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Epidemiology of *Tritrichomonas foetus* in beef bull populations in Florida

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Abstract

The objectives of this study were to estimate the prevalence of herd and individual bull infection with *Tritrichomonas foetus* in a survey of beef bulls in the state of Florida and to perform an epidemiological investigation of risk factors for the disease. Bulls were tested for *T. foetus* colonization by a single preputial scraping and culture. Bull infection prevalence within herds was calculated and relationships with bull, herd factors, and production measurements were determined. The survey included 1984 beef bulls in 59 herds throughout Florida; nine bulls in three small herds (<100 cows) were later excluded from the models. An overall prevalence for *T. foetus*-infected bulls was 6.0% (within-herd prevalence ranged from 0 to 27%). The herd prevalence was 30.4% (i.e. at least one infected bull); infected bulls were found in 11.1 and 39.5% of herds sampled in North and South Florida, respectively. The likelihood of disease was greatest in larger herds in more extensive management settings (≥500 cows, 53.9% prevalence; medium-sized herds of 100–499 cows, 10.0% prevalence). *Tritrichomonas foetus* infection was associated with several bull factors, including age, breed, herd, and herd management practices (bull-to-cow ratio, bulls per breeding group). *Tritrichomonas foetus* infection continues to be prevalent in beef herds in Florida that use natural service.
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Keywords: Trichomonosis; Venereal disease; *T. foetus*; Infertility

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1. Introduction

Tritrichomonas foetus is responsible for substantial reproductive wastage in cattle. Bulls with inapparent infection (colonization) of the prepuce transmit the organism venereally [1]. Susceptible, infected cows may manifest disease by embryonic and early fetal death, abortion, pyometra, fetal maceration, or infertility [2–5]. On rare occasions, infected cows may carry infections into the next breeding season [6]. Economic losses from trichomonosis in beef cattle are associated with culling and replacement of infected cattle, and the loss of calf crop caused by failure or delay in conception [2]. The impact of these losses can be substantial. Wilson et al. [7] projected an annual calf loss attributable to *T. foetus* in replacement heifers in Oklahoma of $2.5 million in 1979 (∼$7.3 million, 2003). In 1958, Fitzgerald, et al. [8] estimated that each infected bull in a large herd was responsible for a loss of $800 per year at that time (∼$3900, 2003). A simulation model estimated a reduction of 14–50% in annual calf crop if prevalence of *T. foetus* in the bull population was 20 and 40%; net return per cow exposed to an infected bull was reduced to 5–35% [9].

A survey reported in 1979 indicated that the prevalence of *T. foetus* in beef bulls in Florida was 7.3% [10]. In a field investigation [11], *T. foetus* was found in beef bulls of a large Florida herd; the ranch-wide prevalence was 11.9%. The prevalence of infection in the 13 separate herds (bull populations) was between 0 and 35.9%. To address the statewide prevalence of the disease, a survey of Florida beef cattle herds was conducted with the following objectives: to estimate the prevalence of herd and individual beef bull infection with *T. foetus* in a sample population within the state; to perform a descriptive and analytical epidemiological investigation of risk factors for the disease; and to assess outcomes of the disease in affected herds.

2. Materials and methods

2.1. Sampling

Estimates indicated that there were approximately 70,000 beef bulls in 13,600 herds of varying sizes in the State of Florida in 1997 (Table 1) [12]. A decision was made to survey herds with at least 50 breeding-age females or a population of approximately 3170 herds.

Table 1
The beef cow inventory for the state of Florida by herd size[a]

Herd size (head)	Herds			Proportion of total (%)
	No.	Percent	No. of cows	
1–49	10,430	76.7	152,690	15.2
50–99	1448	10.6	95,418	9.5
100–499	1389	10.2	277,597	27.7
≥500	333	2.5	477,367	47.6
Total	13,600	100.0	1003,072	100.0

[a] Florida Agricultural Statistics Service [12].

