Effect of Johne's disease on milk production and estimation of genetic parameters for incidence of Johne's disease in New Zealand dairy cattle

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Executive Summary

Lactation performance of cows affected by Johne's disease (JD) was investigated in 122,914 cows distributed in 310 dairy herds of New Zealand.

- Information on prevalence within region was determined. Taranaki showed the highest (1.01%). Prevalence on a herd basis ranged from 0 to 9.35%.
- Correlations between performance traits and JD were all negative, indicating the adverse effect of JD on production.
- For the 2009/10 season, the effect of breed and lactation number on JD positive test results were all significant
- Jersey cows had the highest proportion of positive tests (1.77%), compared to HF (0.57%) and crossbred cows (0.83%).
- The highest proportion of positive tests were between lactations 3-6.
- For the 2009/10 season, milk, fat and protein yields were significantly lower in JD test positive cows. On average, JD positive cows produced 533 kg less milk (14.1%), 26.3 kg less fat (14.2%), 20.8 kg less protein (14.5%) and had 10 days less in milk (4.6%) than JD negative cows. As a result of this, JD positive cows produced 47.1 kg less milksolids in 220 day lactation, which represents 14.3% of the mean.
- Average lifetime performance was also affected, with JD positive cows producing less, with crossbred cows affected to a greater extent.
- Accumulated yields showed a similar pattern with JD positive cows producing less but Holstein-Friesian cows were affected to a greater extent.
- While Jersey cows had a higher proportion of positive tests, the accumulated yields results showed production was negatively affected to a lesser extent than Holstein-Friesian or crossbred cows.
- The estimate of heritability was much lower using a linear model (0.0142) than a threshold logit model (0.226).
- Estimates of phenotypic correlation show very low to no correlation with milk traits analysed.
- The distribution of sire breeding values by breed range from –1 to +5%. Jersey sires had higher breeding values for prevalence of JD than HF, with crossbred sires intermediate.

Introduction

Johne's disease (JD) is a chronic disease of ruminants caused by the pathogen *Mycobacterium avium* subsp. *paratuberculosis* (MAP) causing an intestinal infection that results in a chronic diarrhoea and ill thrift in adult cattle. The disease is known to affect around 12% of dairy herds but thought to affect upwards of 60% of New Zealand herds. However, most infected herds experience only low levels of clinical disease of less than 2 clinical cases per year (Brett 1998).

Johne's disease is considered to adversely affect farm performance and profitability. Based on international studies, JD infection is associated with reduced milk production (Richardson and More 2009; Ott et al. 1999; Smith et al. 2009), increased involuntary culling rates (Ott et al. 1999) and increased calving interval and infertility (Raizman et al. 2007). Buergelt and Duncan (1978) observed an 8% and 16% decrease in milk production in cattle with sub-clinical and clinical JD, respectively. Richardson and More (2009) reported that cows with clinical JD, compared with a control group, showed significantly lower milk yield of 1259.3 kg/lactation representing 20% of the average mean (6000 kg/lactation) in an Irish dairy herd. Ott et al. (1999) reported that in an average US dairy herd, the reduced productivity of milk accounted for US$22 to US$27 per cow, but in high-prevalence herds that reported at least 10% of their cull cows as having clinical signs consistent with JD, the economic losses were over US$ 200 per cow. These high-prevalence herds experienced reduced milk production of over 700 kg per cow per lactation, culled more cows but had lower cull-cow revenues, and had greater cow mortality than Johne's-negative herds.

Smith et al. (2009) reported that cows infected with MAP had monthly decreases of 0.05 to 1 kg in daily milk production relative to uninfected animals, which represent 0.14 to 2.8% of the mean daily yield (35.77 kg) in three commercial dairy herds in the north-eastern of the United States. In a similar study in two Minnesota USA dairy farms, Raizman et al. (2007) reported 84 cows (8% of 1052 cows) with faecal samples that were positive for MAP (46% light, 26% moderate, and 28% heavy shedders). In multivariable analysis, light, moderate, and heavy faecal shedding cows produced on average 537, 1403, and 1534 kg less milk per lactation respectively, representing 5.53, 14.46 and 15.81% of the mean, than faecal negative cows.

