Single-step genomic predictions of a minor breed

(concurrently with the large genomic evaluations of a main breed).

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Who is Finncattle (FIC)?

- FIC represents <1% of milk recorded cows in Finland (in 2019)
- 36,133 animals in pedigree in milk evaluations (1950-2020)
- FIC test-day evaluations are part of Red Dairy cattle DFS* runs
- ~1,000 FIC genotypes available (~200 bulls & 800 cows)

- Aim: Deliver GEBVs to FIC breeders and farmers.

*DFS = Denmark, Finland, and Sweden

Single-step evaluations

Single-step is the target in Nordic Dairy Cattle evaluations

✓ ssGTBLUP with Metafounders

✓ ssGTBLUP with full QP transformation and G_{05}

[Allele frequency = 0.5; inbreeding in A^{-1} and A_{22}; G scaled by tr(A_{22})/tr(G_{05})]

Will RDC single-step evaluations works properly for FIC?

Will FIC genotypes harm RDC single-step evaluations?

Data

- ➢ Test-day records: from 3.6M RDC, 0.86M HOL, and 30K FIC cows
- ➢ Pedigree included 5.9M animals (107K males) with 137 UPG
- ➢ Genotypes: ~170K RDC & 917 FIC

Metafounders concept

ssGBLUP with MF (Legarra et al. 2015; Christensen, 2015).

$$(\mathbf{H}^{\Gamma})^{-1} = (\mathbf{A}^{\Gamma})^{-1} + \begin{pmatrix} 0 & 0 \\ 0 & \mathbf{G}_{\mathrm{w}}^{-1} - \left(\mathbf{A}_{22}^{\Gamma}\right)^{-1} \end{pmatrix}$$

Relationships among MF are described by Γ .

$$\Gamma = 8 * Cov(\mathbf{P})$$

$\mathbf{P}$ - allelic frequencies (AF) across loci in base population.

Use 137 UPG as 137 MF?

- Impossible to calculate AF for each UPG

$$\xcancel{8 * Cov(\mathbf{P}) = \Gamma_{137}}$$

- Structure of pre-gamma ($\Gamma_{\boldsymbol{pre}}$) was defined with covariance function kernel $\boldsymbol{K}$

$$\Gamma_{pre} = \Phi_{pre}\,\boldsymbol{K}\Phi'_{pre}$$ [#1]

$$\boldsymbol{K} = (\Phi'_{pre}\Phi_{pre})^{-1} * \Phi'_{pre}\Gamma_{pre}\Phi_{pre} * (\Phi'_{pre}\Phi_{pre})^{-1}$$ [#2]

