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Beef x dairy matings: opportunities to enhance value and genetic evaluation systems

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Introduction

Widespread adoption of sex-sorted dairy semen has revolutionized genetic management in the dairy sector. According to the National Association of Animal Breeders (NAAB, 2025), U.S. dairy producers used 9.9 million units of gender-sorted semen out of 16.6 million total dairy semen units sold. This efficiency allows producers to generate replacement heifers with a small fraction of inseminations, freeing the remainder for terminal crossbreeding with beef sires. In 2024, U.S. dairy herds utilized 7.9 million units of beef semen (NAAB, 2025). Concurrent contraction of the U.S. beef cow herd has intensified supply–demand dynamics, driving strong market demand for high-quality beef × dairy calves. More than 4 million beef × dairy and dairy feeder cattle are projected to enter the U.S. beef supply chain in 2025, with approximately two-thirds sired by beef bulls (Prins, 2025). Overall, the dairy industry now contributes about 20% of animals to the U.S. beef supply chain.

This integrated beef-on-dairy system has boosted domestic beef semen sales (NAAB, 2025), substantially increased dairy calf revenue, and reduced break-even costs for fluid milk production (Gambonini, 2025). Revenues from beef × dairy calves and cull dairy cows are projected to add $5/cwt to herd revenue, up from ~$1/cwt in 2020, with 51% of the added margin from beef × dairy calves. In 2026, beef revenues are forecast to contribute $4.50–$6/cwt to milk margin and to account for all farm-level profit, potentially offsetting negative margins from milk sales (Gambonini, 2025).

Intensive management of dairy-origin calves—from individual hutches and group housing to conventional feedlot finishing—offers a powerful platform for large-scale phenotypic data collection. Traits including calving ease, birth weight, growth rate, feed efficiency, carcass characteristics, meat quality, animal health, and welfare can be systematically recorded. This extensive dataset presents unique opportunities to accelerate genetic improvement in beef × dairy cattle and native beef populations, as well as to validate genomic predictions across diverse environments.

Beyond current economic gains, additional progress is possible through: 1) development of customized, sector-specific selection indexes for beef sires used on dairy females; 2) targeted breeding of beef bulls that complement dairy cow genetics; and 3) selection of dairy sires for superior carcass and end-product merit in terminal progeny, in addition to milk production traits. Strategies for incorporating commercial pedigree and performance data into national cattle evaluation systems and constructing customized indexes are described below.

Materials & Methods

Beef x dairy carcass trait evaluation prototype. Pedigree and performance data on single-source, commercially produced beef × dairy crossbred calves (n = 57,993) were supplied by the North American Limousin Foundation (NALF). Records included animal EID, birthdate, dam ID, sire ID, NAAB semen cane code of sire of dam and dam's maternal great-grandsire, feedlot and pen identification, on-feed and slaughter dates, and conventional carcass data. Contemporary groups were formed by animal age, feedlot arrival and slaughter dates (constant days on feed within group), feedlot location, and pen ID. After edits, 27,532 records remained, forming 924 unique groups averaging 33 head (range 1–226). The dataset yielded a 26-

generation pedigree of 50,344 animals, including 1,874 sires, 886 paternal grandsires, and 1,294 maternal grandsires. Large sire groups were removed to minimize sire × contemporary group confounding.

Uni- and multivariate mixed sire models were fitted for hot carcass weight (HCW), ribeye area (REA), marbling score (MARB), and 12th rib fat thickness (BF). Models included fixed effects for gender, breed fraction, heterozygosity, linear and quadratic covariates for age at slaughter (days), and contemporary group. Variance components, fixed effect solutions, and animal breeding values were estimated using ASReml version 4.2. Breed and gender contrasts were computed.

These models served as prototypes for a national cattle evaluation using commercial beef × dairy carcass records. NALF now supplies nearly 350,000 carcass records weekly to International Genetic Solutions (IGS) carcass evaluation (Anderson, M., 2026, personal communication). For IGS, animal pedigrees were extended from commercial data and merged with Council on Dairy Cattle Breeding (CDCB) triannual evaluation results (file 38alloff.zip), including cross-references mapping NAAB cane codes to Holstein and Jersey registration/pedigree data. Models were refined and deployed by IGS in routine carcass trait evaluations (Boldt, 2025). Holstein (n = 170) and Jersey (n = 192) sire EPDs (HCW accuracy > 0.30) from the January 13, 2026 IGS evaluation were summarized.

iGENDEC customized terminal sire index construction. Customized selection indexes were developed for Limousin and Holstein sires using the iGENDEC platform (Spangler et al., 2022). iGENDEC is a web-based tool for constructing customized indexes, featuring a stochastic simulation of the North American beef industry with separate modules for beef × beef and beef × dairy systems.

The beef × dairy module was parameterized using publicly available data summarized over 2015–2025, including USDA dressed beef prices, quality/yield-grade premiums/discounts, and beef × dairy performance from Basiel et al. (2025). Resulting marginal economic values (MEV) were used to compute terminal sire indexes for dairy sires (using IGS carcass EPDs) and Limousin sires in beef × dairy systems. Index value descriptive statistics were calculated.

