For further information or to request a copy of the full scientific report detailing the experimental tests and statistical analysis contact:

AgriSearch
97 Moy Road
Dungannon
BT71 7DX
Northern Ireland

T: 028 8778 9770
F: 028 8778 8200
W: www.agrisearch.org

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ARE INTERNATIONAL DAIRY SIRE GENETIC EVALUATIONS RELEVANT TO MILK PRODUCTION SYSTEMS IN NORTHERN IRELAND?

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The Agricultural Research Institute of Northern Ireland,
Hillsborough, Co. Down, BT26 6DR

RESEARCH TEAM
Andrew Cromie
Fred Gordon
Myles Rath[1]
Dennis Kelleher[1]
[1]University College Dublin

Report prepared by
Fiona Young

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10 DAIRY D-13-02
The Effect of the Type of Dietary Supplement on the Performance of the Grazing Dairy Cow

11 DAIRY D-06-98
Are International Dairy Sire Genetic Evaluations Relevant to Milk Production Systems in Northern Ireland?

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OVERALL SUMMARY OF PROJECT

This study investigated the ‘accuracy’ of AI sire proofs generated from international data when applied to daughters of sires used within dairy management systems in Northern Ireland and the Republic of Ireland.

- The project investigated the effect of: environment; nutrition (high concentrate/low concentrate diets); lactation number; and regional and management variations within Ireland on milk yield, protein yield, and fat yield as well as percentage fat and protein. The study examined each of these factors in terms of phenotypic variation or effect of genotype and ultimately the ‘accuracy’ of the AI sire genetic proofs.

- Overall the study found that international AI sire proofs could be used as a reliable indicator for ranking animal’s performance within local dairy management systems. However, the potential genetic benefit obtained from these sires varied depending on the management system employed on the farm. For example, only about 40% of the predicted improvement in milk yield for daughters of sires will be achieved in low concentrate input herds, relative to that predicted from US sire proofs. In contrast 60% of the predicted yield improvement will be achieved with high concentrate input herds.

- Generation of more ‘accurate’ proofs in the future may be assisted by combining performance data from similar management systems across countries rather than the current system, which assesses performance within country, irrespective of any variation in management practices.

INTRODUCTION

Milk production systems in Northern Ireland are predominantly grass-based. With the recent CAP reform, and continued pressure on milk prices, there is a considerable incentive for farmers to maximise the potential of grazed grass and grass silage in order to reduce costs of milk production. At the same time, the range of dairy sires available to dairy farmers, with the exception of New Zealand sires, are almost universally from countries that feed high levels of concentrates to dairy cows. A recent list of the top 20 international AI sires showed that 19 of these sires were proven in high concentrate systems (US, Holland, France or Italy).

The aim of this study was to identify if there was variation in the genetic ranking of dairy sires under local management practices in comparison to their genetic ranking in their country of origin. An animal's phenotypic record, or performance, is commonly described as the sum of a genetic and an environmental effect and is the physical, measurable variation among animals due to a combination of an individual animal's genes and the effects of the environment in which it is kept. In contrast, an animal's genotype is described as the variation solely controlled by its genes. Correlations between genotype and environment can occur when better genotypes are given better environments (e.g. management) and an improvement in phenotype is observed. A common example is milk yield in dairy cattle, where the husbandry practice may involve feeding cows according to their level of production. Alternatively, genotype can respond differently to changes in the environment, such that a phenotypic (e.g. milk yield) difference between genotype A and genotype B is not the same in environment X as it is in environment Y. In this study phenotypic assessment of milk, fat and protein yield and fat and protein percentage were compared among animals of different age and on a variety of management systems within Ireland to determine the effects of genotype.

OUTLINE OF STUDY

The main aim of this study was to assess the suitability of imported AI sire proofs for use in local dairy herds in two main ways. Firstly, the study assessed how much of the genetic advantage suggested in an imported AI bull proof will be established in local dairy farms and secondly, to determine if the ranking of AI sires from imported proofs change when daughters of these sires are evaluated under different management conditions. In more detail, the imported AI sire proofs were assessed to determine the effect of: 1) level of herd nutrition, 2) lactation number and 3) level of herd management (average milk production or variation in milk production) within Ireland.

A National data set comprising of 305-day milk yield data for the years 1992-1995 which consisted of 267,721 lactation records from 149,689 animals within 4268 herds was analysed. This was made up of 243,043 lactation records analysed from 133,550 animals (Department of Agriculture and Food, Dublin, Republic of Ireland) and 101,545 records from 53,596 animals (United Dairy Farmers, Northern Ireland).