Several studies (McNab et al. 1991; Chaffer et al. 2003) have found no significant relationship between JD status and milk production. Few studies have been conducted in New Zealand to estimate the effect of JD on lactational performance. Norton (2007) reported that the prevalence of JD determined by enzyme-linked immunosorbent assay (ELISA) test and faecal culture ranged from 4.5% (95% CI 2.6-6.9) to 14.2% (95% CI 9.2-20.6). Daily milksolids production by JD positive cows was 0.8% less than that of JD negative cows. However in herd D, JD positive cows produced 15.5% milksolids less than JD negative cows daily. This equates to a loss of 53kg of milksolids per 305-day lactation.

Genetic analysis of resistance to JD indicates that estimates of heritability seem to be similar to that for resistance to other diseases, averaging around 0.10. Koets et al. (2000) reported heritabilities for JD of 0.06 for nonvaccinated animals and 0.09 for vaccinated animals in Dutch cows. Gonda et al. (2006) estimated heritabilities using a serum ELISA test of 0.16 (using a linear model) and 0.09 (using a threshold model) in US Holstein cows. In a similar study, Attalla et al. (2010) reported heritabilities using milk ELISA scores of 0.080 (using a

linear model) and 0.0645 (using a threshold model) in US Holstein cows. Hinger et al. (2008) reported a heritability of 0.10 using serum ELISA tests of German Holstein cows. Mortensen et al. (2004) estimated heritability of 0.10 using milk ELISA tests in Danish Holstein cows. The authors of the present study are not aware of estimates of heritabilities for resistance of JD in New Zealand dairy cattle.

The objectives of this study were firstly, to quantify the effects of JD diagnosed by ELISA on milk production, and secondly, to estimate genetic parameters for prevalence of JD in New Zealand dairy cattle.

Material and methods

ELISA test to diagnose Johne's disease

Herds to be tested were identified using a bulk milk test and a commercially available kit assay. The USDA-approved IDEXX MAP Ab Test, based on Institut Pourquier technology, is an enzyme-linked immunosorbent assay (ELISA) for the detection of MAP-specific antibodies in bovine milk, serum or plasma (www.idexx.com).

Routine herd test samples from individual cows within these herds were then used to identify cows for blood testing using the following procedure. Firstly, individual cow samples were bulked into pool samples containing 10 individual cow samples. These pool samples were then tested with the ELISA test, with samples greater that the selected cut-off indicating test reactors within the pool. The individual samples within the positive pools were then individually tested to identify positive test cows which were then confirmed by blood sample. Therefore, cows identified as test positive in this study had 2 positive tests. However, not all cows that were identified as being JD positive by the milk test were subsequently blood tested. In addition, using this pooling system means not all cows in the herds selected were individually tested.

Data

Two data sets were provided by Livestock Improvement Corporation (LIC). The first data set contained 122,914 lactation yields of milk, fat and protein, and days in milk (DIM) from 122,914 cows from different 310 multi-breed herds that produced milk during the 2009/10 production season. Each cow had one lactation record and calving date and lactation number was available as well pedigree and breed composition of the cow, sire and dam. Cows with a breed composition of more than 87.5% Holstein-Friesian (HF), Jersey (JE) and other breeds (OT) were described as pure breed. The rest were described as crossbred (XB) cows. The expected breed heterozygosities for each cow was calculated using the following formulae

$$h_{HFxJE} = \alpha^s_{HF} \alpha^d_{JE} + \alpha^s_{JE} \alpha^d_{HF}$$
$$h_{HFxOT} = \alpha^s_{HF} \alpha^d_{OT} + \alpha^s_{OT} \alpha^d_{HF}$$
$$h_{JExOT} = \alpha^s_{JE} \alpha^d_{OT} + \alpha^s_{OT} \alpha^d_{JE}$$

where h_{HFxJE}, h_{HFxOT} and h_{JExOT} are the expected breed heterozygosity between fractions of HF, JE and OT in the cow, α^s_{HF}, α^s_{JE} and α^s_{OT} are the proportions of HF, JE and OT in the sire, and α^d_{HF}, α^d_{JE} and α^d_{OT} are the proportion of HF, JE and OT in the dam.

