

Non-traditional data sources for use in multi-breed genetic evaluation

A man wearing a light-colored cowboy hat and a blue and white checkered shirt is seen from the back, looking out over a large green field. In the field, there is a herd of cows of various colors, including black, brown, and white. The background features a line of trees and a cloudy sky. The overall scene is a rural farm setting.

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Data Collection In Beef Industry Paradigm

- Data collection has been concentrated in the seedstock industry to make predictions (EPDs/EBVs) for use in commercial beef industry
- Limited amounts of data flow from commercial to genetic evaluations in US

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Other Sources of Data

- Commercial Herds
 - 28.2 million beef cows in the US
- Dairy Herds
 - 9.36 million dairy cows

(USDA, 2024)

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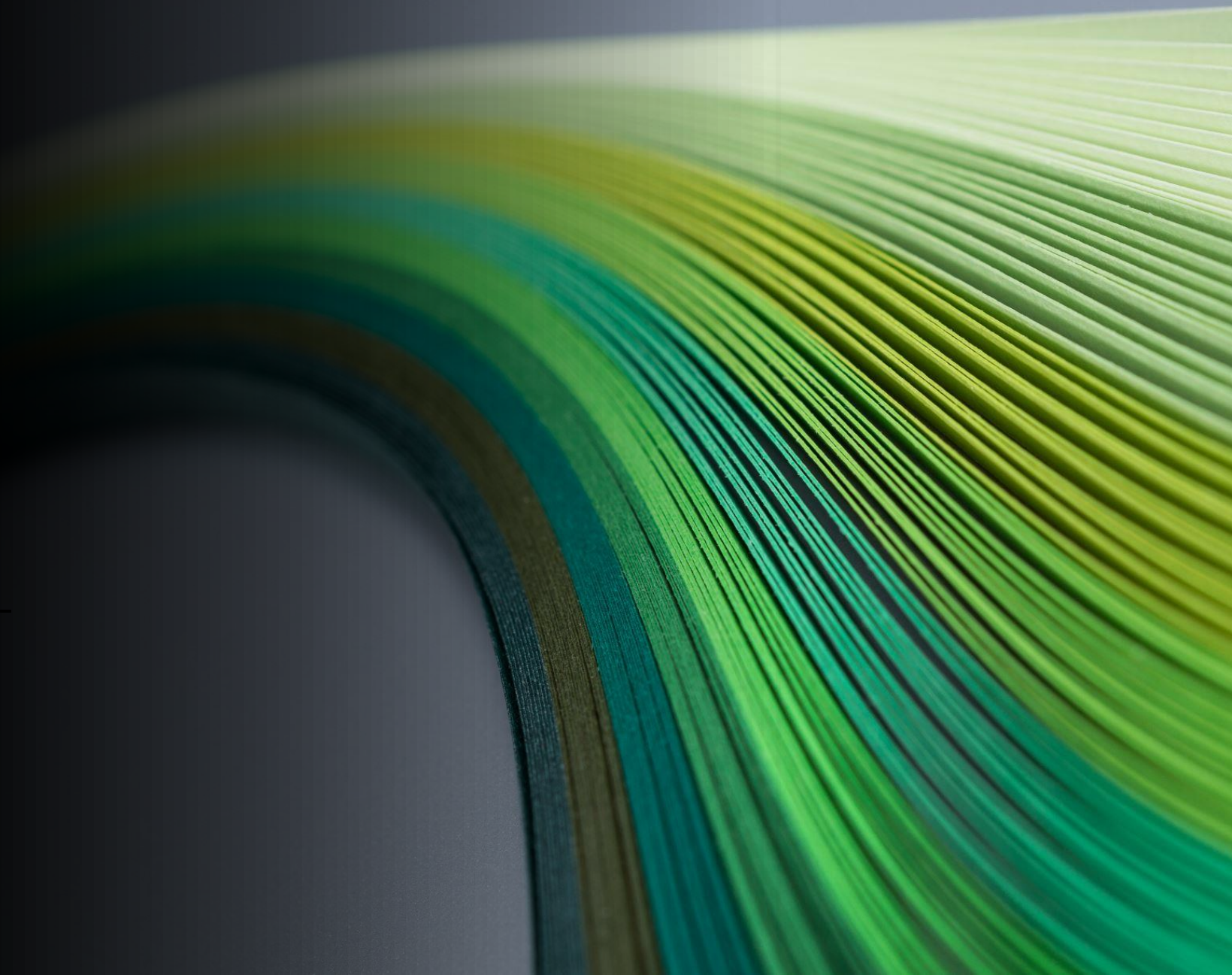
Data Quality And Quantity