From these herds, a stratified random sampling based on herd size was used (Win-episcope 1.0, Wageningen, Netherlands) [13]. To estimate the herd prevalence in Florida beef cattle, a pre-survey estimate of trichomonosis prevalence ($10 \pm 6\%$) was selected to calculate the sample size required (86 herds) to detect the true prevalence. To obtain sufficient participants to meet sample size criteria, 1000 of 3170 producers were randomly selected to receive an informational letter and questionnaire (those having herd size 50–99, 194; herd size 100–499, 585; and herd size ≥ 500, 221), including a request for contact information of those willing to participate in the sampling survey. Those who returned questionnaires with contact information (122: herd size 50–99, 24; herd size 100–499, 65; and herd size ≥ 500, 33) were contacted by telephone to set an appointment to take preputial samples of herd bulls. All respondents were given multiple opportunities (where necessary) to participate.

The sample size estimate of individual bull prevalence was calculated assuming a 10% estimated prevalence, a 1.5% absolute error, and a confidence level of 95%. Thus, 1537 bulls were needed for estimation of individual bull prevalence [13].

2.2. Herd and bull data collection

At the time of sample collection, the owner (or agent) was interviewed using a standardized questionnaire. Data collected for each herd are listed in Table 2. Herd

Table 2
Data collected by questionnaire for each herd participating in the *Tritrichomonas foetus* survey

Herd number	Knowledge level of trichomonosis
Sample identification number	Slightly familiar
Number sampled in the herd	Moderate knowledge
Herd size category	Much Knowledge
Herd size = 50–99 breeding-age females	Month of commencement of breeding season
Herd size = 100–499 breeding-age females	Length of breeding season (days)
Herd size = ≥500 breeding-age females	Ratio of bulls-to-cows, i.e. 1:25
Bull age (years)	Average number of bulls per herd of breeding females
Bull breed	Number of calves weaned
T. foetus culture status (for each individual bull)	Number of females exposed to bulls to produce these
Number of *T. foetus* culture positive bulls in herd	Weaning rate (calves weaned/females exposed)
Herd status for trichomonosis (positive, negative)	Average weaning weight of male calves
Geographical area	Average weaning weight of heifer calves
North Florida	Average weaning weight for all calves
South Florida	Average number of bulls purchased annually
Vaccination status of herd females for *T. foetus*	Total number of bulls in the herd
None, yes	Age at purchase
Administered one time per year	Primary purchase source
No, yes	Raised on ranch
Administered as per label recommendation	General Livestock Auction Market
No, yes	Multiple breed sale
Number of years of annual vaccination	Single breed sale
Month of vaccination (January, etc.)	Private treaty (purchased from individual breeder)
Knowledge of trichomonosis prior to survey	Secondary purchase source
None	Tertiary purchase source
Some knowledge	Previous diagnosis of trichomonosis in herd females

owners were encouraged to have all bulls on the premises sampled, to allow for a more precise estimate of within-herd prevalence. When this was not possible, a subset of at least 20% of bulls was sampled, representing the herd's mature bull population. Ideally, the subset was a random sample, but practically, it was a convenience sample. Bulls were included in the study if they were of breeding age (≥2 years) and were excluded if they had traumatic lesions to the penis or prepuce that could interfere with culture, or if the bulls were from a herd in which a diagnosis of trichomonosis had previously been made.

2.3. Sample collection and evaluation

A modified Diamond's medium was prepared from raw materials every 2 weeks and used for the isolation and cultivation of *T. foetus* [14–16]. Each bull was restrained and a sample taken from the prepuce by vigorous scraping with a clean infusion pipette, and aspiration of smegma from the prepuce near the fornix with a clean syringe attached to the pipette. Scraping technique was deemed adequate if the specimen was mildly blood-tinged and the pipette contained smegma in approximately one-third of its length. A clean examination glove for the hand manipulating the prepuce was used for each bull. Immediately after collection, the specimen was layered on the top of the modified Diamond's medium, kept in an incubator and maintained at 37 °C. Sample evaluation was performed at 24, 48, and 120 h after sample collection. A 0.1-ml sample drawn from the bottom of each tube was placed on a microscope slide and evaluated for trichomonads at $100\times$ magnification using a bright-field microscope. Suspect organisms were then evaluated at $400\times$ to avoid misdiagnosis of non-*T. foetus* trichomonads. The diagnostic characteristics of *T. foetus* included: a protozoal organism $20\,\mu m \times 10\,\mu m$ in size, the presence of three anterior flagella, one trailing posterior flagellum, and a distinct undulating membrane [17].

