Effect of Crossbreeding on Milk Production, Udder Health and Fertility on Dutch Organic Dairy Farms

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Introduction

Organic farming in Europe has developed into a small (about 3% of total agricultural area) but important factor in agricultural production. In the Netherlands, organic dairy farming grew rapidly in the late 1990s. Farmers who converted to organic production had to undergo some major changes in their farm management. The most important changes were no use of chemical fertilizers, restricted use of concentrates, and limited use of antibiotics. Because of these restrictions, the cows have a lower energy intake and do have to combat diseases themselves. This is expected to affect especially the high-producing cows (Padel, (2000)), usually Holsteins. Ten years ago most organic dairy farmers in the Netherlands milked Holstein cows (Nauta et al. (2006)). After conversion many organic farmers started crossing with other breeds, but without clear insight on the effects of crossbreeding in an organic system. Within organic farms there is a large variation in management. To some extent this variation can be captured by soil type and housing system. Both aspects might influence the performance of cows. The aim of this study was to analyze an unique dataset with 24 different breeds and their crosses and to estimate the effects of crossbreeding of the five most prominent breeds with Holstein Friesian cows for milk production, udder health and fertility and to investigate if these effects differ according to soil type and housing systems.

Material and methods

Available data. Organic farms in The Netherlands were approached and 113 out of 325 gave permission to use their data for this study. Data was collected between January 1st, 2003 and February 1st, 2009. Farms had on average a herd size of 50 cows each year. Primiparous cows represented 28.3% of lactations, 23.1% were 2nd lactations. In total, there were 33,788 lactations available on 15,015 individual cows. For these cows, data were collected on breed composition, birth date, age at calving, parity, stage of lactation, calving interval, kg milk production in 305 days, kg fat and protein corrected milk yield (FPCM = (0.337+0.116* %FAT+0.06*%PROT)*KGMILK), log transformed lactation average somatic cell score up to 350 days (SCS = 1000+(1000*(log(SCC)/log(2)))) and calving interval in days (CI).

In total 24 different breeds were present, however, Brown Swiss (BS), Dutch Friesian (FH), Groningen White Headed (GWH), Holstein-Friesian (HF), Jersey (J), and Meuse-Rhine-Yssel (MRY) cattle were presented mostly and had a large spread of crosses (e.g. Purebreds,

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F1-crosses, and backcrosses) present. Holstein-Friesian was the most important breed, with 74.5% of the cows carrying at least 50% Holstein genes.

Farm systems. Farms were separated based on their farming system: (a) soil type of a farm (sand or no sand) and (b) the housing system of a farm (cubicle barn or not). In the data, 49 out of 113 farms farmed on sand, with in total 13,203 lactations. The soil type of the other 64 farms was anything other than sand, like peat meadows, clay, or loess. With regard to the housing system, 84 farms had cubicle barns, corresponding with 26,341 lactations.

Statistical analyses. The data with all breeds and their crosses were analyzed using ASREML (Gilmour et al. (2006)), including a regression on all breed fractions (scaled in classes of 12.5%, from 1 to 8) and the expected heterosis and recombination. Subsequently, least square means were predicted for animals of the five most prominent breeds and crosses with Holstein (F1-offspring), and both between purebred parents and a F1-parent (backcross). The model was the same for all traits (milk, FPCM, SCS and CI):

$$Y \sim \mu + \text{fixed effects} + \sum b_i * \text{breed}_i + b_2 * \text{heterosis} + b_3 * \text{recombination} + \text{animal} + \text{error}$$

In this model, Y = observation on the performance of a production traits on a cow and μ = overall mean. Fixed effects include parity (with four classes, where the last class contains all parities ≥ 4), herd (with 113 classes), year (with 7 classes), season (based on 4 seasons; Jan.–Mar., Apr.–Jun., Jul.–Sep., and Oct.–Dec.). Linear regressions were included for the breed proportions (b_i, with i ranging from 1 to 24), for heterosis (b_2) and for recombination (b_3). A random effect was included for animal, to account for multiple parities of a cow in the dataset, and for the residual term. The interactions with soil types and housing systems were fitted by including an interaction for these factors with all regression coefficients. Because herd effect was already included as a fixed effect separately, the single effects of soil type and housing systems were not included in the model as those traits are entangled with herd.

Results and discussion

Raw average milk production was 6858 kg in 305 days, and 300 kg fat and 235 kg protein. The lactation-average SCS was 1730 (this coincides with appr. 266,000 cells/ml). Predicted milk production, while correcting for effects of parity, herd and the interaction between year and season of calving, is highest for cows that carry 100% HF-genes and lowest for cows that carry 100% GWH-genes (Figure 1). The higher the proportion of Holstein-genes, the higher the predicted milk production, as expected.