The second data set contained all historical lactation yields of milk, fat, protein and lactose, and DIM. Accumulated yields of milk, fat and protein and DIM up to the season 2009/10

were obtained for each cow that was screened for JD in the production season 2009/10. Accumulated yields of lactose were not calculated due to missing yields.

Statistical analysis

This analysis was conducted using data collected from the milk screening performed during the 2009/10 season. All statistical analyses were carried out using SAS (Statistical Analysis System, version 9.3; SAS Institute Inc., Cary, NC, USA). Descriptive statistics and correlations of the traits were obtained using the CORR procedure.

Prevalence of JD (as determined by positive ELISA test) by LIC herd-test region, was analysed after a logit transformation for binomial data using the GLIMMIX procedure with a model that included the fixed effect of region. A cow that tested blood ELISE positive was coded "1" and cows that tested negative were coded "0".

Effects of herd, breed and lactation number on prevalence of JD were estimated with the GLIMMIX procedure with a logit model that included the fixed effects of herd, breed, lactation number, interaction between breed and lactation number and deviation from median calving data included as covariable. Cows with lactation number equal or more than 10 were grouped as lactation number 10.

Lactation yields of milk, fat, protein and lactose, and DIM of the cows that were screened for JD during the 2009/10 season were analysed using the MIXED procedure with a linear model that included the fixed effects of herd, JD status (negative vs positive), lactation number, breed, interaction between JD status and lactation number, interaction between JD status and breed and deviation from median calving data included as covariable. Least squares means and their standard errors were obtained and used for multiple comparisons between JD statuses within lactation number.

Accumulated yields of milk, fat, protein and lactose, and DIM of cows that were screened for JD during the 2009/10 season were analysed with a linear model that included the fixed effect of JD status (negative vs positive), breed and the interaction between JD status and breed. Least squares means and their standard errors were obtained and used for multiple comparisons between JD statuses within breed.

Variance components required for the estimation of heritability for JD were obtained using the statistical package ASREML (Gilmore et al. 2009) with a mixed linear model that included the fixed effect of herd and the random additive genetic animal effect. Proportion of JE and OT and h_{HFxJE}, h_{HFxOT} and h_{JExOT} were included as covariables. The pedigree file included three generations of recorded ancestors of each cow screened for JD in the 2009/10 season. Heritability was calculated as $[\sigma^2_a/(\sigma^2_a + \sigma^2_e)]$ where σ^2_a and σ^2_e are the additive genetic and residual variances, respectively. Variance components were estimated assuming that prevalence of JD have a normal distribution (no transformation) and assuming that prevalence of JD have a binomial distribution and a logit transformation was performed.

Results

Table 1 shows the number of herds by LIC herd-test region that had cows that tested positive for JD (JD+), and the number of cows within those herds that went through the screening process. There were significant differences for JD+ prevalence between regions, with Taranaki having a significantly higher prevalence of JD+ cows than the other regions. The prevalence per herd ranged from 0 to 9.35%.

Descriptive statistics and correlations between lactation performance milk traits are shown in Table 2. The phenotypic correlations between JD and MY, FY, PY and DIM are all negative, indicating the negative effect of JD on production. While these correlations are low, they still represent the negative effect of JD on the dairy industry.

Breed and lactation number had a significant effect on the prevalence of JD+. Table 3 shows the number of cows that tested positive or negative for JD disease by breed group. Jersey cows had the highest proportion of positive tests, with prevalence in crossbred cows intermediate between the two parent breeds.

The interactions between breed, lactation number and deviation from median herd calving date were not significant. Table 4 shows the number of cows that tested positive or negative for JD disease by lactation number. The proportion of JD+ cows increased from lactation 1 to 6 and then declined.

Table 1. Numbers of herds by LIC herd-test region containing cows that tested positive (JD+) or negative (JD-) for Johne's disease during the screening process during the 2009/10 season, with mean and SE of prevalence of JD+.