- Reliability of Data
 - Refers to the degree that you can trust your data
- Ideally have large sets of highly reliable data to make predictions

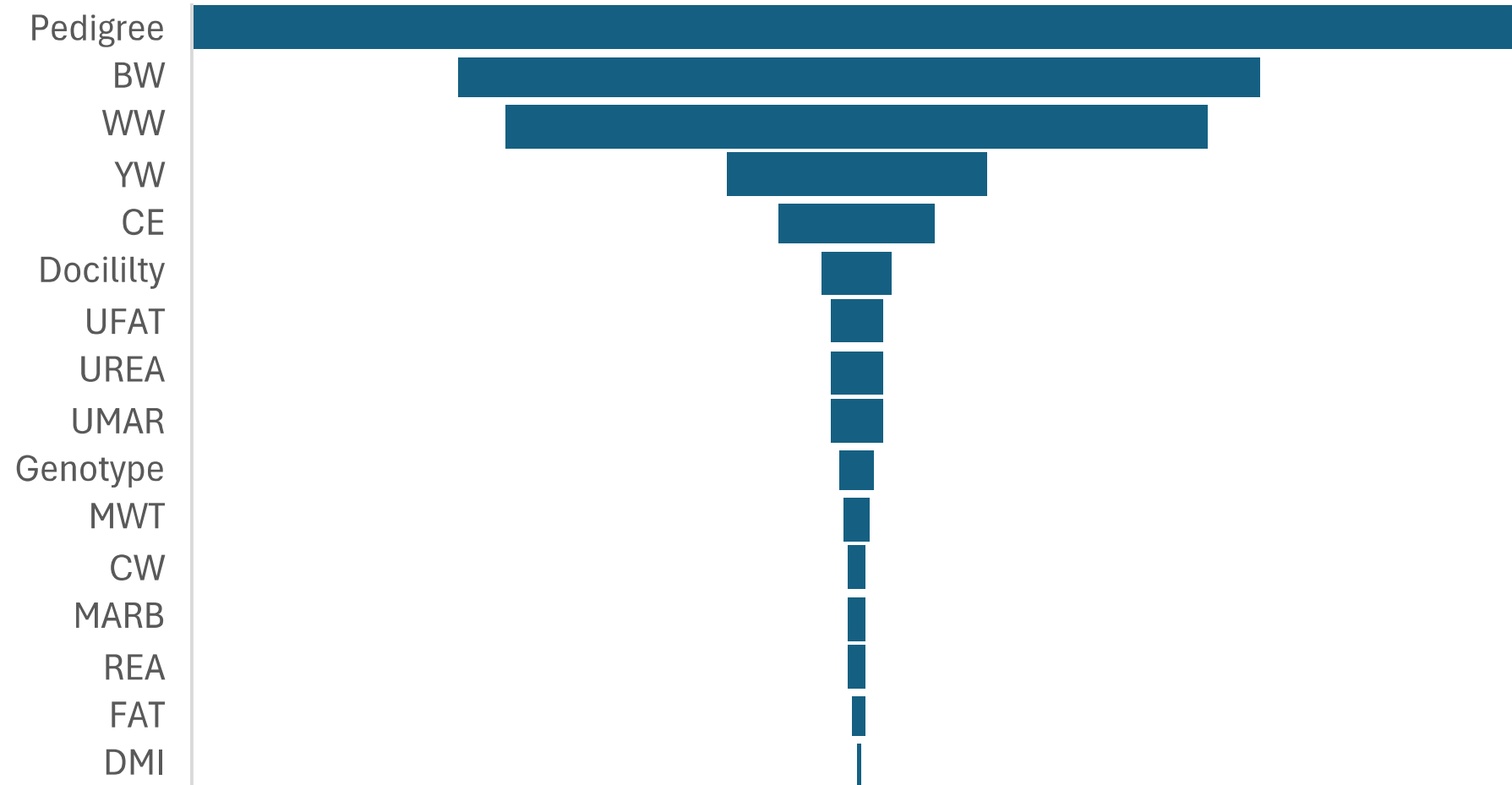
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Breed Association Data Recording Programs