When analyzing the overall data, heterosis had significant effect ($p<0.10$) on milk, FPCM and CI in the favourable direction (i.e. more milk, shorter CI), but unfavourably for SCS (higher cell count). Recombination was unfavourable for the milk traits, but favourable for fertility and udder health. Regression coefficients differed per breed; i.e. the only positive regression coefficient for milk was for HF, but when milk was corrected for fat and protein content, Jerseys gave a positive regression as well. Regression coefficient for udder health (SCS) were favourable for BS, but unfavourable for GWH and Jerseys. Regression coefficient for fertility (CI) was favourable for GWH and unfavourable for HF and BS.
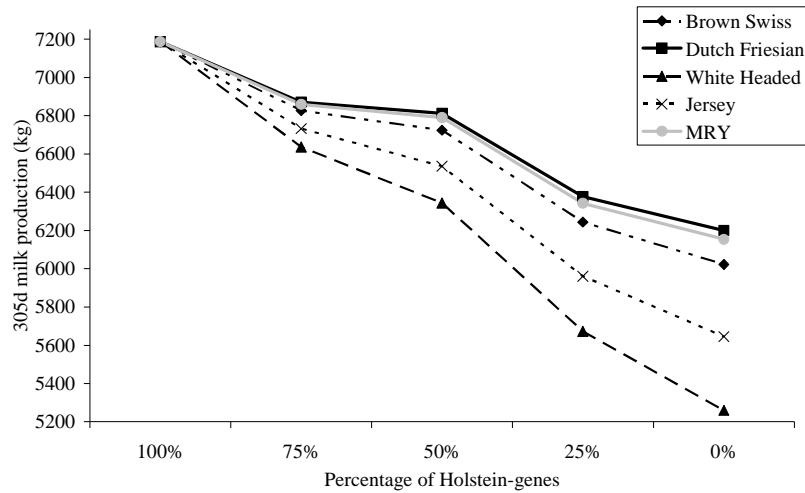
Figure 1: Predicted 305d milk production (kg) per percentage of Holstein-genes and Brown Swiss, Dutch Friesian, Jersey, Groningen White Headed and Meuse Rhine Yssel

The regression coefficients for milk, FPCM, SCS and CI are shown in Table 1 separated per soil type. The soil type of a farm determined directly the composition of the cow's diet. On sandy soil more maize silage was fed to the cows, which has a high energy content, whereas diets on farms with non-sandy soil consisted mostly out of grass silage. Some of the breed effects differed significantly depending on the soil type: regression coefficients of milk on BS, HF, J, and MRY were significantly higher (p<0.10) on farms farming on sand than on farms with other soil types (Table 1). On the other hand, the regression coefficient of SCS on GWH was higher on farms with soil types other than sand, implying a higher cell count and worse udder health. Regression coefficient of CI on Jersey was higher in farms on sand, indicating a longer calving interval.

Table 1: Regression coefficients for milk, fat-protein corrected milk (FPCM), somatic cell score (SCS) and calving interval (CI) based on soil type of the farm (sand *vs.* no sand (No S.))

	Milk		FPCM		SCS		CI	
	Sand	No S	Sand	No S	Sand	No S	Sand	No S
Heterosis	104.9	123.9	124.5	134.3	4.5	3.6	-2.2	-3.1
Recombination	-526.6	-516.5	-312.7	-420.2	-41.9*	-8.9	-3.7	-3.7
Brown Swiss	-6.2*	-75.0	-7.2*	-50.7	-5.2	-4.0	3.2	2.6
Dutch Friesian	-28.3	-25.2	-14.8	-39.3	-1.2	-1.0	-2.0	1.6
White Headed	-113.9	-161.8	-137.4	-160.7	12.1*	4.0	-2.0	-1.4
Holstein	114.7*	79.3	46.5*	74.0	1.0	1.2	3.7	3.7
Jersey	-62.3*	-135.7	-14.3	-59.2	4.1	4.3	2.9*	-0.4
MRY	-7.0*	-66.6	-20.4*	-59.5	1.8	1.0	0.3	-0.9

* p-value <0.10

The farms in this study had either a barn with cubicles or another housing system. Compared to the other breeds, the regression coefficient of milk on HF and MRY (and also FPCM) was higher in a cubicle barn than in barns without cubicles (Table 2). The regression coefficient of udder health on FH or Jersey was significantly higher in non cubicle barns. This might be due to environmental pathogens in the bedding of non cubicle barns causing more mastitis and higher cell counts. Regression of fertility on HF is worse in cubicle barns resulting in higher CI, which might be because of the slippery floor and the cows show their heat less.

Table 2: Regression coefficients for milk, fat-protein corrected milk (FPCM), somatic cell score (SCS) and calving interval (CI) based on housing system of the farm (cubicles (cub.) *vs.* no cubicles (No C.))

	Milk		FPCM		SCS		CI	
	Cub	No C	Cub	No C	Cub	No C	Cub	No C
Heterosis	69.0	183.5	121.5	199.7	1.9	13.7	-1.7	-5.3
Recombination	-583.9	-365.5	-434.9	-267.7	-19.7	-35.6	-8.5	7.6
Brown Swiss	-43.7	-88.7	-17.7*	78.6	-5.5	2.2	3.4	0.7
Dutch Friesian	1.6	-120.1	-5.3	-105.5	-3.5*	6.9	0.4	-2.2
White Headed	-155.5*	-142.9	-162.9	-139.8	6.1*	3.9	-1.6	-1.9
Holstein	107.0*	54.1	97.0*	49.9	0.5	3.0	4.5*	1.4
Jersey	-83.6	-149.2	-20.1	-86.5	1.6*	8.2	1.4	1.2
MRY	-21.5*	-86.7	-24.3*	-90.5	1.3	0.7	0.5	-2.4

* p-value <0.10

Conclusion

Crossbreeding Holstein dairy cows with other breeds (BS, FH, GWH, J, or MRY) decreased milk production (also when corrected for fat and protein content (FPCM)), but improved fertility. Udder health was only improved in some crosses, and not when crossed with GWH or J. Farm management systems (depending on soil type or housing system) affected the regression coefficients on breed components significantly for some breeds. For example, the effect of HF on milk and CI was twice as large in cubicle housing than in other housing systems, and FH had a unfavourable effect on SCS in cubicles, but a favourable effect in other systems. Jersey had a negative effect on fertility only on farms on sandy soil. Hence, breed effects differ across farming systems, also within the organic systems.

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