LIC herd-test region	Number of herds	Number of cows			Prevalence of JD+	SE
		JD-	JD+	Total		
Northland	12	2,988	23	3,011	0.76[b]	0.14
Auckland	80	24,909	232	25,141	0.92[b]	0.06
BoP[1]	10	3,597	26	3,623	0.72[b]	0.14
Taranaki	64	18,653	342	18,995	1.80[a]	0.09
Wtgn[2]	33	11,058	86	11,144	0.77[b]	0.07
S. Island[3]	111	60,463	537	61,000	0.88[b]	0.06
Total	310	121,668	1,246	122,914	1.01	

[a,b] Means with different superscript are significantly different (P<0.001).
[1]Bay of Plenty/East Coast, [2]Wellington/Hawkes Bay, [3]South Island

Table 2. Descriptive statistics and correlations of milk production traits from 122,914 dairy cows that were screened for Johne's disease in 310 dairy herds during the 2009/10 production season in New Zealand.

	N	Mean	SD	Min	Max	MY	FY	PY	LY	DIM	FP	PP	LP	F:P	JD+
						Phenotypic correlations coefficients									
MY	122,914	3,990	1371	165	12715		0.84	0.96	0.84	0.52	-0.41	-0.35	0.16	-0.32	-0.05
FY	122,914	196	60	8	594			0.91	0.72	0.60	0.11	0.04	0.15	0.14	-0.03
PY	122,914	154	49	7	456				0.83	0.57	-0.22	-0.07	0.20	-0.26	-0.04
LY	122,003	177	81	3	647					0.39	-0.33	-0.21	0.64	-0.30	-0.04
DIM	122,914	228	39	61	305						0.10	0.12	0.03	0.05	-0.03
FP	122,914	5.02	0.90	2.00	12.33							0.74	-0.03	0.85	0.03
PP	122,914	3.91	0.38	2.57	6.73								0.09	0.27	0.02
LP	122,003	4.36	1.13	0.11	5.70									-0.11	-0.01
F:P	122,914	1.28	0.16	0.48	2.72										0.03
JD+	122,914	0.01	0.10	0	1										

MY = milk yield, FY = fat yield, PY = protein yield, LY = lactose yield, DIM = days in milk, FP = fat percentage, PP = protein percentage, LP = lactose percentage, F:P = fat to protein ratio, JD+ = a cow testing positive for Johne's disease.

Table 3. Number of cows by breed[1] that tested positive (JD+) or negative (JD-) for Johne's during the 2009/10 production season, and mean (%) and SE of prevalence of JD+.

Breed	JD-	JD+	Total	Prevalence of JD+ (%)	SE
HF	27,332	156	27,488	0.57^a	0.04
JE	31,108	560	31,668	1.77^c	0.07
XB	63,228	530	63,758	0.83^b	0.03
Total	121,668	1,246	122,914	1.01	

[1]HF = Holstein-Friesian, JE = Jersey, XB = crossbred.
^{a,b,c} Means with different superscripts within column are significantly different (P<0.0001).

Table 4. Number of cows by lactation number that tested positive (JD+) or negative (JD-) for Johne's during the 2009/10 production season, and mean (%) and SE of prevalence of JD+.

Lactation	JD-	JD+	Total	Prevalence of JD+ (%)	SE
1	27,112	70	27,182	0.26^a	0.03
2	21,361	189	21,550	0.88^{bc}	0.06
3	20,069	271	20,340	1.33^{de}	0.08
4	14,965	214	15,179	1.41^{de}	0.09
5	12,206	173	12,379	1.40^{de}	0.10
6	9,486	142	9,628	1.48^e	0.12
7	7,171	88	7,259	1.21^{de}	0.13
8	4,306	56	4,362	1.28^{de}	0.17
9	2,393	23	2,416	0.95^{cd}	0.19
10+	2,599	20	2,619	0.76^b	0.17
Total	121,668	1,246	122,914	1.01	

^{a,b,c,d,e} Means with different superscripts within column are significantly different (P<0.05)

Effect of Johne's Disease on milk production per lactation

Table 5 shows the lactation yields of milk, fat, protein and lactose, and DIM by lactation number for the cows that tested positive (JD+) or negative (JD-) for JD during the 2009/10 production season. All yields and DIM were significantly greater in JD- cows on average, with only lactations 2 and 10+ having no significant difference between JD+ and JD-. The effect of JD+ test on milk yield range from decreases of 144 kg (4.9%) to 741 kg (18.5%). This indicates there is an effect on milk yield throughout all age groups in the herd. The greatest production losses are seen in 2nd to 9th lactation cows, which is to be expected as these are most productive age groups (and also corresponds to the greatest numbers of cows tested, Table 4). On average, JD+ cows produced 533 kg less milk (14.1%), 26.3 kg less fat (14.2%), 20.8 kg less protein (14.5%) and had 10 days less in milk (4.6%) than JD- cows.