IGS Database Representation of Data



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Data Collection Programs

- Total Herd Reporting Programs
 - Breed Associations where all animals are part of this program
 - RAAA
 - AGA
 - AHA
 - ASA (Shorthorn)
 - Breed Associations with optional programs
 - ASA (Simmental)
 - AAA
 - NALF

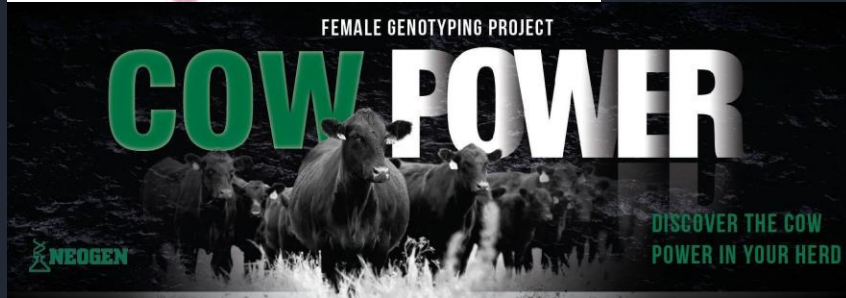
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Total Herd Programs

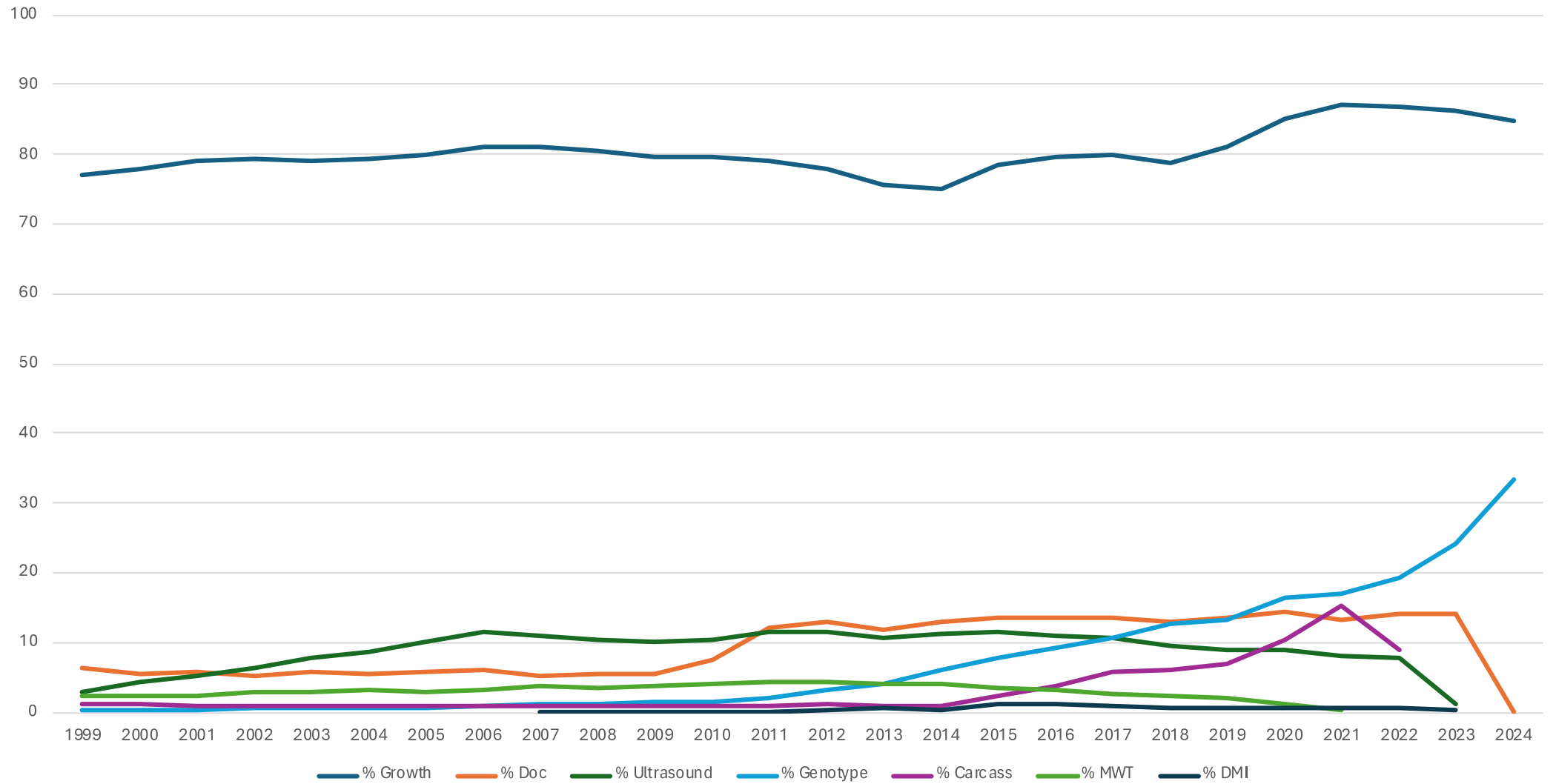
Group	CED	WW	PWG	CW	Milk	Doc	Stay	MARB
THE	.26	.30	.30	.24	.19	.22	.18	.20
Non- THE	.21	.24	.24	.19	.16	.18	.14	.17
Δ_G	0.05	0.90	0.75	1.43	0.45	0.40	0.10	0.03