2.4. Statistical evaluation

Data were evaluated using the statistical software Stata 6.0 (StataCorp, College Station, TX). Independent variables were evaluated individually using two-way tabulation with test for independence (Pearson's chi square test or likelihood ratio). Due to the dichotomous nature of the primary dependent variable, *T. foetus* culture state, the independent variables of interest were made dichotomous and evaluated by multivariable logistic regression [18]. Continuous variables were dichotomized by categorization based on variable medians. Due to the state's large land mass and considerable variability in management styles and types of cattle herds, especially between North and South Florida, herd location was made dichotomous and evaluated as two geographical regions. Herd and individual bull prevalence data was evaluated by a pairwise correlation of all variables to determine which were associated with risk of herd (or individual) infection of *T. foetus*. Each of the herd (or individual) level variables were then evaluated by a univariate analysis to determine the unadjusted odds ratio (OR) and the associated confidence level for each. The logistic regression models were then developed by a forward step-wise selection procedure. SVYLOGIT, a Stata 6.0 logistic regression routine designed for survey data, was used to analyze and evaluate these models. The importance of herd effect on individual

bull prevalence was recognized and specified as the primary sampling unit in that statistical model. Variable interactions were tested. The models selected were evaluated for goodness of fit (Hosmer–Lemeshow Statistic) [18].

3. Results

3.1. Description of the survey population

The survey was performed over a period of 24 months (November 1997 to October 1999). A total of 1984 preputial samples were obtained from bulls in 59 herds located in 27 counties. Response from small herd size owners was low; samples from only three herds of herd size 50–99 head were obtained (9 of 9 herd bulls). Samples were obtained in 30 herds of herd size 100–499 (358 of 413 herd bulls) and 26 herds of herd size ≥500 (1617 of 1964 herd bulls). Each of these two latter herd size categories provided a representative sample size for the respective category (Table 3). The number of bulls tested per herd ranged from 2 to 212 (herd size 50–99, 2–4 head; herd size 100–499, 6–27 head; and herd size ≥500, 15–212 head). The 1984 bulls cultured for *T. foetus* represented 81.8% of all bulls in the surveyed herds (2425), and approximately 2.8% of the population of bulls in Florida in 1997 (Tables 1 and 3). Of those herds not presenting all bulls for test, only six herds presented fewer than half of their bulls (herd size 100–499, 2 of 30 herds; and herd size ≥500, 4 of 26 herds).

The bulls in the survey were from ranches with an inventory of breeding-age females representing 55,211 animals (55 to 6000 animals), a mean of 936 animals or approximately 7.5% of the population of cattle in beef herds having greater than 50 head of breeding females [12]. The exposed females weaned 42,179 calves with a mean of 715 calves per herd (range, 44–4680 calves). The calculated weaning rate (number of calves weaned/ number of females exposed) was 76.8% (74.3–79.3%, 95% CI, range 50–93.1%). The mean calf weaning weight for survey herds was 222 kg (215–229 kg, 95% CI). Weaning weight expressed as kilograms of calf weaned per female exposed to a bull was 172 kg (162–179 kg, 95% CI, range 115–179 kg). Survey respondents purchased 372 bulls (6.3 bulls per herd) in the breeding season prior to the survey. Over fifty percent (52.5%) of survey herds reported purchasing all bulls in their herd from a single seed stock source; these seed stock sources were diverse, coming from within and out of the state. Ten of the 59 herds (16.9%) used a vaccine that included antigens for *T. foetus*. Only 2 of 10 herds

