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Cattle Breed Evaluation at the U.S. Meat Animal Research Centre and implications for commercial beef farmers

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ABSTRACT

Since 1969, 36 sire breeds have been evaluated for topcross performance in a series of experiments (Cycles) in the Germ Plasm Evaluation (GPE) Program. In Cycle VII, the 7 most prominent U.S. beef breeds (3 British breeds: Angus, Hereford, Red Angus; and 4 Continental European breeds: Simmental, Gelbvieh, Charolais, Limousin), comprising 83% of U.S. breed association registrations, are being evaluated. In the 1970's, Continental breeds had greater growth rates and were heavier at weaning, yearling, and maturity. Today British breeds in the U.S. are comparable to Continental breeds for these traits. Steers of Continental sire breeds still excel in retail product yield (%), but those of British sire breeds excel in marbling, an important component of U.S. carcass value, and enjoy a slight ($P < .05$) advantage in tenderness over Continental breeds. Since 1973, current expected progeny differences (EPD) from breed associations and GPE data have been used to estimate breed differences annually. Since 1993 adjustment factors have been calculated to be added to the EPD of 16 breeds to calculate across-breed EPD for growth traits. Multi-breed genetic evaluations are being explored by scientists at three U.S. Universities (Cornell, Georgia, Colorado State). In Cycle VII, DNA was obtained on all sires, dams, and progeny produced in the F1 cross generation, grand progeny, and great-grand progeny to provide for parentage determination, and for identification and validation of quantitative trait loci (QTL). Alternative mating plans are being explored to include additional breeds (> 15), to provide more efficient estimates of direct and maternal breed and heterosis effects, and to facilitate use of QTL in multi-breed genetic evaluations. Our review describes how the U.S. beef cattle breeding industry continues to use the evolving GPE results, and how the Cycle VII DNA samples will be used to provide progressively more accurate predictors of sire EPD on a within-breed or between-breed basis, through groups such as the National Beef Cattle Evaluation Consortium. The opportunities for U.S. cattle breeders arising from new breeding technologies are described, including the potential for similar opportunities to be used in the New Zealand beef industry.

Keywords: beef cattle; breeds; genetic evaluation; QTL.

INTRODUCTION

Variation among and within breeds of cattle is an important genetic resource that can be utilized to increase efficiency of beef production and value of beef products. Genetic variation among breeds can be exploited by crossbreeding or formation of composite populations to match genetic potential with feed resources, the climatic environment, and market targets to meet consumer preferences. Genetic variation within breeds or composite populations can be exploited to make still further improvements in components of efficiency and quality of beef products. In this review, we shall focus on results from Cycle VII of the Germ Plasm Evaluation (GPE) Program in which the seven most prominent beef breeds in the United States (comprising 83% of registrations in breed associations; National Pedigreed Livestock Council, 2005-2006) are being evaluated, namely the Angus, Charolais, Gelbvieh, Hereford,

Limousin, Red Angus and Simmental breeds. The primary objective of this cycle of the program is to characterize quantitative and allelic genetic variation between and within breeds for traits that affect life cycle efficiency of beef production.

MATING PLAN

In Cycle VII of the GPE Program, semen from 22 Angus, 21 Hereford (12 polled, 9 horned), 21 Red Angus, 20 Simmental, 23 Gelbvieh, 23 Charolais, and 20 Limousin sires were used in AI matings to Angus, Hereford, and composite MARC III (1/4 each Angus, Hereford, Red Poll, and Pinzgauer) cows to produce F₁ crosses in the 1999 and 2000 birth years. About half of the sires used in each sire breed were chosen from lists of the 50 most widely used bulls in the breed, according to registrations over the most recent three-year period (a list of 100 sires was considered in Angus because of their relatively

large population size, and a list of 50 horned sires and 50 polled sires was considered in Herefords). The remaining sires chosen represented young herd sire prospects (non progeny-tested ≤ 3 years of age at the time of sampling). For the 2001 calf crop, additional F_1 progeny were produced by the same seven sire breeds out of Hereford and Angus dams, male progeny from which were kept intact and developed for use as F_1 bulls. The male calves born in 2001, sons of four widely used sires based on registrations in each of the seven breeds, were retained to use in natural matings over Cycle VII cows to produce F^2_1 progeny (F^2_1 progeny include an array of F_2 , and various 3- and 4-way crosses that result from exposing F_1 cross females by seven sire breeds and straightbred Angus and Hereford females to F_1 cross bulls by the same seven sire breeds) in a subsequent phase of the experiment.