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Programs to Incentivize Data



Trend of Data Reporting 1999 to 2024



Can We Incorporate Other Sources of Data into the Genetic Evaluation?

- To incorporate data into the evaluation all basics of data recording must be met.
 - Known pedigree information
 - Individual trait recording
 - Known breed percentages
- Are the genetic relationships high between the different data streams to treat as same traits in the genetic evaluation?

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Testing Different Data Streams into IGS Evaluation

- Beef on Dairy
- Commercial Data
 - American Simmental Registration Type D

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Models

- For each analysis, a bi-variate analysis was conducted with phenotypes from a traditional registered BxB data stream was treated as one trait and either the BxD or Commercial animals were treated as a second trait.

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Models

Trait	Fixed Effects
CED	BCG, Sex, Individual outcross, individual breed percent, dam breed percent
BW	BCG, Sex, AOD, Individual outcross, individual breed percent, dam breed percent
WW	WCG, Sex, AOD, Individual outcross, individual breed percent, dam breed percent
PWG	YCG, Sex, Individual outcross, individual breed percent
BF	CarcCG, Age, individual outcross, individual breed percents
CW	CarcCG, Age, individual outcross, individual breed percents
MS	CarcCG, Age, individual outcross, individual breed percents
REA	CarcCG, Age, individual outcross, individual breed percents