[#1] Kirkpatrik et al., 1994
[#2] Tijani et al., 1999

- $\boldsymbol{K}$ was used to extend structure of Γ_{pre} to Γ_{137}

$$\Gamma_{137} = \Phi_{137}\boldsymbol{K}\Phi'_{137}$$

Approaching suitable pre-Gamma matrix

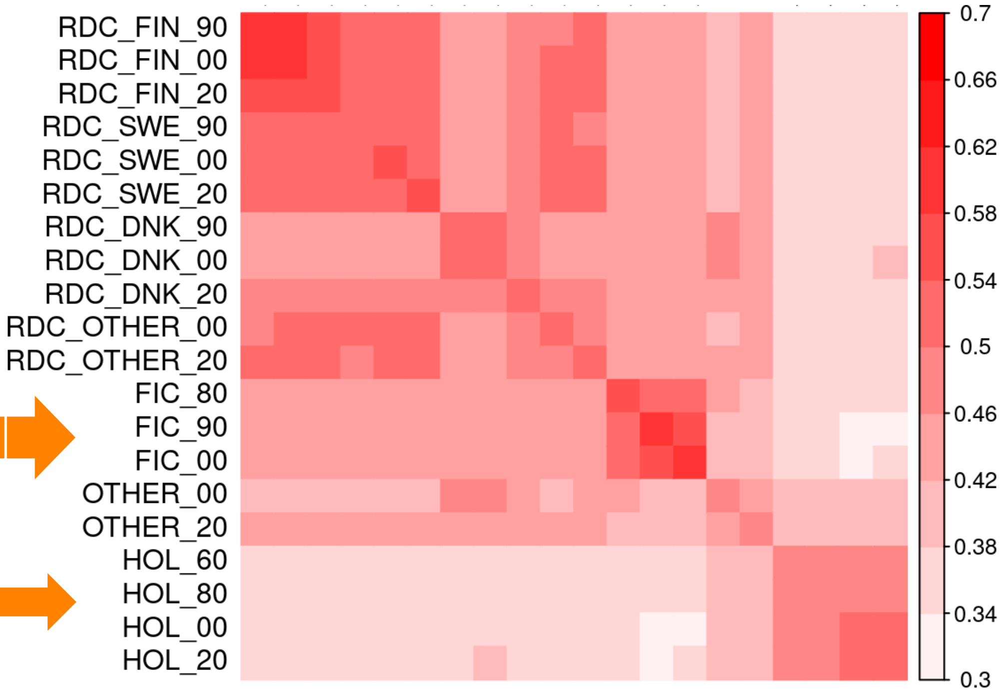
To explore the breeds and changes in population

Groups defined as **breed x time** we treated as M

RDC x 11
FIC x 3
OTHER x 2

Allele Frequencies estimated using BPOP
(Strandén and Mäntysaari, 2020)

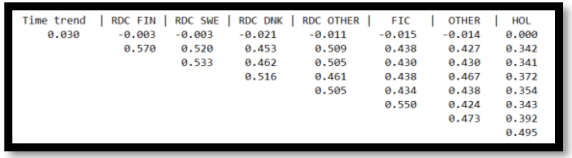
HOL[1] x 4



HOL[1] allele frequencies obtained from NAV Holstein single-step R&D
(see M. Koivula presentation on April 30th 14-15:15)

Expanded Gamma

$K =$



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Time trend   | RDC FIN | RDC SWE | RDC DNK | RDC OTHER |   FIC    |  OTHER  |  HOL
    0.030      -0.003   -0.003    -0.021     -0.011     -0.015    -0.014    0.000
                0.570    0.520     0.453      0.509      0.438     0.427    0.342
                         0.533     0.462      0.505      0.430     0.430    0.341
                                   0.516      0.461      0.438     0.467    0.372
                                              0.505      0.434     0.438    0.354
                                                         0.550     0.424    0.343
                                                                   0.473    0.392
                                                                            0.495
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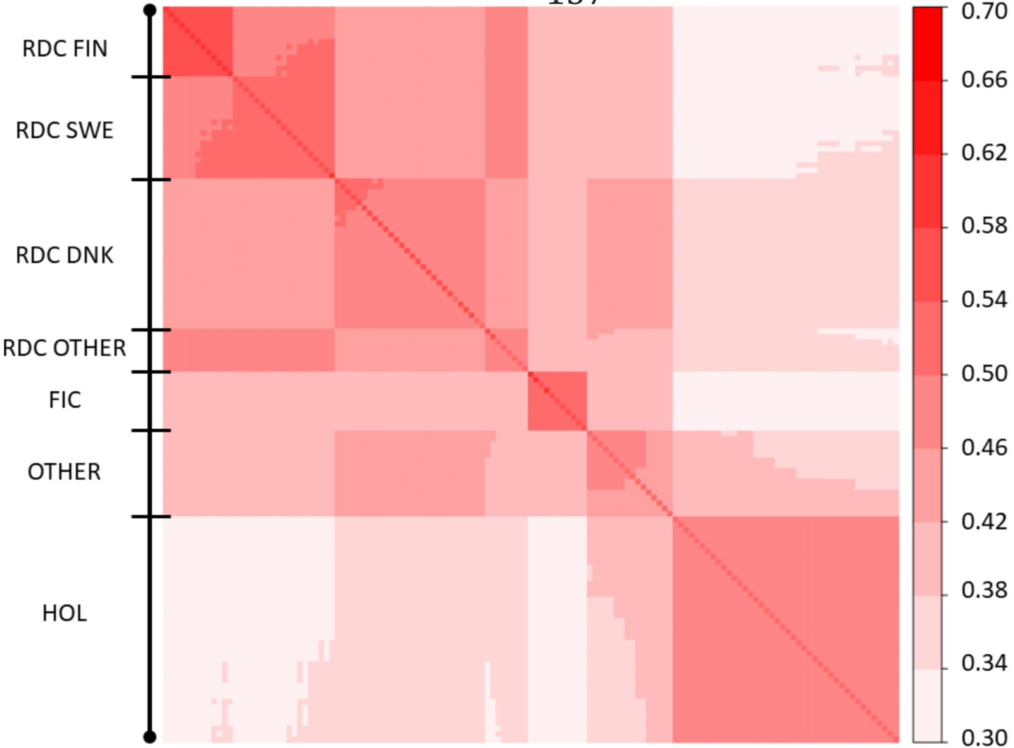
Γ_{20}