In the years 1999 and 2000 combined, about 199 progeny were born and 193 progeny were weaned per sire breed. Male calves were castrated shortly after birth and evaluated for efficiency of postweaning growth from about 200-445 days of age, and then slaughtered for evaluation of carcass and meat characteristics including tenderness of steaks aged to 14 days *post mortem*. About 95 F_1 females per sire breed were evaluated for postweaning growth, age at puberty, and then were mated to MARC III bulls to produce their first calves as 2-year-olds and second calves as 3-year-olds in 2001 and 2002. Subsequently, at 3 through 8 years of age (2003-2008), females have been or will be exposed to the F_1 bulls born in 2001 in natural service multi-sire matings to produce F^2_1 matings. Details of management are described by Cundiff *et al.* (2004).

COMPARISON OF SEVEN PROMINENT BEEF BREEDS IN THE U.S.

Preweaning traits

Breed of sire means for pre-weaning traits of F_1 calves are shown in Table 1, reflecting half of the direct breed effects among these seven prominent breeds. Breed of sire means are shown for percentage calf crop born and weaned per cow exposed, calving difficulty score, percentage unassisted births, birth weight, and 200-day weaning weight, for the F_1 females calving at 2 years of age (Table 2) and at 3-6 years of age (Table 3). Differences between sire breed means shown in Tables 2 and 3 reflect $\frac{1}{4}$ of the direct and $\frac{1}{2}$ of the maternal breed effects among the seven prominent sire breeds.

Angus and Red Angus sired calves required less assistance at calving than those by other British or Continental European sire breeds (Cundiff *et al.*,

2004). Even so, calving ease has improved significantly for calves sired by Continental European breeds, especially Simmental and Gelbvieh, relative to those by British breeds since the Continental European breeds were first introduced into the U.S and evaluated in Cycles I and II of the GPE Program. Sire breed-of-calf differences for birth weight between Continental European and British breeds are less than half as great in recent years as they were 30 years earlier (Cundiff *et al.*, 1986). Sire breed-of-dam differences for calving ease and birth weight for 2-year-old first-calf heifers' progeny are not significant today, reflecting significant improvement in calving ease for Continental breeds relative to British breeds over a 30-year period. Simmental have made the most improvement in calving ease for 2-year-old first-calf heifers. In Cycle I, Simmental-sired 2-year-old females required 6% more assistance than Hereford-Angus reciprocal crosses. In Cycle VII, Simmental sired 2-year-old females required 11% less assistance than 2-year-old Hereford- and Angus-sired crosses. These results, consistent with genetic trends for expected progeny differences (EPD) for birth weight and calving ease reported by breed associations, indicate that Continental European breeds, and especially Simmental which was the first breed to implement EPD for calving ease, have emphasized selection for components of calving ease relatively more than British breeds during this time span.

For 200-day weaning weight, differences among sire breeds were significant for direct (Table 1) and total maternal breed effects (Tables 2 and 3). Continental European breeds that were originally selected for milk production in dual-purpose milk and meat production systems (Simmental and Gelbvieh) still wean the heaviest calves (Tables 2 and 3). However, mean differences between British breeds (Hereford and Angus) and Continental European breeds (Simmental, Gelbvieh, Limousin, and Charolais) are about a quarter as great for direct breed effects (2.5 kg *vs.* 10 kg) and 40% as great for maternal breed effects (4.5 kg *vs.* 11 kg) in the current evaluation as they were 30 years earlier. Differences in reproductive rate (calf crop born and weaned, Tables 2 and 3) and calf survival (for direct effects see Table 1, and total maternal effects see Tables 2 and 3) were not significant in Cycle VII, just as they were not significant in Cycles I or II, 30 years earlier.

