

Genetic parameters of immune response estimated using genetically divergent lines of Holstein-Friesian dairy heifers

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Background

- Fertility research herd (Meier *et al.* 2017)
 - ~540 Holstein-Friesian heifers (2015 born)
 - From assortative mating of high or low fertility parents
- Research aims
 - Underlying physiology driving fertility differences
 - New management strategies
 - New traits to predict fertility ($h^2 = 0.03$)

Immune Response (IR)

- Immunity impacts reproductive function
 - Immune cells key to successful pregnancy (Fair 2015)
 - Post-partum uterine recovery
- Previous IR studies:
 - Heritability (h^2): 0.16 to 0.64
(Mallard *et al.*, 1983; Wagter *et al.*, 2000; Hernández *et al.*, 2006; Thompson-Crispi *et al.*, 2012)
 - Genetic Correlation (r_g) with fertility: -0.19 to 0.20
(Thompson-Crispi *et al.*, 2012)

Objectives

- Estimate genetic parameters in NZ Holstein-Friesian dairy cattle:
 - IR (3 traits) h^2 and r_g
 - IR r_g with Breeding Worth (BW) index traits
 - In NZ, BW composed of 8 traits (including fertility)
- Account for bias due to herd structure

Materials & Methods

- 539 Holstein-Friesian heifers
 - Born across 379 herds (June-Sept 2015)
 - From assortative mating of high/low fertility BV parents
 - High & Low fertility heifer lines
- 7 “Contemporary Groups” (CG)
- Pedigree of 10,992 animals
 - 18 generations deep

Materials & Methods

➤ Immunization protocol (Thompson-Crispi *et al.*, 2012)

- Immunized at ~220 days old
- Antibody-mediated IR (AMIR)
 - HEWL @ days 0 & 14
 - IgG1 conc. @ days 0, 14 & 21

AMIR0 → Control covariate
AMIR14 } Response variates
AMIR21 }

- Cell-mediated IR (CMIR)
 - *C. albicans*/control @ day 21
 - Log skinfold thickness ratio @ day 23

CMIRc → Control covariate
CMIRt → Response variate

Materials & Methods

➤ BLUP mixed model:

$$y = CG + control + a + e, \quad y \in \{AMIR14, AMIR21, CMIRt, nEBV\}$$

- Univariate model $\rightarrow h^2$
- Bivariate model $\rightarrow r_g$

➤ Estimated Breeding Values (EBV) of BW:

- De-regressed (dEBV) by \div reliability (Garrick *et al.* 2009)
- Noise added (nEBV) from $N(0, \sigma_e^2)$
- 100 runs with noise re-sampling \rightarrow mean $r_g \pm SE$

Materials & Methods

- r_g between nEBV and IR also estimated via a Pearson correlation
 - Simple, and used as validation (no SE though)
- Explored herd divergence in fertility
 - Pedigree determined to be deep enough

Results & Discussion

	AMIR14	AMIR21	CMIRt	
AMIR14	0.44 ± 0.14	0.67 ± 0.17	-0.44 ± 0.43	r_g
AMIR21	0.44 ± 0.04	0.47 ± 0.15	-0.07 ± 0.40	
CMIRt	-0.03 ± 0.05	0.01 ± 0.05	0.11 ± 0.10	h^2

r_p

Results & Discussion

		AMIR14	AMIR21	CMIRt
BW trait	h^2	$r_g \pm SE$	$r_g \pm SE$	$r_g \pm SE$
Protein	0.31	-0.10 ± 0.22	-0.13 ± 0.21	-0.39 ± 0.31
Fat	0.33	-0.22 ± 0.21	-0.10 ± 0.21	-0.24 ± 0.29
Volume	0.36	-0.12 ± 0.20	-0.08 ± 0.20	-0.40 ± 0.32
Liveweight	0.35	-0.15 ± 0.17	-0.22 ± 0.17	*
Fertility	0.03	0.09 ± 0.22	-0.17 ± 0.21	-0.04 ± 0.32
SCS	0.12	0.05 ± 0.25	0.03 ± 0.25	0.10 ± 0.39
RSv	0.04	0.03 ± 0.62	-0.08 ± 0.41	0.17 ± 0.58
BCS	0.19	0.02 ± 0.19	-0.15 ± 0.18	0.19 ± 0.27

Conclusions

- IR h^2 low/moderate
 - AMIR & CMIR antagonistic
- } An IR index should have both AMIR & CMIR
- Weak genetic correlations between IR & BW traits
 - IR unlikely helpful as predictor trait ← including for Fertility
 - Selection on IR or BW unlikely to affect each other
 - Caution however, as r_g generally unfavourable still
 - Widespread IR recording impractical
 - Genomic selection reference population