Table 5. Lactation yields of milk (MY), fat (FY), protein (PY) and lactose (LY) and days in milk (DIM) by lactation number of cows that tested positive (JD+) or negative (JD-) for Johne's disease during the 2009/10 production season. Data were collected from 122,914 dairy cows that were screened for Johne's disease in 310 dairy herds.

Lactation		DIM	SE	Milk	SE	Fat	SE	Protein	SE	Lactose	SE
1	JD-	227.4^a	0.19	2,937	6.7	145.5^a	0.36	110.6^a	0.25	113.5	0.36
	JD+	222.0^b	2.71	2,793	97.6	135.7^b	4.62	103.2^b	3.42	109.2	5.36
2	JD-	229.4^a	0.21	$3,639^a$	7.8	178.7^a	0.38	139.8^a	0.28	142.6^a	0.39
	JD+	219.2^b	1.67	$3,270^b$	60.2	159.0^b	2.85	123.7^b	2.11	127.7^b	3.29
3	JD-	229.2^a	0.21	$4,008^a$	7.2	196.3^a	0.37	153.8^a	0.24	158.8^a	0.40
	JD+	213.9^b	1.42	$3,267^b$	51.2	161.7^b	2.43	125.4^b	1.80	126.4^b	2.80
4	JD-	228.3^a	0.23	$4,121^a$	8.2	201.7^a	0.40	157.1^a	0.28	162.8^a	0.44
	JD+	217.3^b	1.59	$3,554^b$	57.3	174.5^b	2.72	134.4^b	2.01	136.1^b	3.14
5	JD-	227.8^a	0.26	$4,126^a$	9.2	201.0^a	0.45	156.7^a	0.33	162.8^a	0.47
	JD+	215.8^b	1.75	$3,404^b$	63.1	167.7^b	2.99	127.8^b	2.22	130.5^b	3.46
6	JD-	226.7^a	0.27	$4,063^a$	10.0	200.0^a	0.45	153.7^a	0.33	159.6^a	0.51
	JD+	218.2^b	1.93	$3,371^b$	69.3	166.7^b	3.29	126.4^b	2.43	128.7^b	3.78
7	JD-	225.3^a	0.30	$3,958^a$	10.3	194.9^a	0.49	149.3^a	0.38	155.2^a	0.58
	JD+	219.1^b	2.42	$3,346^b$	87.1	162.5^b	4.13	125.5^b	3.06	123.9^b	4.76
8	JD-	223.4^a	0.37	$3,866^a$	13.1	187.6^a	0.63	144.4^a	0.46	150.7^a	0.71
	JD+	214.5^b	3.01	$3,350^b$	108.2	165.6^b	5.13	126.6^b	3.80	123.1^b	5.91
9	JD-	222.1^a	0.48	$3,692^a$	17.2	178.9^a	0.82	138.0^a	0.61	141.7^a	0.94
	JD+	199.8^b	4.67	$3,043^b$	168.1	148.4^b	7.96	114.2^b	5.90	111.6^b	9.18
10+	JD-	220.7	0.46	3,524	16.6	171.4^a	0.79	131.6	0.58	135.7	0.90
	JD+	216.1	5.00	3,201	180.0	151.6^b	8.53	119.7	6.32	126.0	9.83
All	JD-	226.0^a	0.17	$3,793^a$	5.9	185.6^a	0.30	143.5^a	0.21	148.3^a	0.30
	JD+	215.6^b	0.99	$3,260^b$	35.4	159.3^b	1.68	122.7^b	1.24	124.3^b	1.94

[a,b] Means with different superscripts within lactation number are significantly different (P<0.05)

Breed and Johne's disease effects on lifetime performance

Average lifetime lactation yields and the impact of JD are shown in Table 6. Holstein-Friesian (HF) cows were the highest yielding, with crossbred cows intermediate between the two parent breeds. There was a negative effect of JD, with JD positive cows having 5 less DIM (2.4%) and producing 346 kg less milk (9.3%), 15.6 kg less fat (8.5%), 12.3 kg less protein (8.8%) and 18.6 kg less lactose (15%).

