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Effect of crossbreeding strategies on long-term rates of genetic gain in New Zealand dairy cattle

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ABSTRACT

Crossbred cows tend to be more profitable than straightbred cows because they fit the present milk payment system and show favourable heterosis for milk traits. This may encourage greater use of crossbred cows eroding the number of potential bull mothers (active cows) thereby reducing genetic progress. The objective of this research was to evaluate the effects of crossbreeding on active cow numbers and genetic gain over 25 years.

A deterministic model was used to calculate the number of cows and the breeding worth (BW) of Holstein-Friesian (F) and Jersey (J) bulls each year. Three strategies were considered: upgrading to F (UPGF); upgrading to J (UPGJ); and some two-breed rotational mating plans. In 1996, sizes of F and J active populations were taken to be 250,000 and 76,400 cows and mean bull BWs were \$72 (F) and \$82 (J).

After 25 years of UPGF the number of active F and J cows were 1,520,000 and 13,000, the BWs of F and J bulls were \$245 and \$213 and genetic gains of F and J bull teams were 8.5 and 4.25 \$BW/year. UPGJ had the opposite effect. Mating 10% of \bullet 2/3F cows to F bulls and 10% of \bullet 1/3F cows to J bulls (ROTATE10) for 25 years led to active F and J populations of 70,200 and 75,800 cows, BWs of F and J bulls of \$227 and \$230 and genetic gains for F and J bull teams equal to 7.0 \$BW/year. Results suggest that widespread adoption of a rotational crossbreeding scheme could be achieved without penalising annual genetic gain in bulls. However, annual recruitment of new active cows should be routinely monitored to ensure long term gain will be maintained.

Keywords: dairy cattle; upgrading; rotational crossbreeding; genetic gain.

INTRODUCTION

The main breeds of dairy cattle in New Zealand are Holstein-Friesian (F), Jersey (J) and Ayrshire with a significant proportion of FxJ crossbred cows (Livestock Improvement Corporation, 1995). Traditionally, breeding schemes have been designed to improve the genetic merit of animals by within-breed selection. The best available cows (cows to breed bulls) in the population are mated to the best available proven bulls (bulls to breed cows). The sons from these matings are progeny tested with 50 to 85 daughters and the best of these (bulls to breed cows) are widely used on commercial cows (cows to breed cows) to breed replacement daughters. Cows available for selection as mothers of young bulls are known as active cows (Macdonald Committee Report, 1992). Active cows may be registered (pedigree) or non-registered (grade) animals provided they are the result of at least three generations of artificial breeding to sires of one breed. Shannon (1989) identified that genetic gain and therefore farm profit is sensitive to the size of the active cow population.

The recently introduced system of genetic evaluation for New Zealand dairy cattle is based on a repeatability animal model across breeds (Garrick *et al.*, 1993; Harris *et al.*, 1996). One feature of this system is that cows of different breeds can be compared on the basis of profit per unit feed consumed (\$ per 4.5 t Dry Matter). Computer simulation results (Lopez-Villalobos and Garrick, 1996) indicate that dairy herds with first-cross FxJ or straightbred

J cows could be more profitable than those herds with straightbred F cows. Therefore, it is likely that dairy farmers would adopt a crossbreeding strategy to maintain crossbred animals or upgrade to the J breed.

Changes in the breed composition of the national herd would have important effects on the availability of bull mothers. Any upgrading to J would reduce the number of active F cows whilst adoption of two-breed rotational crossbreeding would reduce the number of active F and J cows. The objective of this study was to evaluate the effects of crossbreeding strategies on the active cow population and resulting within-breed rates of genetic gain.

METHODS

A deterministic computer model was used to simulate the number and genetic merit of cows and bulls for the next 25 years. The model allowed for crossbreeding strategies, population growth and selection with overlapping generations. Variables and assumptions for the simulation model are listed in Table 1.

Population structure

There were two straightbred populations, Holstein-Friesian and Jersey and one FxJ crossbred cow population. Active cows were those with at least 3 generations of artificial breeding and with \bullet 7/8 of genes of one breed.

Animals were classified into age groups which were characterised by the mean genetic merit and the reliabilities

TABLE 1: Variables and assumptions for the simulation model.

