

Herefords in the Germplasm Evaluation Program at the U.S. Meat Animal Research Center

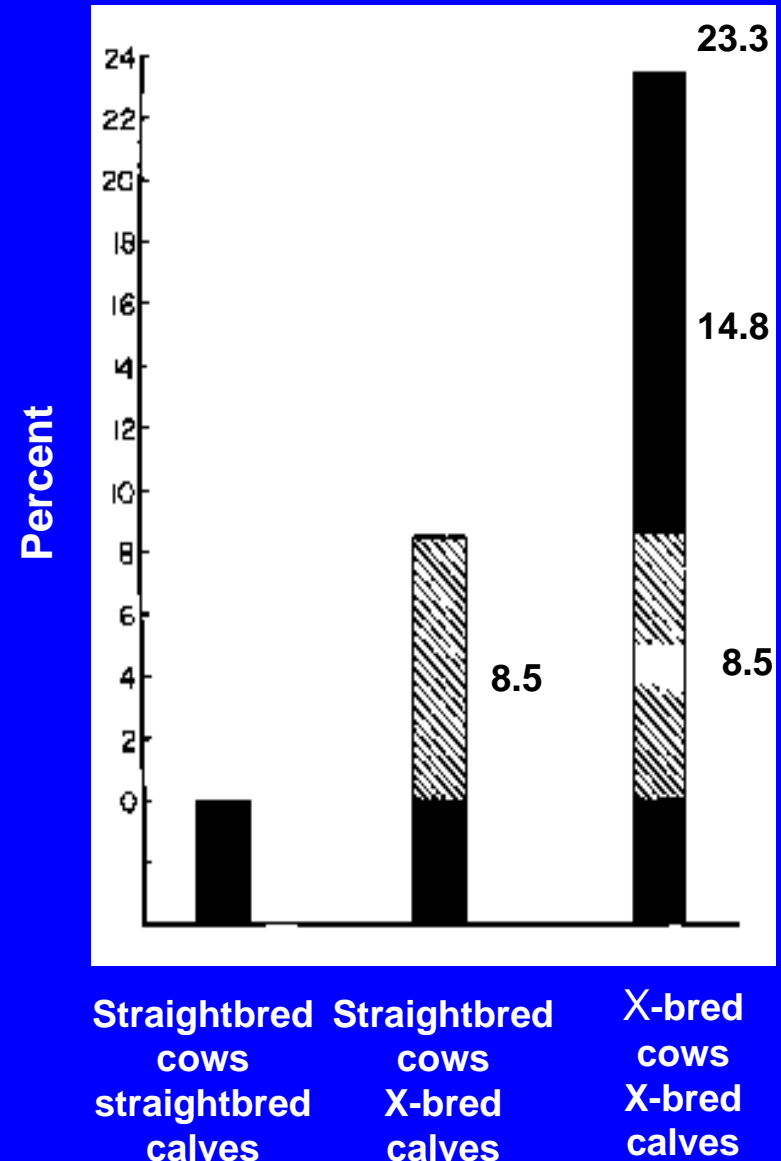
Larry V. Cundiff
MARC-ARS-USDA
Clay Center, NE

American Hereford Association
Young Guns Hereford Conference
U. S. Meat Animal Research Center
Clay Center, NE
August 26, 2005

Heterosis

- Heterosis increases production per cow 20 to 25% in *Bos taurus* x *Bos taurus* crosses and at least 50% in *Bos indicus* x *Bos taurus* crosses in subtropical regions.
- More than half of this effect is dependent on use of crossbred cows.

Weight of Calf Weaned Per Cow Exposed To Breeding



SIRE BREEDS USED TO PRODUCE F₁ CROSSES WITH ANGUS AND HEREFORD DAMS IN THE GERMPLOSM EVALUATION PROGRAM AT MARC^a

Cycle I 70-72	Cycle II 73-74	Cycle III 75-76	Cycle IV 86-90	Cycle V 92-94	Cycle VI 97-98	Cycle VII 99-00	Cycle VIII 01-02
Hereford Angus Jersey S. Devon Limousin Simmental Charolais	Hereford Angus Red Poll Braunvieh Gelbvieh Maine Anj. Chianina	Hereford Angus Brahman Sahiwal Pinzgauer Tarentaise	Hereford Angus Longhorn Salers Galloway Nellore Shorthorn Piedmontese Charolais Gelbvieh Pinzgauer	Hereford Angus Tuli Boran Belg. Blue Brahman Piedmontese	Hereford Angus Wagyu Norweg. Red Sw. Red&Wh. Friesian	Hereford Angus Red Angus Limousin Charolais Simmental Gelbvieh	Hereford Angus Beefmaster Brangus Bonsmara Romosinuano

a

Sire breeds mated to Angus and Hereford females, Composite MARC III (1/4 Angus, Hereford, Red Poll and Pinzgauer) cows were also included in Cycles V, VI, and VII.