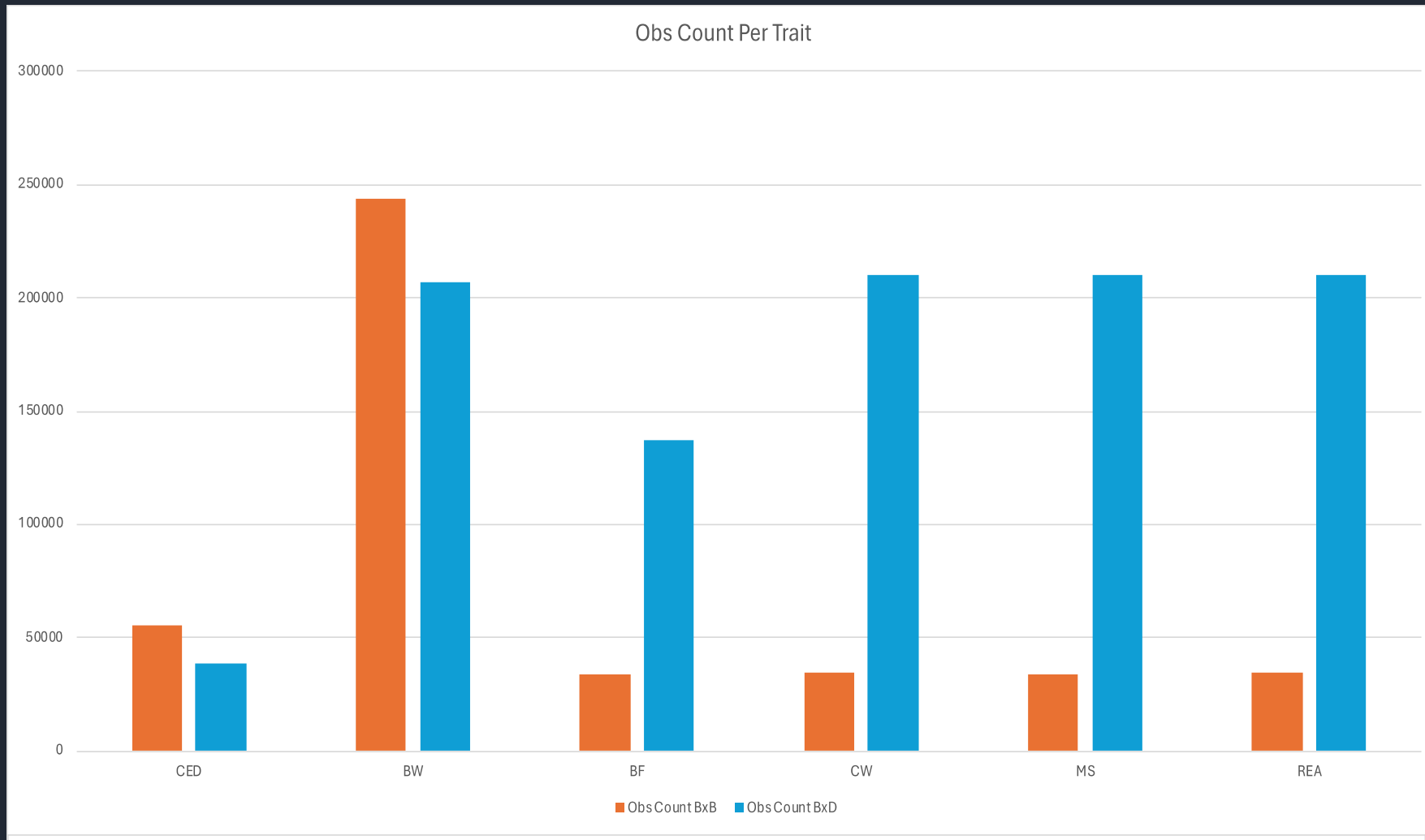


Beef On Dairy Data

Beef On Dairy

- Analysis information
 - All beef on Dairy Records come from a single breeder code
 - For CE and BW data was limited to CG that had 50 or greater animals and sires had 50 or greater progeny in BxD data
 - BxB animals were identified as having a common sire with BxD animal
 - Residual Covariance was set to 0
 - VCE were solved for using JWAS package in Julia
 - 150,000 iterations
 - 50,000 iterations burn in
 - Thinning of every 10 samples

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Beef On Dairy Genetic Parameters

Trait	h^2_{BxB}	h^2_{BxD}	r_g
CED	0.32 (0.30,0.34)	0.06 (0.04,0.07)	0.42 (0.18,0.58)
BW	0.59 (0.58,0.60)	0.78 (0.76,0.80)	0.89 (0.87, 0.91)
BF	0.31 (0.28,0.33)	0.31 (0.29,0.34)	0.95 (0.93,0.96)
CW	0.33 (0.30,0.36)	0.21 (0.20,0.23)	0.81 (0.75,0.88)
MS	0.48 (0.46,0.51)	0.48 (0.45,0.51)	0.95 (0.92, 0.97)
REA	0.32 (0.30,0.35)	0.29 (0.27,0.31)	0.83 (0.77, 0.90)