	Value									
COW POPULATION										
Total 1996 population										
Holstein-Friesian; Jersey and FxJ crossbred cows	1,613,000;		509,400;		453,000					
Active cows										
Holstein-Friesian; Jersey	250,000;		76,400							
Age structure, genetic merit, and reproductive and survival parameters										
Age at calving (years)	2	3	4	5	6	7	8	9	10	
Lactation number	1	2	3	4	5	6	7	8	9	
Percentage of cows	21.1	18.8	15.6	12.5	10.2	7.8	6.2	4.7	3.1	
Mean 1996 genetic merit (\$BW) ^a										
Holstein-Friesian	22.5	20.8	19.8	16.9	10.5	3.1	3.4	3.7	2.0	
FxJ Crossbred	30.0	27.2	28.0	25.6	18.2	9.7	10.0	9.6	6.5	
Jersey	34.0	27.5	27.9	26.4	20.6	12.9	14.0	11.5	6.9	
Reliability (%)	37	42	43	45	46	46	48	48	48	
Mortality rate (%) ^b	1.4	1.2	1.3	1.2	1.1	1.0	1.1	1.1	1.4	
Culling rate (%)	12.0	15.8	17.0	19.2	21.5	23.3	27.0	32.7	98.6	
Services per conception	1.3									
Percentage of cows mated to AB bulls	84									
Percentage of female calves recorded	95									
Number of active cows selected to produce a progeny tested bull	4.2									
Percentage of cows selected as cow dams	95									
BULL POPULATION										
Number of semen doses per proven sire per year	from 116,000 to 250,000									
Age at sampling	12 months									
Genetic merit and survival parameters										
Age (years)	1	2	3	4	5	6	7			
Mean 1996 genetic merit (\$BW)										
Holstein-Friesian	83.7	77.5	75.8	74.8	71.9	65.5	58.1			
Jersey	96.4	89.0	82.5	82.9	81.6	75.6	67.9			
Reliability (%) ^c	0	0	0	0	85	85	85			
Culling + Mortality rate (%)	10	10	10	10	10	10	10			
Maximum number of years of use of a proven sire	3 years									
Size of progeny group	60 to 85									
Number of bulls selected to breed bulls	3 per breed									
Number of bulls selected to breed cows =	<u>number of cows to be artificially inseminated x services per conception</u> semen doses per bull per year									

^a Livestock Improvement Corporation (personal communication); BW = breeding worth

^b data from Harris (1989).

^c based on 85 daughters.

of genetic evaluations. Cows calved from 2 to 10 years of age with the proportions within age classes are shown in Table 1. Cows older than 10 years were culled at the end of their lactation. Growth of the cow population depended on mortality and culling rates, sex ratio (1:1, male to female) and proportion of calving losses (0.09, Macdonald Committee Report, 1992). Number of animals were updated each year using a herd-growth model (Upton, 1989). The intake of male calves for each breed depended on the predicted number of cows to be inseminated in five years time.

Selection pathways

Selection of cows and bulls was on an index (breeding worth, BW) which is calculated as $BW = \sum v_j \hat{g}_j$ where v_j is the economic value in dollars of trait j and \hat{g}_j is the estimated breeding value of the individual for trait j . Traits

contained in BW were cow liveweight and 270-day lactation yields of milk volume, fat and protein. Standard deviation of true BW (known as aggregate genotype, T) was calculated as \$25. Reliabilities of genetic evaluations (represented as the squared correlation between T and estimated BW) were based on the number of lactation records for individual cows and information from the 60 to 85 first crop daughters for bulls.

Four selection pathways (Rendel and Roberston, 1950) were considered, cows to breed cows, bulls to breed cows, cows to breed bulls and bulls to breed bulls. Selection of animals to be parents of the next generation was undertaken by truncation across age classes based on normal distribution theory using the algorithm proposed by Ducrocq and Quaas (1988). All other selection and culling decisions were assumed to be independent of the index.

Average annual rates of genetic gain were calculated from the total increase in BW of the bull teams for the simulation period divided by the length of the simulation (25 years). Asymptotic annual genetic gains were taken as the increase in BW of the bull teams in the last year of simulation.

Crossbreeding strategies

Three crossbreeding strategies were considered: upgrading to Holstein-Friesian (UPGF), upgrading to Jersey (UPGJ) and some two-breed rotational crossbreeding (ROTATE1, 10 and 50). For UPGF, all F and FxJ crossbred and half of J cows were mated to F bulls and the remaining J cows were mated to J bulls. For UPGJ, all J and FxJ crossbred and half of F cows were mated to J bulls and the remaining F cows were mated to F bulls.