Table 3
The number of herds (and bulls) sampled for *Tritrichomonas foetus* by geographical area and herd size

| | Herd size (head) | | | |
	50–99	100–499	≥500	Total
North Florida	3 (9)	13 (166)	5 (225)	21 (400)
South Florida	0 (0)	17 (192)	21 (1392)	38 (1584)
Total	3 (9)	30 (358)	26 (1617)	59 (1984)

used the vaccine as recommended by the manufacturer, i.e. two injections in the initial immunization year, 2–4 weeks apart, with the second injection given <30 days before the beginning of the breeding season. Generally, only a single injection immunization schedule was used. Of survey herds, three indicated that a diagnosis of trichomonosis had been made through submission of aborted specimens to a diagnostic lab, but no prior testing of bulls had been performed.

Of the 1984 bulls cultured for *T. foetus*, 119 bulls (6.0%) were culture positive. These 119 bulls were from 17 of the 59 surveyed herds. This represented an unstratified herd prevalence of 28.8% (16.9–40.7%, 95% CI). Due to the inadequate sampling of herds with 50–99 head, this category was not included in the analysis by herd size (three herds and nine bulls). Subsequent analysis included 1975 bulls (119 culture positive) and 56 herds. Thus, the survey estimated an unstratified herd prevalence for trichomonosis in Florida beef cattle herds with 100 and greater breeding-age females to be 30.4% (18–43%, 95% CI). Two of 18 herds were positive in North Florida (11.1% prevalence; 0–27.0%, 95% CI; Table 4) and 15 of 38 (39.5% prevalence; 23.0–55.8%, 95% CI) were positive in South Florida.

The age of the bulls in the surveyed herds ranged from 2 to 15 years. The mean age was 5.0 years (4.9–5.1 years, 95% CI); 92.5% of bulls were 2–8 years of age. There were 22 different breeds represented in the survey including *Bos taurus*, *Bos indicus*, and their crosses. Ninety-one percent of the bulls were of seven breeds: Angus, Hereford, Brangus, Charolais, Beefmaster, Braford, and Brahman (Table 5).

Herd size of 100–499 head had a herd prevalence of 10% (3 of 30 herds), while herd size of ≥500 head had a 53.9% herd prevalence (Table 6). The univariate unadjusted OR of a herd size of 500 or greater breeding-age females having at least one culture positive *T. foetus* bull in the herd was 10.5 times more likely than that of a herd of 100–499 breeding-age female herd ($P < 0.001$).

For herds with culture positive bulls, the estimate of within-herd prevalence ranged from 1.8 to 27%, with a mean of 11.9%. Herds with fewer than 500 breeding females (three culture positive herds) had a mean within-herd prevalence of 24.4%; herds with over 500 had a mean within-herd prevalence of 9.2%. The herd prevalence of infected bulls was 17.9 and 11.1% in North and South Florida, respectively.

The surveyed herds used primarily multiple-sire breeding groups (mean, 7.6 bulls per group). The 9% of herds that used single sire breeding groups were all *T. foetus* negative

Table 4
The number of survey herds with culture-positive *Tritrichomonas foetus* bulls by geographical area

Herd status[a]	Geographical area		
	North Florida	South Florida	Total
Negative	16	23	39
Positive	2	15	17
Total	18	38	56
Prevalence (%)	11.1	39.5	30.4

[a] Herd status: negative status, no bulls with *T. foetus* positive cultures; positive status, one or more bulls with *T. foetus* positive cultures.