1). Level of herd nutrition

Of these 4268 herds, information on level of concentrate input (kg/cow/year) was available for 665 herds. This information was obtained from four recognised herd management programmes: Teagasc Dairy Mis; Richardson's/Irish Fertilizer Industries Milk Chek; Department of Agriculture for Northern Ireland Milk Manager; and Kingswood Computing. High input herds were defined as the top 25% of herds on concentrate input/cow/year, whereas, the low input herds were the bottom 25% of herds on concentrate input/cow/year usage. The difference in mean concentrate input between high and low concentrate herds was 1,009kg concentrate/cow/year.

2). Lactation number

A comparison was made of multiple lactation data (Table 1). This comparison examined the genetic ranking of the sires in subsequent lactations i.e. if a sire ranked first in the 1st lactation, would it remain first in the 2nd and 3rd lactation. The study assessed the phenotypic effects on milk, fat and protein yield and fat and protein percentage.

Table 1. The number of records within each lactation and the total number of records for high and low concentrate herds.

	High concentrate herds	Low concentrate herds
First Lactation	11,211	6,190
Second Lactation	5,694	3,144
Third Lactation	2,774	1,627
Fourth Lactation	831	560
Total	20,510	11,521

3). Herd management within Ireland

Herds in the national dataset (4268 herds) were categorised into high and low categories on the basis of (i) herd average milk yield, (ii) within-herd variation in milk yield, (iii) season of calving and (iv) region within Ireland. The respective herd average milk yield and within-herd variation in milk yield was calculated during the 4-year period of the study. High and low categories were defined as the top and bottom 25% of herds ranked on herd average milk yield or within herd variation in milk yield.

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Kingswood Computing

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Department of Agriculture and Rural Development of Northern Ireland

SUMMARY AND IMPLICATIONS FOR THE INDUSTRY

In general, international AI sire proofs provide a relatively accurate indicator of sires' daughter's performance in local management systems, irrespective of the levels of concentrate input or type of management system.

- In high and low concentrate herds, for milk, fat and protein yield, US bull proof results indicate that, on average, only 60% (high concentrate) and 40% (low concentrate) of the perceived advantage in a US bull proof is found in the performance of daughters under local conditions. However, there was little evidence of any scaling effect on fat or protein percentage.

- The generation of sire proofs from heifer yield lactation data are relatively accurate indicators of how that animal will perform in subsequent lactations.

- Neither herd management nor regional variation within Ireland affected the relative accuracy of US bull proofs, only as management systems became further from the US system did the accuracy of the US bull proof decline.

- In the future, one improvement in the generation of sire proofs may be to combine sire information (e.g. daughter individual milk records) from similar production environments (across several countries) into one evaluation. For example, raw data from low yielding, spring calving herds in Ireland could be combined with data from New Zealand and Australia to give one combined analyses of information from low input, seasonal milk production systems. Similarly raw data from high yielding herds in Ireland could be included with data from the USA, Canada, or the Netherlands to give one combined analyses of information from high input, all-year round calving systems. This would result in a more meaningful and accurate international sire proof for future use by the dairy farmer.

REVIEW OF FINDINGS

1). Level of herd nutrition (Heifer only)

- There were large differences between high concentrate (approximately 1.5 t concentrate/cow/year) and low concentrate (approximately 0.5 t concentrate /cow/year) herds in additive genetic and phenotypic variances (and heritabilities) for milk, fat and protein yield, but not for fat and protein percentage (Table 2).

Table 2. Performance of high and low concentrate herds.

	High concentrate herds			Low concentrate herds		
	Average	Maximum	Minimum	Average	Maximum	Minimum
Concentrate (kg/cow/year)	1,514	2,830	1,237	505	663	128
Milk yield (kg/cow/year)	5,887	9,604	3,956	4,496	6,068	3,374
Fat yield (kg/cow/year)	227.3	353.9	142.9	170.3	125.5	237.3
Protein yield (kg/cow/year)	189.2	315.7	128.5	147.7	196.2	112.9
Fat (%)	3.88	4.47	3.13	3.80	4.31	3.07
Protein (%)	3.22	3.61	3.01	3.29	3.48	3.05

- High concentrate herds had higher milk yields (+1,391kg/cow/year) with a higher proportion of cows calving in the winter months. These herds also yielded 90.5kg more combined fat and protein per lactation. Fat percentage of milk was also marginally higher with the high concentrate herds than low concentrate herds (3.88% compared to 3.80%). In contrast, milk protein was marginally higher in herds feeding low levels of concentrate than in herds feeding high levels of concentrate (3.29% compared to 3.22%).