For rotational crossbreeding strategies, cows were classified according to their proportion of F genes into three groups: (i) $\bullet 2/3F$, (ii) $<2/3F$ and $>1/3F$ and (iii) $-1/3F$. Cows in group (ii) were mated half to F bulls and half to J bulls. For ROTATE1, 1% and 99% of cows from groups (i) and (iii), respectively, were mated to F bulls. For ROTATE10, 10% and 90% of cows from groups (i) and (iii), respectively, were mated to F bulls. And for ROTATE50, 50% of cows from groups (i) and (iii) were mated to F bulls.

RESULTS

The F population was the dominant genetic group at the start of the simulation (1,613,000 cows; Table 1). After 25 years of UPGF, this population increased to 2,994,000 cows at the expense of the J and FxJ crossbred populations (Table 2). The F active cow population increased from 255,000 to 1,520,000 whilst the J active population was reduced from 76,000 to 13,000 cows (Table 3). The average annual genetic gains in the F and J bull teams were 6.9 and 5.3 \$BW and approached an asymptotic rate of 8.5 and 4.3 \$BW (Table 4). The BWs of the bulls teams were \$245 and \$213 in the year 2020/21 (Table 5).

Upgrading the dairy cattle population to Jersey (UPGJ) for 25 years, increased the J population to 2,774,000 but produced a large proportion of FxJ crossbred cows in the early years (Table 2). The size of the J active population increased to 1,410,100 cows whilst the F active population was reduced to 41,100 in the year 2020/21 (Table 3). The average annual genetic gains in the F and J bull teams were 6.0 and 6.6 \$BW and approached an asymptotic rate of 5.5 and 8.3 \$BW (Table 4). The BWs of the bull teams in the year 2020/21 were \$221 and \$248 (Table 5).

Two-breed rotational crossbreeding strategies increased the size of FxJ crossbred population at the expense of straightbred F and J populations (Table 2). After 25 years of ROTATE50 the size of the F and J active populations were 333,000 and 303,000 cows (Table 3), the average annual genetic gains in the F and J bull teams were 6.6 and 6.3 \$BW and approached an asymptotic rate of 7.8

TABLE 2: Total number of cows by breed or cross under different crossbreeding strategies (UPGF, upgrading to Holstein-Friesian; UPGJ, upgrading to Jersey and ROTATE^a, two-breed FxJ rotational crossbreeding).

Strategy	Cows ^b	Year		
		2000/01	2010/11	2020/21
UPGF	F	1,795,000	2,482,000	2,994,000
	FxJ	475,410	274,700	77,110
	J	367,300	97,500	25,700
UPGJ	F	1,163,000	308,800	81,300
	FxJ	883,100	847,800	244,000
	J	593,000	1,702,000	2,774,000
ROTATE1	F	722,000	7,770	15,210
	FxJ	1,686,300	2,839,900	3,068,390
	J	228,600	12,910	15,390
ROTATE10	F	812,000	81,800	138,200
	FxJ	1,566,300	2,655,300	2,810,100
	J	259,100	121,600	149,300
ROTATE50	F	1,228,000	634,700	656,700
	FxJ	1,013,300	1,810,400	1,843,500
	J	396,800	413,400	597,300

^a The number (x) after ROTATE indicates the percentage of cows with $\bullet 2/3$ F genes which were mated to F bulls and the percentage of cows with $-1/3$ F genes which were mated to Jersey bulls. Cows with $<2/3$ F and $>1/3$ F genes were mated half to F bulls and half to J bulls.

^b F = Holstein-Friesian, J = Jersey

TABLE 3: Number of active cows under different crossbreeding strategies (UPGF, upgrading to Holstein-Friesian; UPGJ, upgrading to Jersey and ROTATE^a, two-breed FxJ rotational crossbreeding).

Strategy	Cows	Year		
		2000/01	2010/11	2020/21
UPGF	Friesian	512,000	1,180,000	1,520,000
	Jersey	85,700	43,600	13,000
UPGJ	Friesian	277,000	138,000	41,100
	Jersey	170,000	829,000	1,410,000
ROTATE1	Friesian	116,000	3,750	7,730
	Jersey	35,000	6,360	7,820
ROTATE10	Friesian	149,000	39,100	70,200
	Jersey	46,200	59,800	75,800
ROTATE50	Friesian	301,000	299,000	333,000
	Jersey	96,800	200,000	303,000

^a The number (x) after ROTATE indicates the percentage of cows with $\bullet 2/3$ F genes which were mated to F bulls and the percentage of cows with $-1/3$ F genes which were mated to Jersey bulls. Cows with $<2/3$ F and $>1/3$ F genes were mated half to F bulls and half to J bulls.

and 7.5 \$BW (Table 4). The BWs of the bull teams in the year 2020/21 were \$237 (F) and \$239 (J) (Table 5).