In examining the breed x JD status interaction it can be seen that the largest negative impact on production caused by JD was seen in crossbred cows.
- Decreases in DIM in JD positive cows ranged from 4 less days milking (1.7%) in HF cows compared to 5 (2.3%) in Jersey cows and 8 (3.4%) in crossbred cows.
- For milk yield, decreases ranged from 300.6 kg (7.3%) in HF cows compared to 264.8 kg (8.1%) in Jersey cows and 472.5 kg (12.4%) in crossbred cows.
- For fat yield, decreases ranged from 13.3 kg (7.2%) in HF cows compared to 14.9 kg (8.4%) in Jersey cows and 27.5 kg (12.9%) in crossbred cows.
- For protein yield, decreases ranged from 10.3 kg (7%) in HF cows compared to 10.3 kg (8%) in Jersey cows and 16.2 kg (11.3%) in crossbred cows,
- For lactose yield, decreases ranges from 19.3 kg (13.8%) in HF cows compared to 12.4 kg (11.8%) in Jersey cows and 24.2 kg (18.9%) in crossbred cows.

Table 6. Lactation yields of milk (MY), fat (FY), protein (PY) and lactose (LY) and days in milk (DIM) by breed[1] of cows that tested positive (JD+) or negative (JD-) for Johne's disease during the 2009/10 production season. Data were collected from 122,914 dairy cows that were screened for Johne's disease in 310 dairy herds.

Breed		Num of lactations	DIM	SE	MY	SE	FY	SE	PY	SE	LY	SE
HF		112,624	224.4	0.85	3953.3^a	22.3	180.3^a	1.06	142.5^a	0.81	129.8^a	2.61
JE		135,429	222.9	0.56	3156.6^b	14.8	170.0^b	0.71	124.1^c	0.54	98.9^c	2.32
XB		263,068	223.3	0.58	3581.5^c	15.3	180.2^a	0.73	133.7^b	0.55	116.1^b	2.33
	JD-	506,148	226.3^a	0.23	3738.8^a	6.1	184.6^a	0.29	140.2^a	0.22	124.3^a	2.14
	JD+	4,973	220.8^b	0.94	3392.8^b	24.6	169.0^b	1.18	127.9^b	0.89	105.7^b	2.63
HF	JD-	112,036	226.3^a	0.26	4103.6^a	6.8	186.9^a	0.33	147.7^a	0.25	139.5^a	2.15
	JD+	588	222.5^b	1.65	3803.0^b	43.2	173.6^b	2.07	137.4^b	1.57	120.2^b	3.69
JE	JD-	133,117	225.4^a	0.27	3289.0^a	7.0	177.5^a	0.33	129.2^a	0.25	105.2^a	2.15
	JD+	2,312	220.3^b	1.04	3024.2^b	27.3	162.6^b	1.31	118.9^b	0.99	92.8^b	2.79
XB	JD-	260,995	227.1^a	0.24	3823.7^a	6.4	189.4^a	0.31	143.8^a	0.23	128.1^a	2.14
	JD+	2,073	219.4^b	1.09	3351.2^b	28.7	170.9^b	1.38	127.6^b	1.04	103.9^b	2.84

[1]HF = Holstein-Friesian, JE = Jersey, XB = crossbred.
[a,b] Means with different superscripts within breed are significantly different (P<0.05).

Accumulated lactation yields and the impact of JD are shown in Table 7. Holstein-Friesian cows were the highest yielding, with crossbred cows intermediate between the two parent breeds. There was a negative effect of JD, with JD positive cows having 65 less DIM (6.9%) and producing 2106 kg less milk (12.7%), 88 kg less fat (10.8%), 76 kg less protein (11.9%) and 22 kg less lactose (4.5%).