- Phenotypic variances in yields of milk, fat, and protein, and fat percentage were higher in high concentrate herds. Similarly, additive genetic variances in milk and protein yield were almost four times as high in the high concentrate herds, resulting in much higher estimates of heritability (h^2) for milk and protein yield in these herds (0.40 and 0.34) compared to the low concentrate herds (0.20 and 0.15).

- Heritability estimates for fat yield and protein percentage were also higher with the high concentrate herds. In contrast, the heritability of fat percentage was higher in herds feeding low levels of concentrate (0.55) compared to those feeding high levels of concentrate (0.48).

- The observed heterogeneity of genetic variance and heritability for yield traits were strongly related to level of herd concentrate input, with cows in high concentrate herds able to express their genetic merit more fully compared to cows in low concentrate herds.

- In general, there was good agreement in the relative rankings of sires across both high and low concentrate herds for all five production traits, especially percentage fat and percentage protein. These results indicate that, on average, milk production proofs from countries that feed high levels of concentrate to dairy cows are reasonably accurate predictors of the genetic merit for local milk production systems (See Figure 1). For example, four of the top 10 sires for milk yield with low concentrate herds also ranked within the top 10 sires for high concentrate herds.

- There was a significant effect of management on milk, fat and protein yields when grouped by herd variation in milk yield or herd average milk yield (Table 3).

- Differences in the magnitude of additive genetic variation between high and low herds for milk, fat and protein yield were largest for herds grouped on the basis of ‘variation in milk yield’ (3.5 times greater in high herds), followed by herds grouped on ‘average milk yield’ (2.4 times greater), ‘season of calving’ (1.7 times greater) and region (1.5 times greater).

- Effects of the herd management level on estimates of genetic correlation for milk, fat and protein yield, indicated that, as differences in management and herd environment became more pronounced, there was evidence of a decline in the genetic correlation for both milk and protein yield, but not for fat yield.

- Estimates of heritability for milk and protein yield were greater in high herds than in low herds for all herd environments. Estimates of heritability in high herds ranged from 0.43 to 0.44 for milk yield and from 0.36 to 0.42 for protein yield. In contrast, estimates of heritability in low herds ranged from 0.32 to 0.37 for milk yield and from 0.30 and 0.35 for protein yield. Heritabilities for fat yield were similar between high and low herds for all herd environments (except when grouped on season).

- There was no evidence of significant re-ranking of US sire proofs and sire proofs in high or low yielding herds for any of the production traits, with an average reliability of 0.89, 0.86 and 0.79 respectively. However the response to improved genetic merit (based on US sire proofs) was greater in high yielding herds compared with low yielding herds.

3.) Herd management within Ireland

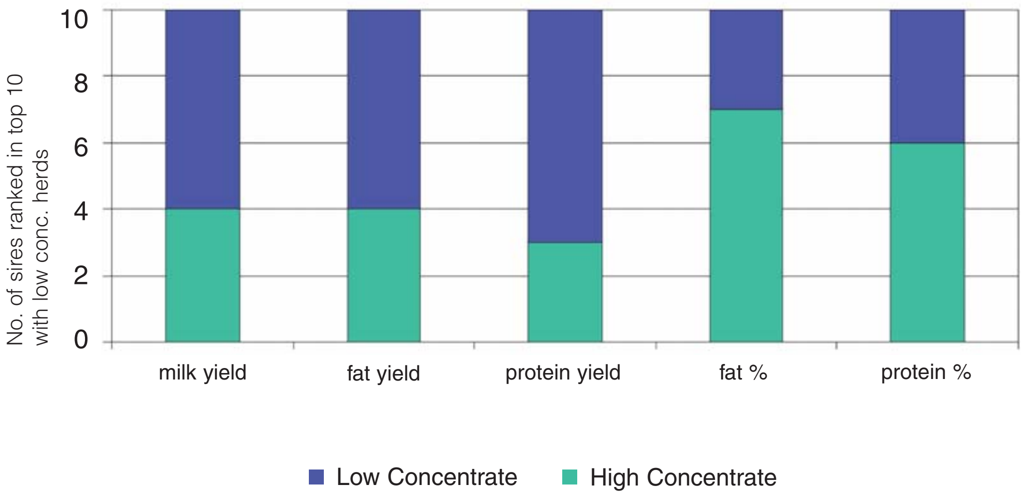
- Differences in herd average milk yield between high (top 25%) and low categories (bottom 25%) were largest for ‘average milk yield’ herds (2,223 kg) followed by ‘season of calving’ herds (1,316 kg), ‘variation in milk yield’ herds (1,297 kg) and herds from different regions (896 kg) respectively (Table 3).

