Genotype by environment interaction through first lactation of dairy cattle in California and New England.

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INTRODUCTION

- Current US National Dairy evaluation does not account for Genotype-by-environment interactions
- This GxE interaction could cause a potential sire reranking
  - Rerankings provide information to breeders and farmers for selection
- One important GxE interaction could be geographical location, which can be modeled as phenotypes in each region as a different trait

OBJECTIVE

- Calculate the genetic parameters and sire reranking in order to assess the existence of GxE interaction in the first lactation of US Holstein cows raised in California (CA) and New England (NE)

MATERIALS AND METHODS

- **4,500,000** first lactation records from CA cows
- **500,000** first lactation records from NE cows
- First lactation used to ensure animal expressed phenotypes without culling poorly adapted cattle
- **50,000** animals selected based on contemporary groups of 30+ daughters (repeated 10x)
- Two Models used to calculate genetic parameters for milk yield, fat, and protein
  - Single Trait
  - Two Trait
- Model included random additive genetic, herd-by-sire interaction, and residual effects
  - Averages calculated using average information restricted maximum likelihood algorithm
- Breeding values calculated using complete data
- Ranking of high accuracy bulls across the two regions were evaluated
- Bulls with **30+** daughters were ranked using single trait analysis EBS and number of common bulls in top 30 ranked were assessed

$$Y = Xb + Za + Whs + e$$

Where **y** represents a vector of phenotypes, **b** is the vector of fixed effects, **a** is the vector of random additive genetic effects, **hs** is the herd by sire random effects, and **e** is the vector of the random residual effects. **X** is the incidence matrix of the fixed effects management group, which includes age, parity of the dam, and birth year. The **Z** is the incidence matrix of the additive genetic random effect. **W** is the incidence matrix that relates the records to the herd by-sire-random effects.

State	Trait	Genetic Additive Effect	Herd By Sire (HXS)	Residual Effects	Heritability (H2)	Standard Error
Single Trait						
CA	Milk	2.54E+06	6.71E+05	1.29E+07	0.16	1.69E-02
NE		4.99E+06	2.60E+05	9.53E+06	0.34	1.66E-02
CA	Protein	1.51E+03	3.61E+02	1.00E+04	0.13	1.51E-02
NE		3.16E+03	1.87E+02	7.84E+03	0.29	1.62E-02
CA	Fat	2.83E+03	6.02E+02	1.94E+04	0.13	1.47E-02
NE		6.66E+03	3.24E+02	1.49E+04	0.31	1.63E-02
Single Trait (Combined States)						
CA & NE	Milk	4.43E+06	4.04E+05	1.07E+07	0.29	1.32E-02
CA & NE	Protein	2.50E+03	2.77E+02	8.74E+03	0.22	1.21E-02
CA & NE	Fat	5.06E+03	4.83E+02	1.70E+04	0.22	1.22E-02
Two Trait						
CA	Milk	2.87E+06	5.69E+05	1.26E+07	0.18	0.01
NE		5.07E+06	2.37E+05	9.39E+06	0.34	0.01
CA	Protein	1.51E+03	3.51E+02	1.00E+04	0.13	1.48E-02
NE		2.88E+03	2.55E+02	8.23E+03	0.25	1.06E-01
CA	Fat	2.73E+03	5.63E+02	1.74E+04	0.12	1.34E-02
NE		4.88E+03	4.11E+02	1.48E+04	0.22	9.23E-02

RESULTS

Proportion of Effects based on Model
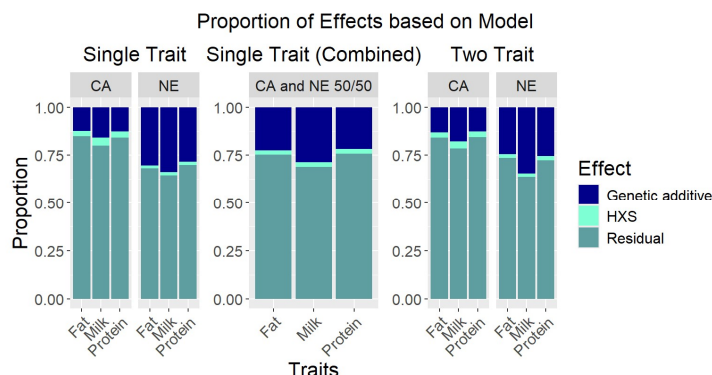
- Variant components indicate modest GxE between CA and NE
- Genetic correlations between fat and protein were .87 and .80 respectively
- Correlation between breeding values of high accuracy bulls
  - .83 for milk
  - .84 for protein
  - .86 for fat
- Bulls in top 30 of **both** CA **and** NE
  - 9 for milk
  - 6 for protein
  - 4 for fat

Top Ranked Bulls in BOTH regions vs only ONE region
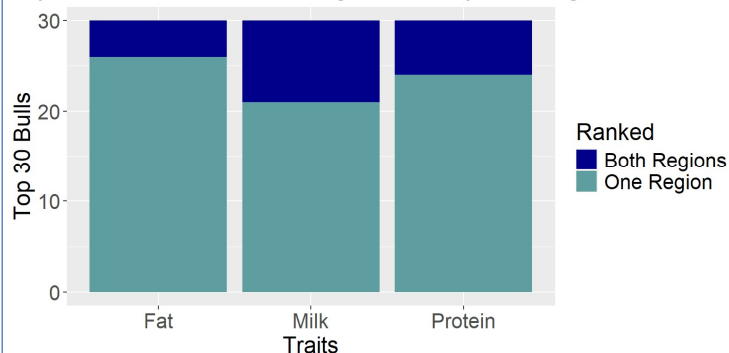
CONCLUSIONS AND FUTURE STEPS

- Sire reranking is significant as the list of top ranked bulls differs between the regions
- Next steps
  - Evaluate GxE interactions using somatic cell score
  - Perform genome-wide association study to study genomic regions associated with the three traits in CA and NE

ACKNOWLEDGMENT

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