Acknowledgements

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- In-kind support from LIC and CRV Ambreed
- DairyNZ farm & technical staff for data collection
- Dorian Garrick for input to address herd divergence

Q & A

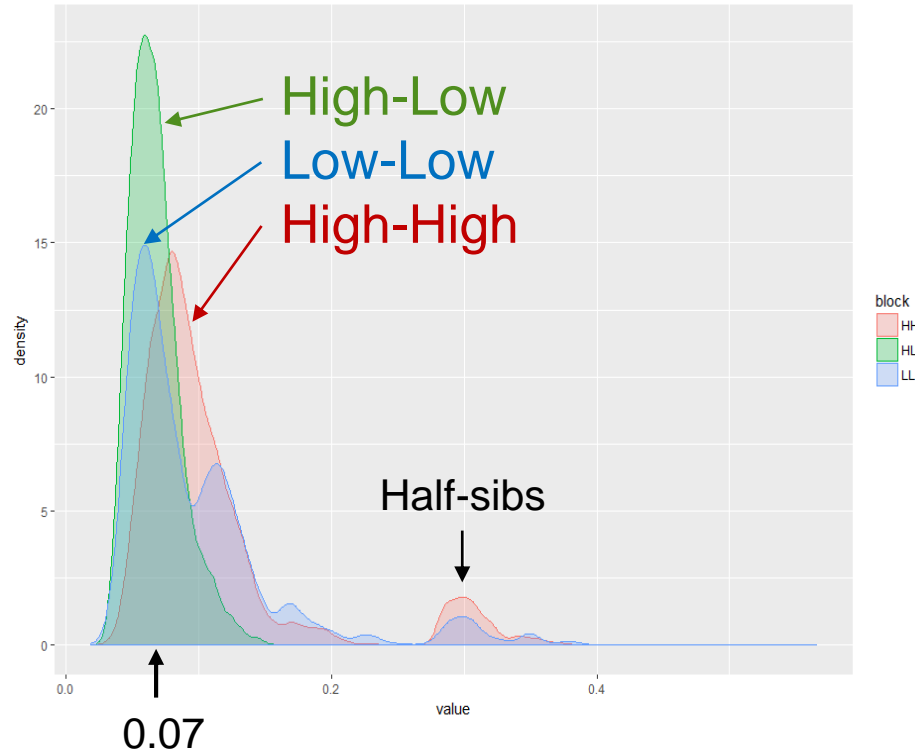
Materials & Methods

- r_g with EBV verified by Pearson correlation

From IR univar → $\frac{\sigma_{IR}^2 \times \sigma_{EBV}^2}{\text{COV}(\sigma_{IR}^2, \sigma_{EBV}^2)}$ ← Resid. from bivar. *fixed* model;
 $\sigma_e^2 \approx \sigma_a^2$ as EBV genetic est.

- SE not available
- Accounting for fertility divergence
 - If divergence between lines present in founders, and
 - If fertility $r_g > 0$ with trait X, then
 - Model for X req. 2 gen. distributions
 - Fertility line term (GG or fixed effect)

Materials & Methods



- Distribution of A-matrix heifer coefficients
 - Apart from sibs, both within- & between-line ~ 0.07
 - \therefore pedigree deep enough; 1 genetic distribution ok

		AMIR14		AMIR21		CMIRt	
BW trait	h^2	Resampling	Pearson	Resampling	Pearson	Resampling	Pearson
Protein	0.31	-0.10 ± 0.22	-0.05	-0.13 ± 0.21	-0.06	-0.39 ± 0.31	-0.05
Fat	0.33	-0.22 ± 0.21	-0.15	-0.10 ± 0.21	-0.03	-0.24 ± 0.29	0.05
Volume	0.36	-0.12 ± 0.20	0.00	-0.08 ± 0.20	0.02	-0.40 ± 0.32	-0.08
Liveweight	0.35	-0.15 ± 0.17	-0.16	-0.22 ± 0.17	-0.18	*	0.33
Fertility	0.03	0.09 ± 0.22	0.10	-0.17 ± 0.21	-0.05	-0.04 ± 0.32	-0.07
SCS	0.12	0.05 ± 0.25	-0.01	0.03 ± 0.25	-0.03	0.10 ± 0.39	0.06
RSv	0.04	0.03 ± 0.62	-0.01	-0.08 ± 0.41	-0.01	0.17 ± 0.58	0.19
BCS	0.19	0.02 ± 0.19	0.05	-0.15 ± 0.18	-0.09	0.19 ± 0.27	0.08