Postweaning growth and efficiency

Following weaning at about 202 days of age and an additional adjustment period of about 30

Table 1: Least squares means by breed of sire for preweaning traits of F₁ calves by seven prominent sire breeds in the U.S.

Sire breed of calf	No. calves	Calvings unassist. %	Calving diff. sc	Birth wt. (kg)	200-dwt. (kg)
Hereford	190	95.6	1.24	41.0	237.7
Angus	189	99.6	1.01	38.1	241.9
Red Angus	206	99.1	1.06	38.3	238.7
Simmental	201	97.7	1.10	41.8	251.0
Gelbvieh	209	97.8	1.10	40.2	242.2
Limousin	200	97.6	1.13	40.6	235.3
Charolais	199	92.8	1.40	42.5	245.0
LSD < .05		3.6	.21	1.5	6.4

Table 2: Least square means by breed of dams sire for reproduction and maternal traits of F₁ females producing their first calves at 2 years of age (2001 and 2002).

Sire breed of female	No.	Calf crop		Calving diff. score	Unassist. Births %	Birth Wt (kg)	200-d wt. per calf (kg)
		Born %	Wnd. %				
Hereford	80	92	70	1.9	74	37.0	187.4
Angus	84	83	76	2.0	72	36.2	192.2
Red Angus	104	86	76	2.2	68	35.5	188.1
Simmental	98	86	69	1.5	86	36.1	200.3
Gelbvieh	109	79	68	2.2	64	37.9	202.9
Limousin	109	85	73	2.0	68	36.4	194.7
Charolais	97	87	73	2.1	69	37.0	195.2
LSD < .05		14	15	.6	19	2.0	9.5

Table 3: Least squares mean by breed of dams sire for reproduction and maternal traits of F₁ females producing calves at 3-6 Years of Age (2002-2005 calf crops).

Sire breed of female	No.	Calf crop		Calving diff. score	Unassist. Births %	Birth Wt. (kg)	200-d wt. per calf (kg)
		Born %	Wnd. %				
Hereford	244	94	91	1.16	96.9	43.0	233.1
Angus	241	95	89	1.03	98.4	41.2	239.0
Red Angus	288	89	85	1.19	96.4	40.7	234.8
Simmental	294	90	87	1.02	98.9	41.8	249.4
Gelbvieh	305	90	86	1.11	97.8	42.3	248.8
Limousin	303	95	91	1.06	98.7	42.7	240.1
Charolais	293	90	86	1.30	94.5	42.3	243.9
LSD < .05		7	8	.21	3.7	1.6	8.7

Table 4: Least squares means by breed of sire for final weight and carcass traits of F₁ steers taken to a constant age (445 days) at slaughter.

Sire breed	No.	Postweaning average daily gain (kg)	Final wt. (kg)	Retail product		Marbling sc	USDA Choice %	WB shear (kg)
				%	(kg)			
Hereford	97	1.47	599.6	60.7	217.8	526	65.4	4.12
Angus	98	1.51	619.3	59.2	221.3	584	87.6	4.02
Red Angus	93	1.48	604.7	59.1	215.1	590	89.9	4.15
Simmental	92	1.48	617.9	63.0	237.0	527	65.7	4.30
Gelbvieh	90	1.41	595.0	63.8	231.1	506	57.7	4.51
Limousin	84	1.41	583.0	63.7	228.5	504	56.9	4.31
Charolais	95	1.46	611.2	63.5	237.3	517	61.9	4.34
LSD < .05		.06	18.4	1.3	7.3	28	10.7	0.31

days, steers were assigned to replicated pens within sire breed and fed separately by sire breed. Details of feeding and management are described by Cundiff *et al.* (2004). Steers were sampled randomly from within each pen and slaughtered serially in four or five slaughter groups spanning about 48 days to assess carcass traits and efficiency of gains in alternative intervals of evaluation (0 days on feed to the mean number of days fed = 187 days), weight intervals (340 to 590 kg, an initial and final weight bracketed by all breed groups), a USDA Quality grade of Low Choice (0 days on feed to the time each breed group expressed a small degree of marbling [marbling score = 500]), a fat thickness endpoint (0 days on feed to the time each breed group expressed the mean fat thickness of 1.1 cm), a fat trim endpoint (0 days on feed to the time each breed group expressed the mean fat trim of 24.8%), and a retail product endpoint (0 days until each breed group produced the mean weight of totally trimmed-boneless retail product of about 225 kg).