Table 5
The breed representation in the survey population of Florida beef bulls and prevalence of *Tritrichomonas foetus* by breed among that population

Breed	No. of bulls	No. of herds	Population (%)	No. of positive culture	Prevalence (%)
Angus	454	14	23.0	56	12.3
Brangus	247	10	12.5	7	2.8
Braford	155	3	7.8	5	3.2
Beefmaster	166	4	8.4	5	3.0
Brahman	135	8	6.8	3	2.2
Charolais	235	9	11.9	16	6.8
Hereford	414	14	21.0	18	4.3
Limousin	42	3	2.1	1	2.7
Simmental	37	4	1.9	7	18.9
Other	90	17	4.6	1	1.1
Total	1975			119	6.0

herds. The 91% of herds that used more than one bull per breeding group (range 3–31, mean 8.6 per group) had a mean within-herd prevalence of 11.9%. Of herds with multiple-sire breeding groups, the mean number of bulls per group in *T. foetus* negative herds was 7.7 bulls per group, whereas that of *T. foetus* positive herds was 10.3 bulls per unit. The surveyed herds purchased 0–30 bulls annually (mean of 6.3 bulls per year). *Tritrichomonas foetus* culture negative herds purchased a mean 4.0 bulls per year, while *T. foetus* positive herds purchased an average 11.9 bulls per year. Of the 10 herds that had a history of at least one vaccination, 5 herds were positive for *T. foetus*. The mean within-herd prevalence of the 12 culture-positive, but unvaccinated herds was 13%, whereas, the mean within-herd prevalence of the five culture-positive, vaccinated herds was 8% ($P > 0.10$).

3.2. Logistic regression of the herd prevalence data

In the herd level logistic regression model (Table 7), herd size ($\geq$500 breeding-age females) and bull-to-cow ratio (less than 24 breeding-age females to one bull) were

Table 6
The number of survey herds with culture-positive *Tritrichomonas foetus* bulls by herd size

Herd status[a]	Herd size (head)		
	100–499	$\geq$500	Total
Negative	27	12	39
Positive	3	14	17
Total	30	26	56
Prevalence (%)	10.0	53.9	30.4

[a] Herd status: negative status, no bulls with *T. foetus* positive cultures; positive status, one or more bulls with *T. foetus* positive cultures.

Table 7
The multivariable logistic regression model of herd prevalence of trichomonosis in Florida beef bulls

Herd status	Odds ratio	95% CI[a]		P-value
Herd size <500	1.0			
Herd size ≥500	12.8	2.4	68.3	0.004
Bull-to-cow ratio = 1:>25	1.0			
Bull-to-cow ratio = 1:25	3.5	0.3	37.8	0.302
Bull-to-cow ratio = 1:<25	12.8	1.1	144.5	0.039

Hosmer–Lemeshow $\chi^2 = 1.42$ ($P = 0.84$).
[a] 95% CI is 95% confidence interval of the odds ratio.

significant risk factors for trichomonosis in Florida beef herds. Large herds or a greater bull-to-cow ratio, each resulted in a 12.8 times greater likelihood of a bull within the herd being culture positive for *T. foetus* ($P = 0.004$ and 0.04, respectively).

3.3. Individual bull prevalence

The survey's unstratified individual bull prevalence was 6.0% (4.9–7.0%, 95% CI). Evaluation of prevalence by geographical area indicated that South Florida had a higher bull prevalence than North Florida ($P = 0.006$; Table 8). Bull age was also a risk factor ($P < 0.0001$). Bulls that cultured negative for *T. foetus* had a mean age of 5.0 years (range 2–15 years), whereas culture-positive bulls had a mean age of 5.8 years (range 2–12 years). Breed of bull appeared to be associated with *T. foetus* culture status (Table 4) and was evaluated.

3.4. Multivariable logistic regression models for individual bull prevalence

Bos taurus bulls were six times more likely to culture positive than *Bos indicus* bulls. Within *B. taurus* bulls, Simmental (OR = 13.4, 3.6–49.5, 95% CI), Charolais (OR = 13.6, 3.9–40.5, 95% CI), and Angus bulls (OR = 12.7, 3.0–54.1, 95% CI) were more likely to culture positive for *T. foetus* than *Bos indicus* bulls (Table 9). Other breeds were not statistically significant in the model. Where >10 bulls per breeding group were used, there was an associated increase in likelihood of an individual bull having a *T. foetus* culture-positive status. As the bull-to-cow ratio increased (lower cow numbers per bull, i.e.