Mating 10% of $\bullet 2/3F$ cows to F bulls and 10% of $-1/3F$ cows to J bulls (ROTATE10) for 25 years led to active F and J populations of 70,200 and 75,800 cows (Table 3), BWs of F and J bulls of \$227 and \$230 (Table 5) and the asymptotic annual gains for F and J bull teams were equal to 7.0 \$BW (Table 4).

TABLE 4: Average and asymptotic annual rate of genetic gain in the bull teams under different crossbreeding strategies (UPGF, upgrading to Holstein-Friesian; UPGJ, upgrading to Jersey and ROTATE^a, two-breed FxJ rotational crossbreeding).

Strategy	Bull team	Rate of genetic gain (\$BW ^b /year)	
		Average	Asymptotic
UPGF	Friesian	6.9	8.5
	Jersey	5.3	4.3
UPGJ	Friesian	6.0	5.5
	Jersey	6.6	8.3
ROTATE1	Friesian	5.5	6.3
	Jersey	5.5	6.3
ROTATE10	Friesian	6.2	7.0
	Jersey	5.9	7.0
ROTATE50	Friesian	6.6	7.8
	Jersey	6.3	7.5

^a The number (x) after ROTATE indicates the percentage of cows with $\frac{2}{3}$ F genes which were mated to F bulls and the percentage of cows with $\frac{1}{3}$ F genes which were mated to Jersey bulls. Cows with $<\frac{2}{3}$ F and $>\frac{1}{3}$ F genes were mated half to F bulls and half to J bulls.

^b breeding worth

TABLE 5: Breeding worths (\$) of Friesian and Jersey bull teams under different crossbreeding strategies (UPGF, upgrading to Holstein-Friesian; UPGJ, upgrading to Jersey and ROTATE^a, two-breed FxJ rotational crossbreeding).

Strategy	Bull Team	Year		
		2000/01	2010/11	2020/21
UPGF	Friesian	89.5	170.0	245.3
	Jersey	101.3	164.0	213.3
UPGJ	Friesian	89.5	164.3	221.3
	Jersey	101.3	170.5	247.5
ROTATE1	Friesian	89.5	145.0	208.5
	Jersey	101.3	149.8	212.5
ROTATE10	Friesian	89.5	156.5	226.8
	Jersey	101.3	160.3	229.5
ROTATE50	Friesian	89.5	165.8	237.3
	Jersey	101.3	166.3	239.0

^a The number (x) after ROTATE indicates the percentage of cows with $\frac{2}{3}$ F genes which were mated to F bulls and the percentage of cows with $\frac{1}{3}$ F genes which were mated to Jersey bulls. Cows with $<\frac{2}{3}$ F and $>\frac{1}{3}$ F genes were mated half to F bulls and half to J bulls.

DISCUSSION

Shannon (1989) and Garrick and Rendel (1992) concluded that the size of the active cow population has a significant effect on the rate of genetic gain of New Zealand dairy cattle. This was supported in the current study. For all crossbreeding strategies, the size of the active cow population affected the within-breed average annual genetic gain and average BW of bulls. UPGF increased the F active population and reduced the J active population, and as a result, the average annual genetic gain

and BW of F bulls were higher than those for J bulls (Table 4). Similarly but in opposite trend, UPGJ reduced the F active population and increased the J active population. Therefore, the average annual genetic gain and BW of F bulls were lower than those for J bulls. Compared to UPGF and UPGJ strategies, all two-breed rotational crossbreeding strategies reduced the size of F and J active populations with a subsequent decrease in the within-breed average annual genetic gains.

Rotational crossbreeding schemes seem to be an alternative to make use of within-breed selection and heterosis effects. The strategy where 10% of predominantly Holstein-Friesian cows were mated to Holstein-Friesian bulls (ROTATE10) led to active F and J populations of about 70,000 cows with similar annual genetic and BW of bulls to those achieved with larger active cow populations (UPGF or UPGJ). This strategy maintains the current breeding scheme without penalising the genetic gain in bulls and at the same time allows for an increase in the number of crossbred cows.

CONCLUSIONS

Results from this study confirm that the size of active cow population affects the rate of genetic gain but these results also suggest that rotational crossbreeding schemes could be implemented without penalising genetic gain in bulls.

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