Breed of sire means for postweaning average daily gain, final slaughter weight at 445 days of age, and several carcass traits are shown in Table 4. Results indicate that today, progeny of British and Continental European breeds do not differ significantly in postweaning average daily gain or final live weight at 445 days of age. In evaluations conducted 30 years earlier, Continental European breeds had significantly faster average daily gains and were 1-3 standard deviations heavier at yearling ages. Results from Cycle VII are consistent with EPD genetic trends reported by the respective breed associations. The EPD genetic trends indicate that response to selection for growth to weaning or yearling ages has been about twice as great for British breeds as Continental European breeds (Table 5). As a result of these relative changes in growth rate, British and Continental European breeds no longer differ significantly in efficiency of post weaning gain to age or weight end-points (Table 6). However, to fatness endpoints (1.1 cm fat thickness, 25% carcass fat trim, or small degree of marbling [marbling score = 500]), progeny by British sire breeds are still significantly more efficient than those by Continental European sire breeds. To weight of retail product endpoints, (*i.e.* 225 kg), progeny by Continental European sire breeds were still significantly more efficient than progeny by British sire breeds.

Carcass traits

Sire breeds differed significantly ($P < .05$) for retail product yield (%) and weight, marbling, percentage grading USDA Low Choice or more,

and Warner Bratzler shear force at the average age of slaughter of 445 days (Table 4). Results indicate that differences between Continental European and British breeds for percentage of retail product, marbling, and tenderness remain nearly as great today as they were 30 years ago, a result that is not surprising because EPD for carcass traits have only been introduced for most breeds in recent years. Although, British and Continental European breeds do not differ significantly in live weight at the same age, Continental European sire breeds still produced progeny with significantly heavier retail product (15 kg) due to higher retail product yields (3.9%) at the same age (445 days) than British sire breeds. Steers by British sire breeds had significantly greater marbling and a higher percentage of carcasses grading USDA Choice than those by Continental European sire breeds.

Reproduction and maternal performance

Breed of sire means for 400-day weight, 550-day weight, 18-month height, frame score, age at puberty, and pregnancy rate are shown in Table 7. Effects of sire breed were significant for all traits summarized except pregnancy rate. Results indicate that female progeny of Continental European sire breeds are not necessarily heavier or taller at yearling ages than those by British breeds. On the contrary, Gelbvieh sired females were significantly lighter than Angus, Red Angus, and Hereford sired breeds at 400 days, but not significantly different at 550 days of age. Sire breeds that have had a long history of selection for milk production (*e.g.* Simmental and Gelbvieh), still produced females that reached puberty at younger ages (average 329 days) than those that have not been selected for milk production (Limousin, Charolais, Hereford, Angus or Red Angus: average 346 days). Differences among sire breeds for pregnancy rate of yearling females were not significant. Similarly, differences among sire breeds for reproduction rates at 2 years of age (Table 2) or at 3-6 years of age (Table 3) were not significant in recent or earlier evaluations.

Cow size

Breed of sire means for height, condition score (1 for very thin to 9 for very fat), weight, and weight adjusted for condition score of the F₁ females are shown in Table 8. Females by Continental European and British breed sires did not differ significantly in estimates of cow weight or height at 5 yrs of age, with one exception: Gelbvieh are significantly lighter than females by other sire breeds. Results indicate that the reduced cow weight for Gelbvieh is associated with strong negative genetic trends for birth weight in the

Table 5: Mean annual change in estimated progeny difference (EPD) for growth traits (kg/yr)^a.