In examining the breed x JD status interaction it can be seen that the largest negative impact on production caused by JD was seen in HF cows.

- Decreases in DIM in JD positive cows ranged from 76 less days milking (8.2%) in HF cows compared to 48 (4.9%) in Jersey cows and 71 (7.6%) in crossbred cows.
- For milk yield, decreases ranged from 2507 kg (13.2%) in HF cows compared to 1357 kg (9.7%) in Jersey cows and 2457 kg (14.5%) in crossbred cows.
- For fat yield, decreases ranged from 102 kg (12.4%) in HF cows compared to 70 kg (8.7%) in Jersey cows and 90 kg (10.9%) in crossbred cows.
- For protein yield, decreases ranged from 89 kg (13.7%) in HF cows compared to 57 kg (9.8%) in Jersey cows and 58 kg (9.3%) in crossbred cows,
- For the number of lactations, decreases ranges from 0.25 (5%) in HF cows compared to 0.17 (3.4%) in Jersey cows and 0.23 (4.8%) in crossbred cows.

Table 7. Accumulated yields of milk (aMY), fat (aFY) and protein (aPY), days in milk (aDIM) and number of lactations (aNL) by breed[1] of cows that tested positive (JD+) or negative (JD-) for Johne's disease during the 2009/10 production season. Data were collected from 122,914 dairy cows that were screened for Johne's disease in 310 dairy herds.

Breed		N	aDIM	SE	aMY	SE	aFY	SE	aPY	SE	aNL	SE
HF		27,488	892^a	18.2	17,723^a	363	769	17.8	637^a	13.7	4.86^a	0.09
JE		31,668	961^b	9.7	13,254^c	193	772	9.5	554^b	7.3	4.91^a	0.05
XB		63,758	897^a	9.9	15,727^b	197	782	9.7	609^a	7.4	4.70^b	0.05
	JD-	121,668	949^a	1.4	16,621^a	28	818^a	1.4	638^a	1.0	4.93^a	0.01
	JD+	1,246	884^b	15.2	14,515^b	302	730^b	14.9	562^b	11.4	4.71^b	0.08
HF	JD-	27,332	930^a	2.7	18,977^a	55	820^a	2.7	681^a	2.1	4.98	0.01
	JD+	156	854^b	36.3	16,470^b	723	718^b	35.6	592^b	27.3	4.73	0.19
JE	JD-	31,108	985^a	2.6	13,933^a	51	807^a	2.5	582^a	1.9	5.00	0.01
	JD+	560	937^b	19.2	12,576^b	382	737^b	18.8	525^b	14.4	4.83	0.10
XB	JD-	63,228	933^a	1.8	16,955^a	36	827^a	1.8	652^a	1.4	4.81^a	0.01
	JD+	530	862^b	19.7	14,498^b	392	737^b	19.3	567^b	14.8	4.58^b	0.10

[1]HF = Holstein-Friesian, JE = Jersey, XB = crossbred.
^{a,b} Means with different superscripts within breed are significantly different (P<0.05).

Estimates of variance components and heritability and breeding values for prevalence of Johne's disease

Estimates of variance components using first lactation records and all lactation records are presented in Table 8. The estimate of heritability for JD using a linear model is much lower than the estimate of heritability using a threshold logit model. Estimations of phenotypic correlation shows very low to no correlation between JD+ and the milk traits as shown in Table 2.

The distribution of sire breeding values by breed (Figure 1) ranged from -1 to +5%. The JE sires had higher breeding values for prevalence of JD than HF, while crossbred (XB) sires had intermediate breeding values for the prevalence of JD.

Table 8. Estimations of variance components and heritability for prevalence of Johne's disease (JD) in New Zealand dairy cattle, in which JD was treated as either 0 or 1 as a trait without transformation (Not trans) or as a binomial (Logit) transformation.