Table 8
Tritrichomonas foetus culture status of individual bulls by geographical areas

No. of bulls	Geographical area		
	North Florida	South Florida	Total
Negative	348	1477	1865
Positive	12	107	119
Total	391	1584	1975
Prevalence (%)	3.1	6.8	6.0

Table 9
The odds ratios, P values, and confidence intervals as determined by a multivariable logistic regression for the model of individual bull prevalence of trichomonosis in Florida beef cattle

	Odds ratio	95% CI		P-value
Breed[a]				
Angus	12.7	3.0	54.1	0.001
Brangus	2.2	0.4	11.1	0.334
Braford	2.7	0.4	19.4	0.331
Beefmaster	3.0	0.7	13.3	0.145
Charolais	13.6	3.9	40.5	0.000
Hereford	2.8	1.1	7.1	0.031
Limousin	3.1	0.3	33.2	0.348
Simmental	13.4	3.6	49.5	0.000
Bulls/group[b]	3.9	1.7	8.9	0.002
Age[c]	2.2	1.1	4.3	0.022
Bull:cow ratio[d]	2.2	1.1	4.3	0.030
Knowledge of T. foetus[e]	0.3	0.2	0.7	0.003
Geographical area[f]	4.4	1.9	10.3	0.001

[a] Bull breed (note: the reference (ref.) group for bull breed is *Bos indicus* bulls).
[b] Bulls per breeding group (<10 (ref.) or ≥10 bulls).
[c] Bull age (2–5 years of age (ref.), ≥5 years).
[d] Bull-to-cow ratio (<1:25 or ≥1:25 (ref.)).
[e] Yes or no (ref.).
[f] North (ref.) or South Florida.

1 to 15–24), the risk (OR = 2.1) for an individual bull to be culture positive for trichomonas increased. Bulls >5 years were 2.2 times more likely to have trichomonosis when compared to bulls ≤5 years, where all other factors were held constant ($P < 0.02$). An evaluation of age by culture status, sorted by geographical area (Table 10), indicated that the mean bull age was younger in South Florida where the prevalence of trichomonosis was significantly higher. A bull in South Florida was four times more likely to be culture positive than a bull from North Florida. Herd size was not statistically significant in the individual bull prevalence model. Herd owner knowledge of trichomonosis was associated with *T. foetus* culture status of a bull within the herd; herd owners/agents without a knowledge of the disease were about 3.3 times more likely to have a bull with trichomonosis, all other factors being constant.

There was no effect ($P < 0.87$) of herd infection status for trichomonosis on data collected for herd pregnancy percentages and weaning weights. Weights could not be

Table 10
Tritrichomonas foetus culture status by mean bull age and geographical area

Area	Culture status	Observations	Age (years)	P-value
North Florida	Negative	379	5.4	
	Positive	12	7.7	0.00
South Florida	Negative	1477	4.9	
	Positive	107	5.6	0.00

adjusted to day of age at weaning since age at weaning was not available in most herds. Only a few herds had production data summarized (4 of 56 herds); all were *T. foetus* negative. Weaning percentage (number of calves weaned per exposed females) analysis, as reported by producers, indicated that there were no differences by herd status ($P < 0.27$).