Sire breed	Birth weight	Weaning weight	Yearling weight	Milk
Hereford (1979 – 2004)	0.069	0.42	0.86	0.23
Angus (1979-2004)	0.047	0.68	1.29	0.34
Mean	0.058	0.55	1.08	0.28
Simmental (1985-2004)	-0.022	0.24	0.50	-0.03
Gelbvieh (1984-2004)	-0.035	0.11	0.36	0.02
Charolais (1990-2002)	0.011	0.41	0.60	0.04
Limousin (1985-2005)	0.024	0.40	0.73	0.12
Mean	-0.006	0.29	0.55	0.04

^aTaken from EPD genetic trends available on web sites of the American Hereford Association, American Angus Association, American Gelbvieh Association, American International Charolais Association, the American Limousin Foundation, and personal communication with the American Simmental Association.

Table 6: Breed of sire means for feed efficiency (live weight gain, g/MJ) for alternative intervals and endpoints.

Sire breed	Time 187d	Weight change 340 to 590 kg	Fat thick. 1.1 cm	Marbling score 500	Fat trim 24.8%	Retail product weight 225 kg
Hereford	14.16	13.82	14.47	14.00	14.45	13.64
Angus	13.54	13.42	14.23	14.59	14.31	13.18
Red Angus	13.33	13.04	13.83	14.43	14.00	12.58
Simmental	13.73	13.78	13.30	13.56	13.37	14.43
Gelbvieh	13.25	13.04	12.87	12.82	12.82	13.52
Limousin	13.90	13.35	13.49	13.28	13.54	14.11
Charolais	13.04	13.04	12.49	12.70	12.56	13.73
LSD < .05	0.89	1.03	0.81	0.79	0.79	1.00

Table 7: Least squares means by breed of sire for growth and puberty traits of heifers in Cycle VII of the GPE Program (1999-2000 calf crops).

Sire breed of female	No.	400-d weight (kg)	550-dayweight (kg)	18-mo height (cm)	Frame score	Age at puberty (d)	Pregnancy Rate (%)
Hereford	81	381.5	430.9	128.4	5.5	357	94
Angus	85	394.2	424.5	127.2	5.3	343	88
Red Angus	106	393.7	432.5	126.9	5.2	342	91
Simmental	103	385.3	435.8	130.2	5.9	342	90
Gelbvieh	111	366.1	418.4	128.8	5.6	329	83
Limousin	109	373.6	423.3	129.9	5.8	377	87
Charolais	103	375.4	430.7	129.5	5.8	358	91
LSD ≤ .05		14.0	14.7	1.6	.3	16	13

Table 8: Least squares means by breed of sire for height, condition score, and weight of F₁ cows (adjusted for condition score) at 5 years of age.

Breed	No.	Five-yr-old height, cm	Five-yr-old cond. Score ^a	Five-year-old Weight ^a (kg)
Hereford	56	135.4	7.00	679 (644)
Angus	62	134.4	7.22	681 (640)
Red Angus	68	134.4	7.40	685 (639)
Simmental	70	137.4	6.98	669 (637)
Gelbvieh	68	135.0	6.77	627 (600)
Limousin	80	137.4	6.95	663 (631)
Charolais	69	137.3	7.09	669 (622)
LSD<.05		0.8	0.28	29 (26)

^aCondition scores were assigned on a scale from 1 = very thin to 9 = very fat.

^bEstimates for Hereford, Angus, and Red Angus were adjusted to the level of heterosis expected in three-way F₁ crosses (estimate of 18.9 kg was added to five-year-old weight and 16.6 kg was added to five-year-old weight adjusted for condition score). Means shown in parentheses were adjusted to a condition score of 5.5. Actual condition scores for the F₁ cows were relatively high (mean = 7.0) because their calves were weaned about 40 days earlier than usual due to drought conditions.

Gelbvieh breed, contrasted to slightly positive or null genetic trends for birth weight in other breeds. These results are consistent with preliminary results from a selection experiment at the USMARC, in which response to selection for lighter birth weight and heavier yearling weight, reduced birth weight and mature cow weight significantly while yearling weight was increased (Bennett, G.L. pers. comm.). The lack of differences among breeds for cow weight and height, contrast sharply with comparisons made 30 years earlier when cows by Continental European sire breeds were on average 6 cm (4.5%) taller and about 33 kg (4.8%) heavier than those by British sire breeds.