Results & Discussion

Prototype carcass trait evaluation highlighted both expected and unanticipated challenges with commercial data, including missing observations, incomplete records, and coding inconsistencies. Given the large volume, high sire representation, and substantial contemporary groups, extensive record cleaning was avoided. Instead, the effort focused on optimal contemporary grouping. Commercial practices sorted calves by arrival weight into pens until full, resulting in variable days on feed within slaughter-date/pen groups despite narrow birthdate windows. Contemporary groups were thus constrained by days on feed.

Convergence issues arose from large contemporary groups dominated by a single sire (~20% of calves were from two sires, often mated to distinct cow breed groups). Removing these groups reduced sire × contemporary group confounding and improved model stability.

A key concern for IGS integration was trait definition and variance component similarity between beef × dairy and native beef data. Incorporating massive commercial data risked overpowering existing evaluations and causing unintended sire reranking if there was large divergence in variance component estimates or other interactions. Prototype analyses therefore examined heritabilities and genetic correlations relative to native beef literature.

Heritability and genetic correlation estimates from the prototype (Table 1) generally aligned with native beef literature values (Table 2; Marshal, 1994; Koots et al., 1994), supporting integration. The main exception was higher marbling heritability in beef × dairy cattle. Even

so, these similarities justified proceeding with beta development at IGS using the prototype grouping strategies and existing BOLT variance components.

Table 1. Heritabilities, covariances (below diagonal), and genetic correlations (above diagonal) with standard errors for hot carcass weight (HCW), marbling (MARB), ribeye area (REA) and 12th rib fat thickness (FT) for beef x dairy crossbred cattle.[1.]

Trait	HCW (SE)	MARB (SE)	REA (SE)	BF (SE)
HCW	**0.29 (**0.07)	0.50 (0.14)	-0.12 (0.19)	0.50 (0.14)
MARB	1262.8 (507.0)	**0.70 (0.14)**	-0.44 (0.15)	0.56 (0.12)
REA	-3.58 (5.53)	-29.02 (12.74)	**0.41 (0.10)**	-0.38 (0.16)
FT	1.80 (0.74)	4.55 (1.61)	-0.04 (0.02)	**0.51 (0.11)**

[1] h^2 from univariate analysis; r_g from bivariate analysis

Table 2. Literature values for heritability, phenotypic and genetic correlations of hot carcass weight (HCW), marbling (MARB), ribeye area (REA) and 12th rib fat thickness (FT).[1, 2.]

Trait	HCW	MARB	REA	FT
HCW	**0.41**	0.25	0.48	0.29
MARB	0.15	**0.35**	-0.21	0.35
REA	0.45	0.06	**0.37**	0.01
FT	0.37	0.24	-0.11	**0.44**

[1] Heritabilities on diagonal (bold); phenotypic correlations below diagonal; genetic correlations above diagonal.

[2] Heritability estimates from Marshal 1994; genetic and phenotypic correlations from Koots et al. (1994)

Terminal indexes for Holstein sires revealed substantial carcass merit variation. iGENDEC MEV were: HCW $1.94, REA $14.97, FT –$105.52, MARB $51.18, Feed Intake –$48.99, Calving Ease Direct $1.50. MEV reflect expected net profit change per mating per unit trait change (others constant). FI was excluded due to unavailable EPDs; focus remained on carcass differences. Carcass EPD ranges in the selection criteria were: HCW 89 lb, REA 1.4 in², MARB 1.17 units, FT 0.15 in. Resulting index values ranged from $56.99 to $254.59, indicating nearly $200/mating difference between top- and bottom-ranked sires. Selection for improved carcass merit in dairy sires is clearly justified. While US beef and dairy selection systems have not yet been integrated, the concepts are gaining traction internationally. The Irish Cattle Breeders Federation has implemented indexes for beef sires used in terminal mating systems (the Dairy Beef Index; ICBF 2026a) as well as the incorporation of carcass, fertility, milk components, calving ease and health traits into an index for integrated milk and beef production (Economic Breeding Index, ICBA 2026b).

Conclusions

Intensive management of dairy-origin calves—from hutches to feedlot finishing—enables systematic, large-scale recording of industry-relevant phenotypes across the value chain, potentially including traits like disease resistance and other well-being traits. The commercial dairy beef data stream offers exceptional opportunities to accelerate genetic improvement in beef × dairy and native beef cattle and to validate genomic predictions across environments.

Substantial differences in value among dairy sires are unsurprising, given the limited historical selection for carcass traits. Yet, with beef × dairy calves (and cull cows) forming a critical revenue stream for U.S. dairies, dairy bulls' genetic contribution to terminal calf value warrants attention. Dairies retaining ownership of beef × dairy calves should consider combined milk/carcass merit indexes for sire selection. Further gains are achievable via customized,

sector-specific indexes for beef sires on dairy females to exploit breed complementarity, and targeted breeding of complementary beef bulls using selection index tools.

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