SCOPE FOR PROGENY-TESTING OF DAIRY SIRES
FOR CONFORMATION

K. Meyer, E. B. Burnside, K. Hammond, A. E. McClintock

Animal Genetics and Breeding Unit[1]

University of New England, Armidale, New South Wales 2351

G. D. Gillan

Holstein-Friesian Association of Australia

504 Racecourse Road, Flemington, Victoria 3031

INTRODUCTION

Sire ranking systems for conformation generally utilise all lactation classifications and are likely to be subject to selection bias if only the most recent record of a cow is used or if breed policy prevents downgrading upon reclassification. While the importance of classifier effects has been recognised and taken into account, herd effects have frequently been ignored. Recently, the method of Best Linear Unbiased Prediction (BLUP) (Henderson 1973), which is widely used in sire evaluation for dairy production traits, has been applied to evaluate sires for conformation of their daughters. Concurrent research has identified the importance of herd effects which are generally included in these BLUP evaluation procedures.

Relatively large herd sizes in Australia and mandatory scoring of registered Holstein-Friesian heifers for conformation make a sire evaluation on a within-herd basis, utilising only first classification records, feasible. This paper describes the analysis of first lactation records and the resulting BLUP sire evaluation procedure for type, implemented in Australia in December 1983.

MATERIAL AND METHODS

First classification records were obtained for 18 132 Australian Holstein-Friesian heifers, classified between twenty-one and fifty-four months of age. Data comprised twenty-six type traits, scored in three or six categories, and total score (see Table 1) from three rounds of classification between 1981 and 1983. For the analysis, records were transformed to 'objective scores' (Snell 1964) between 0 and 100. The model of analysis included herd-round-classifier (HRC) subclasses as fixed and sires as random effects, fitting age at classification as a linear and quadratic covariable within subclasses. Using a univariate Restricted Maximum Likelihood procedure (Patterson & Thompson 1971), genetic parameters were estimated from a subset of the data, consisting of 10 263 records in 1693 HRC for 299 sires with at least eight effective daughters in the full data set. After estimating variances for 'compound' traits, covariance components were obtained by difference and modified to ensure resulting correlation estimates within bounds and compatible with each other (see Meyer *et al.* 1984)

A BLUP sire evaluation for 2597 bulls was carried out for each trait, utilising the heritability estimates obtained and incorporating pedigree information — that is, sire and maternal grandsire identities, available for 1460 bulls. Regressions of mean progeny on

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Table 2: Traits analysed with abbreviations used, mean scores, and phenotypic variances (s²), proportion of total sums of squares explained by different effects in the model of analysis, and estimates of heritability (h²) and genetic correlation (rg) with total score

	Trait	Abbrev.	Mean* Score	S^2†	\multicolumn{4}{c}{Proportion (in %) of Total Sums Squares due to}	h^2	SE§	r_g with TSC
					HRC	Age	Sires	Residual			
1.	Total Score	TSC	—	—	37.3	1.6	5.9	55.2	0.438	0.058	—
2.	General Appearance	GAP	3.41	0.63	32.4	1.2	5.1	61.3	0.337	0.049	0.96
3.	Dairy Character	DCH	3.95	0.68	31.2	1.4	6.1	61.3	0.396	0.054	0.91
4.	Capacity	CAP	3.80	0.73	33.0	5.8	4.8	56.3	0.351	0.050	0.73
5.	Rump	RUM	3.59	0.73	31.2	2.5	3.8	62.4	0.252	0.041	0.73
6.	Feet and Legs	F&L	3.77	0.62	28.9	0.1	1.9	69.0	0.094	0.024	0.48
7.	Mammary System	MSY	3.49	0.63	31.1	0.5	5.1	63.3	0.322	0.047	0.92
8.	Fore Udder	FUD	3.63	0.66	28.9	0.9	4.0	66.1	0.245	0.040	0.91
9.	Rear Udder	RUD	3.72	0.69	29.8	0.1	4.8	65.3	0.290	0.044	0.87
10.	Size	SIZ	1.99	0.51	34.6	3.2	5.0	57.2	0.321	0.047	0.65
11.	Stature	STA	1.87	0.53	33.4	2.4	5.9	58.3	0.415	0.056	0.68
12.	Style	STY	1.85	0.48	29.7	1.3	3.5	65.5	0.191	0.035	0.78
13.	Dairyness	DAI	1.62	0.51	31.4	0.7	3.3	64.7	0.181	0.034	0.77
14.	Muzzle Width	MUZ	1.25	0.46	26.8	2.4	2.4	68.5	0.114	0.026	0.33
15.	Chest	CHE	1.43	0.54	26.2	3.7	3.3	66.9	0.181	0.034	0.40
16.	Loin	LOI	1.26	0.45	23.4	0.0	2.5	74.1	0.109	0.025	0.34
17.	Rump Width	RUW	1.38	0.50	30.8	2.9	3.5	62.8	0.203	0.036	0.46
18.	Pin Setting	PST	1.24	0.57	20.6	0.1	2.8	76.5	0.139	0.029	−0.23
19.	Rear Heel	RHL	1.88	0.39	26.8	0.0	1.9	71.3	0.085	0.023	0.16
20.	Bone Quality	BON	1.05	0.22	18.2	0.1	1.5	80.2	0.065	0.020	0.24
21.	Rear Legs Set	RST	1.30	0.47	25.3	0.2	2.2	72.4	0.096	0.024	−0.28
22.	Udder Texture	UTX	1.19	0.40	24.4	0.2	3.2	72.2	0.186	0.034	0.63
23.	Fore Attachment	FAT	1.92	0.30	22.0	0.9	2.1	75.1	0.095	0.024	0.66
24.	Rear Attachment	RAT	1.88	0.43	25.4	0.1	2.5	72.0	0.117	0.026	0.62
25.	Median Suspensory Ligament	MSU	1.36	0.50	25.8	0.2	3.5	70.6	0.170	0.032	0.56
26.	Fore Teat Placement	FTP	2.03	0.49	23.4	0.2	3.6	72.9	0.166	0.032	0.42
27.	Rear Teat Placement	RTP	1.15	0.39	22.2	0.1	2.1	75.6	0.085	0.022	0.37

* Expected value: 3.5 for traits 2 to 9 and 2.0 for traits 10 to 27, respectively.
† Expected value: 1.04 for traits 2 to 9 and 0.58 for traits 10 to 27, respectively.
§ Approximate large sample standard error (= lower bound) of h².

sires' breeding value were calculated for 223 sires with 1150 sons. For eighty bulls with fifteen or more effective daughters, type proofs were contrasted to corresponding production proofs (ABVs, January 1983) for milk-yield, and fat-yield and content.

RESULTS AND DISCUSSION

As Table 1 shows, herd-round-classifier effects explained between 18 per cent (BON) and 37 per cent (TSC) of total sums of squares. Age at classification accounted for 5.8 per cent (CAP) to 2.4 per cent (STA) for traits related to body size and 1.6 per cent or less otherwise. Heritability (h^2) estimates ranging from 44 per cent (TSC), 42 per cent (STA), and 40 per cent (DCH) to 10 per cent or less for F&L, RHL, RST, BON, and RTP were on average higher than corresponding 'all-lactation' values (see Bowden 1982 for references). Sire-son regressions showed good agreement with their expected values. Little association was found between proofs for type and production.

ACKNOWLEDGMENTS

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