-level antibody distributions and herd-level antibody prevalences

- Herds with similar BM-ELISA results can have significantly different proportions of seropositive animals within the herd
- EDF-curves revealed that the variation observed in the predicted within-herd seroprevalence in the regression models is likely a result of individual animal variation in serum antibody titres in these herds.

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