ACROSS BREED AND MULTI-BREED EVALUATIONS

Expected progeny differences (EPD) have provided an effective tool for significant genetic change in most breeds for birth weight, direct and maternal weaning weight, and yearling weight. EPD technology has had a greater impact on growth than other traits because they have been recorded over a longer period of time. EPD for calving ease were introduced by the American Simmental Association in the early-1980's and by the American Gelbvieh Association in the mid-1980's. Most breeds have relied on use of direct (as opposed to maternal) birth weight EPD as the basis for genetic improvement in calving ease. By the mid-1990's EPD for scrotal circumference were included in genetic evaluations of the Hereford and Limousin breeds and they have been included in more recent evaluations of the Angus, South Devon, Charolais, Gelbvieh, Salers, and Beefmaster breeds. Some breeds have introduced EPD for stayability (Red Angus, Salers, and Gelbvieh), docility (Limousin and Salers), mature weight (Angus, Simmental, and Salers) and mature height (Angus, Limousin) in recent years. EPD for carcass traits were introduced in the late 1990's. Records on carcass traits were sparse, so EPD were not available for very many sires. However, with development and increased use of ultrasound technology, EPD for ribeye area, fat thickness, and intramuscular fat (marbling) have been provided for at least three years by 11 breeds (Angus, Red Angus, Hereford, Shorthorn, Limousin, Simmental, Charolais, Gelbvieh, Maine Anjou, Salers, and Brangus). Recently we estimated coefficients of regression for carcass traits in steers ($n = 2,602$) produced in the GPE Program at the USMARC on EPD for their sires (402 sires) from 2005 genetic evaluations for these 11 breeds (Van Vleck *et al.*, 2007). Regression coefficients of 1.07

$\pm .17$ for marbling, $2.8 \pm .35$ for fat thickness, and $0.88 \pm .19$ for ribeye area indicated that that EPD can predict with reasonable precision genetic variation in these carcass traits.

However, EPD can not be used to compare individuals of different breeds because they have been computed using separate data sets and analyses for each breed. Also, each breed has its own base point (EPD = 0.00). We have developed procedures to estimate adjustment factors that can be added to within-breed EPD to estimate across breed expected progeny differences (AB-EPD). The basic steps were given by Notter & Cundiff (1991) with refinements by Nunez-Dominguez *et al.* (1993), Cundiff (1994), Van Vleck & Cundiff (2006). Each year data that have been obtained over all the years in the GPE Program are combined with current EPD from breed associations to estimate factors that can be added to EPD for individuals of 16 different breeds for across breed comparisons. The AB-EPD for birth weight, weaning weight, yearling weight, and milking ability (as reflected in progeny weaning weights) are most useful to commercial producers purchasing bulls of two or more breeds to use in systematic crossbreeding programs.

In recent years, effectiveness of genetic evaluations has been improved by development and use of multi-breed genetic evaluations (BIF, 2002; Pollak & Quaas, 2005). The Multi-breed genetic evaluations have been an important development, especially for producers of F_1 seedstock and composite breeds. In these evaluations, EPD of the contributing breeds and composite populations can be expressed on a common base. Accuracy of this approach is highly dependent on seedstock producers that have cattle of multiple breeds and the assumption that they are managed comparably in contemporary groups. Multi-breed evaluations utilize a Bayesian approach of analysis that depend on prior estimates of heterosis and breed effects reported in the scientific literature (*e.g.* Long, 1980; Gregory & Cundiff, 1980; Cundiff *et al.*, 1993; Gregory *et al.*, 1999). A number of breed associations have recently asked for an industry-wide multi-breed national evaluation of beef cattle. The National Beef Cattle Evaluation Consortium (NBCEC) has begun developing prototypes for such evaluations and a number of breeds have contributed to this prototype. While the industry is unlikely to adopt a single National Cattle Evaluation in the near future, a development that would eliminate the need for AB-EPD factors, it is likely that many single breed genetic evaluations will be consolidated into fewer multi-breed evaluations in the next several years.