Table 3: Average milk, fat, and protein yield for ‘average milk yield’ herds, ‘variation in milk yield’ herds, ‘season of calving’ herds and herds from different regions within Ireland.*

	‘Average Milk Yield’ Herds	‘Variation in Milk Yield’ Herds	‘Season of calving’ Herds	Herds from different regions
Milk yield (kg)				
High	6,140	5609	5584	5600
Low	3,917	4312	4268	4704
Fat yield (kg)				
High	233.3	211.3	214.1	223.3
Low	145.8	161.6	159.0	176.7
Protein yield (kg)				
High	199.0	182.6	179.6	177.4
Low	128.4	140.6	140.0	153.9

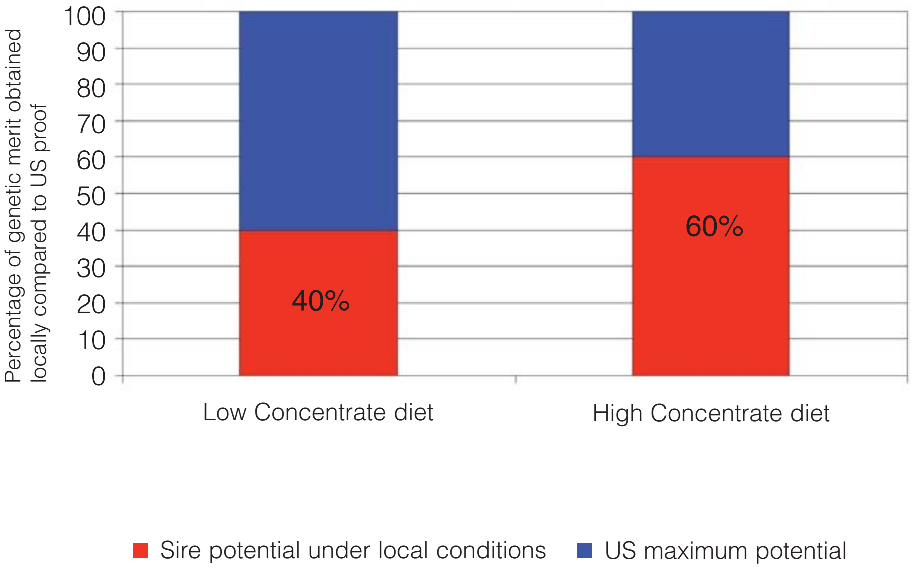
*High and low categories were defined as the top and bottom 25% of herds ranked on average milk yield and variation in milk yield within herds.

Figure 1. Number of sires ranked in the top 10 sires with low concentrate herds who also ranked in the top 10 with high concentrate herds, when ranked for milk yield, fat yield, protein yield, percentage fat and percentage protein.



- Interbull proofs in the US were higher for high concentrate herds for all five production traits and were significantly higher for milk yield (P=0.017). These results suggest that, due to environmental restriction in low concentrate herds, only about 40% of the yield improvement predicted for daughters from sires will be achieved, relative to that predicted in the US. In contrast in high concentrate herds, 60% of the yield improvement predicted in the US will be achieved (See Figure 2).

Figure 2. Average genetic merit potential obtainable from US sire proofs when managed locally on low and high concentrate systems.



2). Multiple lactation

- Results of the analyses of subsequent lactations were found to be very similar to the results of heifer analyses, both total phenotypic variance and additive genetic variances were greater in high concentrate herds for milk, fat and protein yield, although the magnitude of difference in additive genetic variances for these traits was not as dramatic as those obtained using heifer data.

- Estimates of heritability were still higher in high concentrate herds for milk yield (0.32 vs 0.25) and protein yield (0.29 vs 0.19) and were the same for fat yield (0.25) across HC and LC herds. Additive genetic variances were also higher for fat and protein percentage in high concentrate herds – as were heritabilities (0.55 vs 0.51 and 0.59 vs 0.52 for fat and protein percentage respectively).

- Estimates of the genetic correlation between high concentrate and low concentrate herds were above 0.87 for all five production traits throughout subsequent lactations. Similarly, estimates of genetic correlation between lactation 1 and lactation 2 and between lactation 1 and lactation 3 were above 0.84 in high concentrate herds and above 0.86 in low concentrate herds for all five production traits, indicating that cows with greatest genetic merit in lactation 1 were essentially the same cows with greatest genetic merit in lactations 2 and 3.