BEEF BREED REGISTRATIONS

National Pedigreed Livestock Council, 2003-2004

Breed	Registrations	%	Breed	Registrations	%
Angus	281,965	40.0	Brahman	11,000	1.6
Hereford	69,316	9.8	Salers	10,286	1.5
Charolais	55,034	7.8	Santa Gertrudis	7,500	1.1
Limousin	49,600	7.0	Longhorn	7,459	1.1
Simmental	45,000	6.4	Chianina	6,679	.9
Red Angus	42,178	6.0	Braunvieh	4,100	.6
Gelbvieh	31,664	4.5	Corriente	3,211	.5
Shorthorn	22,430	3.2	Tarentaise	1,600	.2
Brangus	22,311	3.2	Highland	1,500	.2
Beefmaster	21,242	3.0	Pinzgauer	664	.1
Maine Anjou	12,544	2.2	TOTAL	707,283	100

SIRE BREED MEANS FOR FINAL WEIGHT AND CARCASS TRAITS OF F1 STEERS (445 DAYS)

Sire Breed	N	Final wt lb	Retail <u>product</u> %	lb	Marb- ling sc	USDA Choice %	WB shear lb
Hereford	97	1322	60.7	480	526	70	9.1
Angus	98	1365	59.2	488	584	95	8.9
Red Angus	93	1333	59.1	474	590	93	9.2
Simmental	92	1363	63.0	522	528	66	9.5
Gelbvieh	90	1312	63.8	509	506	58	9.9
Limousin	84	1286	63.7	504	504	57	9.5
Charolais	95	1349	63.7	523	517	62	9.6
LSD \leq .05		40	1.3	16	17	0.7	0.6

SIRE BREED MEANS FOR REPRODUCTION AND MATERNAL TRAITS OF F1 FEMALES MATED TO PRODUCE THEIR FIRST CALVES AT 3-5 YEARS OF AGE (2002-2004)

Sire Breed of female	No rec.	Calf crop		Calving diff. score	Unassist. births %	Birth wt. lb	200-d wt per calf cow exp	
		born %	wnd. %				lb	lb
F – test		ns	ns	ns	ns	ns	**	ns
Hereford	180	96	93	1.12	97.9	91.7	498	464
Angus	175	94	90	1.01	100.0	88.5	515	460
Red Angus	205	91	87	1.23	95.5	87.2	503	441
Simmental	214	90	88	1.03	99.1	88.2	535	463
Gelbvieh	220	89	86	1.07	98.8	89.8	527	452
Limousin	219	94	89	1.02	99.6	90.2	513	456
Charolais	210	94	91	1.18	97.2	91.3	522	475
LSD \leq .05		7	8	--	--	--	10	45

Maternal performance of Hereford, Angus, Red Angus, Simmental, Gelbvieh, Limousin, and Charolais sired two-year old females

Differences in reproduction rate, and calf survival to weaning not significant.

Contrasts between British (H and A) and Continental European breeds (S, G, L, and C) are about 1/4th as great for direct (5.5 vs 22 lb) and half as great for maternal (10 vs. 17 lb) breed effects in the current evaluation as they were to 30 years ago.



Four-yr-old cow weights unadjusted and adjusted for condition score

Breed Group	Unadjusted Wt, lb	Adjusted Wt, lb
F test	*	*
Hereford	1360^a	1348^a
Angus	1348^a	1342^{ab}
Red Angus	1342^a	1321^{ab}
Simmental	1357^a	1353^a
Gelbvieh	1273^b	1282^b
Limousin	1320^{ab}	1330^{ab}
Charolais	1344^a	1339^{ab}
LSD <.05	54	51

* P < .05

Genomics Populations (Cycle VII)

- Identify and validate QTL and favorable alleles in populations directly tied to industry
- Incorporate into EPDs using multi-loci/multi-trait genetic prediction