Pollak & Quaas (2005) argued, based on Rodriguez-Almeida *et al.* (1997), that multi-breed genetic evaluations should incorporate experimental data, either directly or as Bayesian priors. Otherwise various effects that are confounded such as direct and maternal breed and heterosis effects are likely to be partitioned poorly and bias EPD estimates. Diallel crossing experiments conducted over at least two generations efficiently provide for partitioning of direct and maternal heterosis and breed effects. The scientific literature contains many estimates of general heterosis but estimates for many specific crosses have not been reported, or at best are poorly estimated. A significant number of estimates have been reported for British x British breeds (*e.g.* Hereford, Angus, Shorthorn, and Red Poll) and for crosses of certain British breeds with the Brahman breed (*e.g.* Long, 1980). However, only a few estimates are available for specific crosses of British X Continental European breed crosses, Continental European X *Bos indicus* breeds, not to mention tropically adapted breeds that have recently been introduced into North America (*e.g.* Tuli, Boran, Senepol, and Romosinuano). Furthermore, as noted above, breed effects change over time as a result of differential selection emphasis. Thus, it is important to estimate current direct and maternal breed effects on a continuing basis, either by experimentation or by use of current EPD for sires sampled in previous experiments to adjust to current breed average EPD, to account for genetic trends (*e.g.* Notter & Cundiff, 1991).

We are altering our mating plans in the GPE Program at the USMARC to provide contemporary contrasts of a variety of crosses to more effectively partition direct and maternal breed and specific heterosis effects. In previous cycles of the GPE Program we have evaluated reproduction and maternal performance of F₁ females by mating them to produce 3-way crosses by sires of a breed other than that represented in any of the F₁ cross females (*e.g.* Braunvieh were used in Cycle I, Simmental in Cycle II, III, and IV, and Charolais were used in Cycles V, VI, and VIII on females calving at 3-8 years of age). In cycle VII, the F₁ females by seven prominent sire breeds are being mated to F₁ cross bulls by the same seven sire breeds out of Hereford and Angus dams in natural service multi-sire matings to produce F₂¹ progeny. In each of four breeding pastures per year, about 150-160 cows are run together and exposed to seven F₁ bulls, each a son of one of the seven prominent sire breeds. The F₂¹ females are being retained for evaluation of reproduction and maternal performance when mated to additional F₁

sires to produce fourth generation progeny. All resulting F₂¹ and fourth generation progeny are being genotyped to determine parentage. The variety of resulting genotypes include an array of F₂s (*e.g.* HA x HA), various backcrosses (*e.g.* HA x A, SH x H), partial backcrosses (*e.g.* HA x SA, HA x GH, *etc.*), and 4-way cross (*e.g.* SA x LH) progeny which will be pooled with data from previous phases of the experiment (*e.g.* purebred Hereford and Angus, F₁ crosses, 3-way crosses) to estimate direct and maternal breed and heterosis effects. Breed and heterosis effects will be estimated by fitting a linear regression coefficient for each dependent variable (*e.g.* weight) on the proportion of direct or maternal breed effect (*e.g.* 0.0, 0.25, 0.5, 1.0 Hereford, *etc.*) or heterosis effect (*e.g.* purebred = 0.0, F₁cross = 1.0, backcross = .5 *etc.*).

My colleagues are planning additional changes in mating plans. Simulation analyses are being conducted to determine the optimum mating design for estimation of direct and maternal breed and heterosis effects. They are considering including 16-20 breeds in the program in a series of matings that include all pure breeds (or backcross matings to grade up to purebreds), reciprocal F₁ crosses or backcrosses to partition direct and maternal breed effects, as well as additional F₂¹ matings. The intent is to optimize the mating structure to facilitate more effective multi-breed genetic evaluations. Data are being obtained on a comprehensive series of traits characterizing calving ease, pre-weaning growth, rate and efficiency of post-weaning growth, carcass composition, meat quality, age and weight at puberty, reproduction rate, cow size, and longevity consistent with previous cycles of the GPE Program and following protocols that are consistent with industry practice.