4. Discussion

The prevalence of *T. foetus* in this report (30.4% herd prevalence and a 6.0% individual bull prevalence) was similar to the prevalence for a large cow-calf enterprise in Florida reported previously [11], where the segregated herd prevalence in 13 units on a single ranch ranged from 0 to 35.9%, and the ranch-wide individual bull prevalence was 11.9%. These results were also within the range reported in bull populations of other studies in other areas (range, <1–38.5%). Three such reports describe bulls tested in livestock markets or abattoirs; prevalence in these populations was between 0.2 and 7.8% [7,10,19]. Abbitt and Meyerholz [10] reported a 7.3% prevalence (8 of 109 cull Florida beef bulls were culture positive for *T. foetus*). A comparison of the prevalence proportions between the 1979 survey and the current survey suggested that there was no apparent change in the prevalence of trichomonosis from 1979 to 1998 in the state of Florida. The 1979 survey, however, did not report herd of origin and thus limits direct comparisons. Two studies reported herd investigations involving compromised reproductive performance in cows bred by infected bulls. Skirrow et al. [20] reported a 38.5% prevalence of *T. foetus* infection in 195 beef bulls in California. Kimsey et al. [21] reported a prevalence of 5.8% in 328 bulls. In a survey of 729 bulls in 57 herds in California, the prevalence of infection in sampled bulls was 4.1% [22]; of herds surveyed, 15.4% had at least one infected bull and a within-herd prevalence that ranged from 4.0 to 38.5%. These studies validate the need for epidemiological investigations to identify risk factors associated with disease and improve prevention and control. A principal strength of the current survey was the scope of the study. Sampling herds throughout the state gave a broad representation of risk factors and the large number of observations improved the likelihood that the sample population truly represented the target population.

Evaluation of herd prevalence indicated that there were substantial levels of trichomonosis in Florida beef cattle herds. The results suggest that herds with 500 or more breeding-age females are at significantly greater risk of having trichomonosis. The herd size and cattle density in South Florida makes *T. foetus* more of a threat to the South Florida beef industry than those in the northern part of the state.

Bulls per breeding unit and the bull-to-cow ratio are management factors that could affect exposure to *T. foetus*. Where owners used more than 10 bulls per unit, the likelihood that an individual bull would have a culture-positive *T. foetus* status increased. As the ratio of bull-to-cows increased (lower cow numbers per bull), the odds for an individual bull to be culture positive increased. These practices were apparently used by producers to increase conception rates in large herds where cow density per acre was low and acreage was large. These practices seem to lend themselves to increasing the within-herd prevalence of the disease. It is assumed that each of these practices increased the number

of potential sexual contacts and thereby increased the probability that an individual bull might be or become positive.

Evaluation of herd production data was limited by the accuracy of information supplied by the producer. Weaning percentages and weaning weights for participating herds did not demonstrate a significant difference by trichomonosis herd status. Unfortunately, weights could not be adjusted to day of age at weaning, which would have better reflected differences. Only a few herds (4 of 56) had production data summarized, and all were *T. foetus* negative. The long breeding season commonly used in Florida may permit compensatory increases in weaning rate, and thus losses associated with *T. foetus* may be difficult to recognize. In the Florida case report [11], an age-adjusted mean weaning weight of calves provided a time referenced value across breeding units that showed a significant association between the mean adjusted weaning weight per bull exposed cow and the breeding unit prevalence of bull infection. Clark et al. [2] reported herd calving percentages of 30% for heifers infected with *T. foetus* during their first bull exposure, and prolonged calving intervals that were significantly different from those of non-infected heifers. Overall, calf production was reduced by 18%. Skirrow et al. [20] recorded an increase in pregnancy percentage from 74 to 85% following elimination of the disease in an affected herd.

The evaluation of vaccination effect on herd status and within-herd prevalence was hampered by the low numbers of surveyed herds with a history of vaccination against *T. foetus*. Only 10 of the 56 herds had used any vaccination protocol against this agent. Of these, only two administered the vaccine as per manufacturer's recommendations.

The survey model reaffirms bull age as a significant risk factor for infection within the bull population. Bulls ≥5 years were twice as likely to culture positive. In the Florida case report [11], the mean age of all bulls was 4.1 years and the mean age of *T. foetus* infected bulls was 5.5 years ($P < 0.05$). These findings agree with other reports of a predilection for colonization in older bulls (i.e. >4 years of age; [2,22,23]). It has been theorized that older bulls have deeper and more numerous crypts on the mucosal surface of the prepuce than younger bulls and this provides a protective, more conducive environment for development of the permanent carrier state (that also increases the probability of transfer of the organism) [1,5]. Alternately, older bulls may be more active, assertive breeders. Use of young bulls in *T. foetus*-infected herds has been a management tool used to control losses associated with the disease. Older bulls are more likely to become infected and remain so, but infection is clearly possible in younger bulls [20], perhaps associated with the increased herd prevalence of disease. This was evident as age of infected bulls was compared in this study between North and South Florida. Although age was a significant risk factor for infection, it was very likely also influenced by the prevalence of disease in the population.