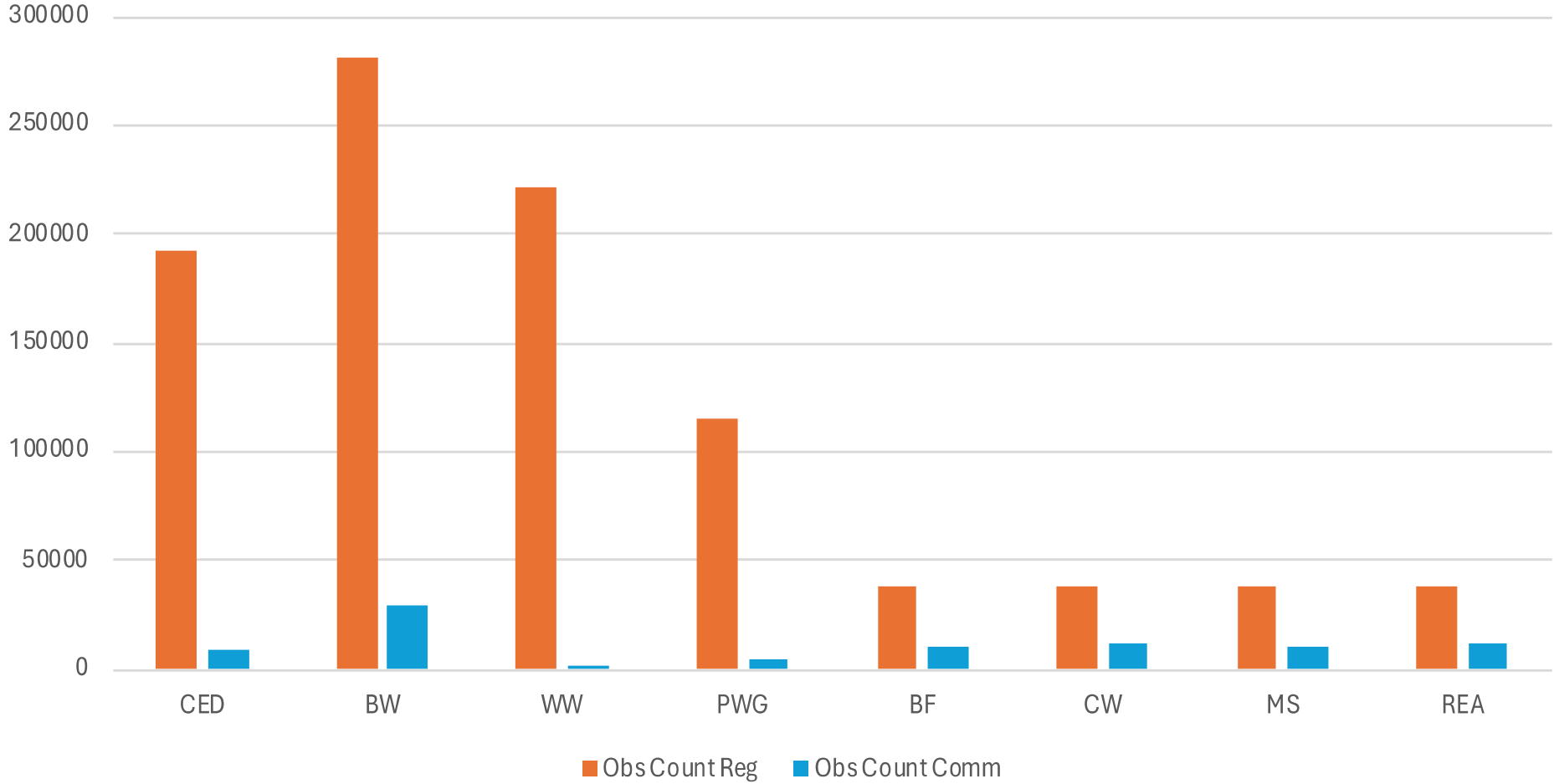
Commercial Data

ASA Registration Type D Animals

- Analysis information
 - A list of breeder codes were provided by ASA
 - For CE, BW, and WW data was limited to CG that had 50 or greater animals and sires had 50 or greater progeny in commercial data data
 - Registered animals were identified as having a common sire with commercial animal
 - Residual Covariance was set to 0
 - VCE were solved for using JWAS package in Julia
 - 150,000 iterations
 - 50,000 iterations burn in
 - Thinning of every 10 samples

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Obs Count Per Trait



Genetic Parameters

Trait	h^2_{reg}	h^2_{comm}	r_g
CED	0.28 (0.27,0.29)	0.36 (0.24,0.46)	0.93 (0.86,0.97)
BW	0.59 (0.58,0.60)	0.60 (0.58,0.63)	0.85 (0.81,0.90)
WW	0.42 (0.40,0.43)	0.41 (0.31,0.50)	0.89 (0.78,0.97)
PWG	0.23 (0.22,0.24)	0.26 (0.20,0.32)	0.92 (0.85,0.97)
BF	0.32 (0.29,0.35)	0.37 (0.33,0.42)	0.91 (0.80,0.96)
CW	0.34 (0.31,0.37)	0.32 (0.26,0.38)	0.73 (0.53,0.85)
MS	0.52 (0.49,0.55)	0.46 (0.42,0.51)	0.96 (0.94,0.97)
REA	0.34 (0.32,0.37)	0.38 (0.33,0.43)	0.93 (0.86,0.98)

Looking to the Future

- Continued and increased use of these types of records
- More diversity of animals used in these different data sources
- Opportunity to collect records more easily in these populations than registered herds

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Conclusions

- Genetic relationships among traits are high
- More generally this shows that genetic predictions with data collected in seedstock herds can cause genetic improvement in commercial populations.

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Questions?

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