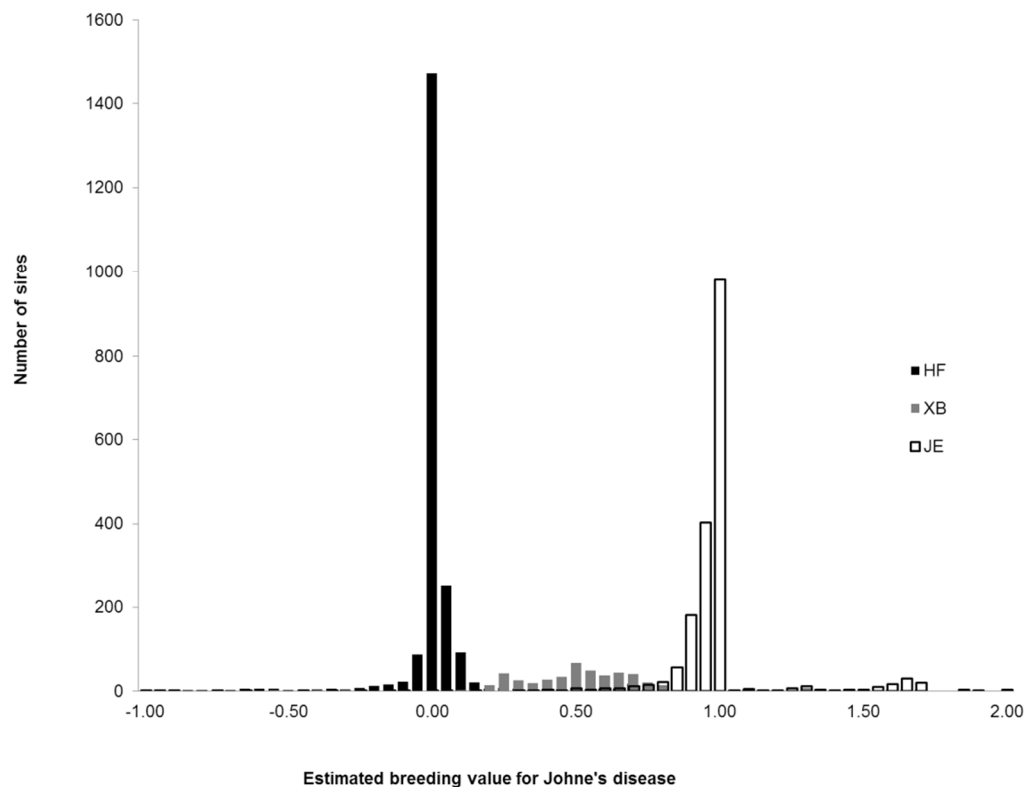| Parameter	Not trans	SE	Logit	SE
Genetic additive variance	0.0001	0.00002	0.963	0.144
Residual variance	0.0098	0.00004	3.290	
Phenotypic variance	0.0098	0.00004	4.253	0.144
Heritability	0.0142	0.00230	0.226	0.026

Figure 1. Distribution of the number of sires with estimated breeding values for Johnes's disease.

Conclusion

The average prevalence of JD in this study was 1.01% with a range from 0 to 9.35% per herd. Few studies have been conducted in New Zealand to estimate the effect of JD on lactation performance. The average prevalence reported in this study is lower than that reported by Norton (2007) where the prevalence of JD by ELISA and faecal culture ranged from 4.5% (95% CI 2.6-6.9) to 14.2% (95% CI 9.2-20.6).

Production estimates were calculated using data from the 2009/10 production season and JD positive cows produced 47.1 kg milksolids less than JD negative cows in 220 days, which represents 14.3% of the mean. This value is similar to the predicted loss of 53kg milksolids per a 305-day lactation (15.5% of the mean) reported in a New Zealand herd (Norton 2007).

Heritability estimates were calculated two ways. The estimate of heritability of 0.0142 (using an untransformed linear model) for prevalence of JD obtained in this study was lower than the average value of 0.10 reported in elsewhere (Koets et al. 2000; Attalla et al. 2010; Hinger et al. 2008; Mortensen et al. 2004). However, the estimate of heritability of 0.226 using a threshold model is higher than the values reported using a similar threshold model, 0.09 by Gonda et al. (2006) and 0.06745 by Attalla et al. (2010). Gonda et al. (2006) reported a value of heritability of 0.16 using a linear model.

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