Bos taurus bulls were six times more likely to culture positive than *Bos indicus* bulls. Within the *Bos taurus* group, several breeds were more likely be culture positive for *T. foetus*, namely, Simmental, Charolais, and Angus. Several studies have examined breed predilections, but a clear association has not been reported [10,22]. BonDurant et al. [22] showed a greater prevalence among *Bos taurus* breeds than *Bos indicus* or crossbred bulls, but could not attribute biological significance to the finding because of a lack of equal distribution of breeds across all herds. Similarly, in the present study, there was not an equal distribution of breeds across breeding units/herds, and additionally, information

regarding source of bulls was not available to clarify the reason for the breed differences observed. Breed-related anatomical differences could contribute to a greater prevalence of infection in specific breeds. As described for the age association, one breed or breed-type may develop a preputial environment more conducive to establishment and maintenance of colonization than another. Another explanation might relate to differences in libido or other sexual behaviors, i.e. repeated, multi-sire breedings within a breed or breed-type of bulls. Further investigations are warranted to delineate breed association with *T. foetus* infection.

Owner familiarity with trichomonosis seemed to be associated with a reduced risk of disease in the individual bull; owners/agents in our survey that reported a knowledge of the disease were about 70% less likely to have culture-positive bulls. In the survey results, the unadjusted probability of an individual bull being culture positive in North Florida decreased from 6.9 to 3.7% when owners had knowledge of the disease. In South Florida, where the disease was more prevalent, the predicted probability of individual bulls being *T. foetus* positive where owners had no knowledge of trichomonosis was 19.9%, in contrast to 5.4% where they had knowledge of the disease. It appeared that owner knowledge of the disease had a protective effect and that education concerning this disease would most likely aid in its control.

The primary limitation of this study was the inability to obtain a true random sample. Surveys use convenience sampling because they depend on an acceptance or willingness to participate that is often out of the control of the investigator. An effort was made by personal contact to encourage the prompt return of the questionnaire and a commitment to present bulls for sampling. Multiple dates and opportunities were provided. There was also a potential for geographical bias. The inherent regional differences within the State of Florida may have influenced the level of knowledge of disease and owners perception of the disease's importance. The direction of the bias was likely to overestimate the overall herd prevalence, since those with some familiarity with, or concern for, the disease were more likely to participate. Another important limitation was an apparent lack of accuracy relative to herd production data. Many producers did not have production records and were unable to accurately estimate production parameters, particularly weaning numbers, exposed females, pregnancy percentages, and weaning weights. It is suspected that this would impose a bias to lessen the expected differences in weaning rates and weaning weights of trichomonosis-infected herds compared to those without the disease. As a result, no clear outcome effect was evident from the survey data concerning production data and *T. foetus*. The study was also limited by a single preputial sample. Since the sensitivity of the diagnostic method is estimated to be 81–90%, it is anticipated that the true prevalence could be slightly higher than that reported.

In conclusion, the prevalence of *T. foetus* in this report (30.4% herd prevalence and a 6.0% individual bull prevalence) was similar to the prevalence previously reported in Florida. Infected bulls were found in 11.1 and 39.5% of herds sampled in North and South Florida, respectively. The likelihood of disease was greatest in larger herds under more extensive management settings (≥ 500 cows, 53.9% prevalence, in contrast to medium-sized herds from 100 to 499 cows with a 10.0% prevalence). *Tritrichomonas foetus* infection was associated with several bull factors, including age, breed, herd, and herd management practices, such as bull-to-cow ratio and bulls per breeding group. *Tritrichomonas foetus*

infection continues to be prevalent in beef herds in Florida that use natural service and a reproductive disease of concern.

Acknowledgements

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