MOLECULAR GENETIC VARIATION AMONG AND WITHIN BREEDS

Another objective of the GPE Program is to identify and fine-map QTL regions that affect quality of beef and efficiency of production. DNA has been obtained on parents, progeny, and grand-progeny produced in Cycles V, VI, and VIII of the program. However, the primary populations supporting this effort are those being produced in Cycle VII. DNA has been obtained on all sires, dams, F₁, F₂¹ and fourth generation (F₁ x F₂¹) progeny described above. These matings result in three- and four-generation families that will be used to identify or fine-map QTL, in collaboration with other scientists at USMARC. Phenotypes are being recorded on approximately 2,750 F₂¹ animals

produced from 2003 through 2007.

These F_1 progeny provide a resource for collaborative efforts of scientists in the nutrition, carcass and meats, reproduction, and animal health units working in the comprehensive genomics program at USMARC to identify QTL and genes affecting important traits in beef cattle. The F^2_1 steers are being individually fed to measure intake, feed efficiency, and their components. Comprehensive carcass and meat data are being obtained on the steers to measure carcass composition and tenderness traits. The F^2_1 females are being retained to measure traits related to reproduction and maternal traits in females when they are mated to additional F_1 sires.

QTL will be discovered by genotyping across the whole genome followed by combined linkage and disequilibrium analyses. Markers identified elsewhere will be validated by genotyping and association analyses. The sources of genomic information for these analyses are the linkage generated by sires in larger half sib families and the allele associations from smaller sire families and the F_1 dams which have a larger number of sires. Analyses utilizing variance components to evaluate linkage and association are most appropriate because there are many families.

Whatever form DNA testing takes, it is unlikely that it will thrive without being integrated into genetic evaluation systems to improve EPD estimates for important traits. For about a decade, my colleagues (Gregory, Echternkamp, Van Vleck, Allan and Thallman) have been using three QTL along with phenotypic records for twinning rate and ovulation rate recorded on pubertal heifers to improve prediction of breeding values for twinning rate in a population under selection for twinning rate at the U.S. Meat Animal Research Centre. We anticipate that similar methodology can be utilized in national cattle evaluations. Although, challenges in infrastructure and statistical methods remain to be resolved, beef cattle breeders will be simply unable to effectively integrate a myriad of DNA test results with the dozen or more EPD that are currently available to them for economically relevant traits. We are optimistic that decision support systems such as those described by Garrick (2005) can and will be developed to provide for this opportunity.

Experimentation has had a great impact on use of breeding systems that exploit heterosis and utilize breed differences to match genetic potential with the environment, feed resources and consumer preferences for lean and tender beef products. In the late 1960's, about 90% of the U.S. beef cows were straightbred Herefords, Angus, and Shorthorns. Today, it is estimated that 75% are

crossbred or composite cows. Reports of registrations in breed associations (National Pedigreed Livestock Council, 2005-2006) indicate that at the present time, about 60% of the germ plasm used in U.S. beef production originates from breeds of British origin (primarily Angus, Hereford, Red Angus, and Shorthorn), 32% from breeds of Continental European origin (primarily Charolais, Simmental, Limousin, and Gelbvieh), and 8% of American origin (e.g. Brahman, Santa Gertrudis, Brangus, and Beefmaster). Experimentation with target species such as beef cattle will be even more important in future development of technology for genetic improvement than it has been in the past. It is difficult to measure components of complex traits such as feed efficiency, tenderness and other quality attributes of beef products, resistance to diseases, age at puberty and other reproduction traits in industry herds. Complex traits such as these can be measured in experimental populations. If the experimental populations are representative of those used in the industry, algorithms can be derived to compute EPD based on DNA and phenotypic data obtained in experimental herds and only DNA data obtained in industry herds. Once sufficient markers are identified to account for significant genetic variation in seedstock populations, significant progress can be made from selection for traits that can only be measured in intensively managed experimental populations.

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