$$\Phi_{137} \boldsymbol{K} \Phi'_{137}$$

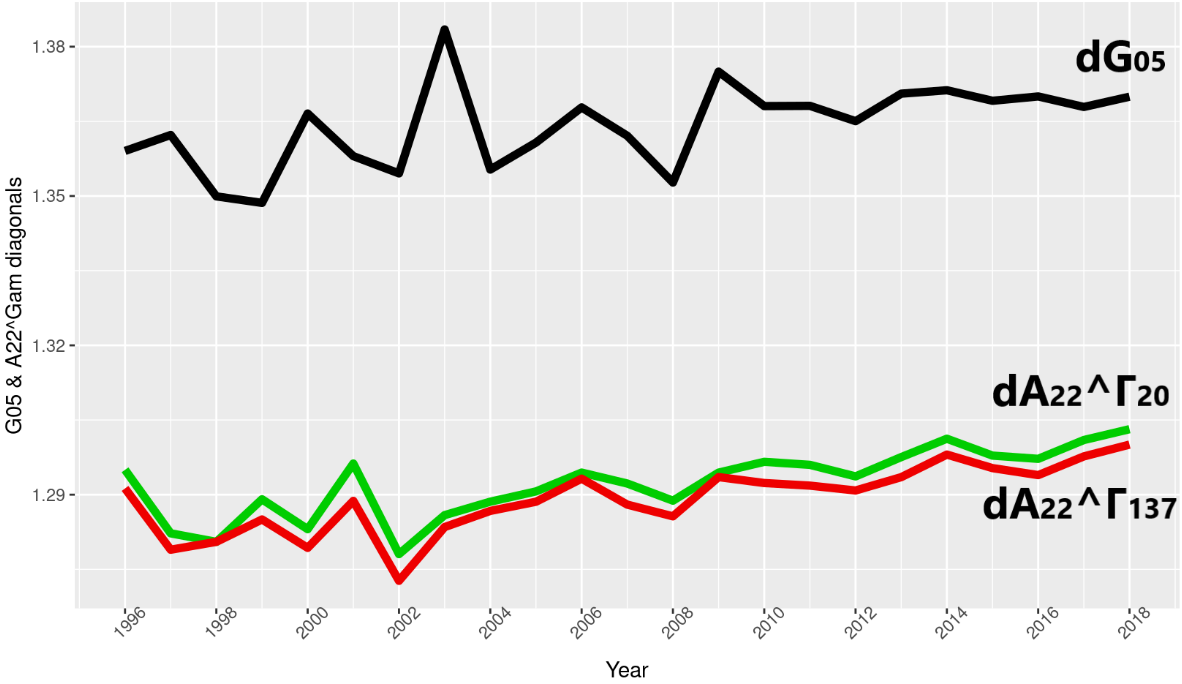
Γ_{137}



Relationship matrix diagonals

All genotyped animals

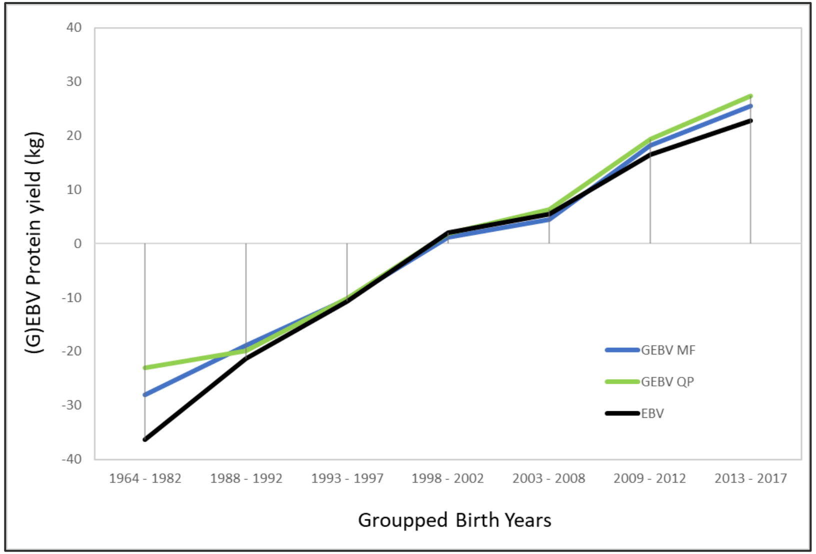
FIC only



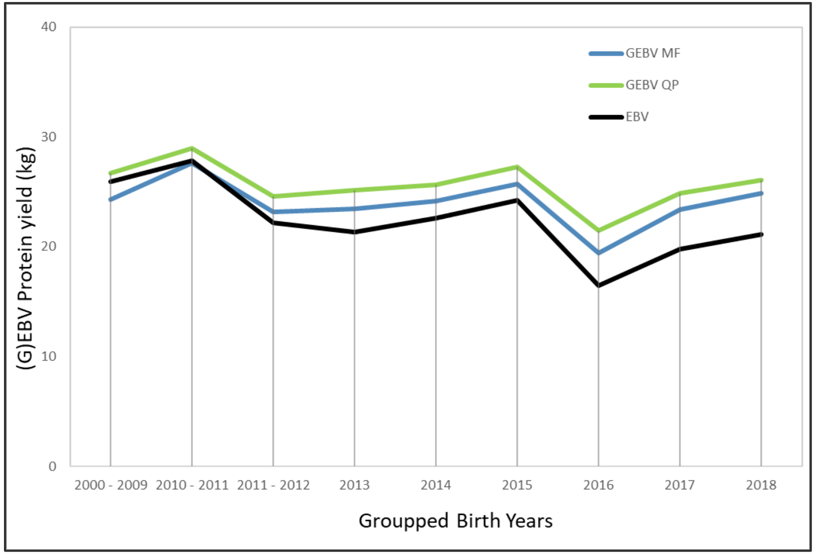
		Correlation
		G_{05}
Diagonals	A_{22}	0.59
	$A_{22}^{\Gamma 20}$	0.56
	$A_{22}^{\Gamma 137}$	0.59
Off-diagonals	A_{22}	0.63
	$A_{22}^{\Gamma 20}$	0.68
	$A_{22}^{\Gamma 137}$	0.67

Genomic prediction. Protein yield genetic trends.

Genotyped FIC Bulls (181 anim.)



Genotyped FIC Cows (700 anim.)



*GEBV MF – ssGTBLUP with MF

GEBV QP – ssGTBLUP with full QP transformation and G_{05}

EBV – Test-Day Animal Model

FIC validation

Bulls with reliability >50% in full data.

Legarra & Reverter (2018) validation test for FIC animals.

Model	m(GEBV)-m(GEBVred)	b_1 (±SE)	R^2
Protein (21 individuals)			
ssGTBLUP MF	-3.98	0.79 (±0.13)	0.66
ssGTBLUP QP	-4.22	0.90 (±0.15)	0.66
EBV	-3.13	0.82 (±0.18)	0.53
Milk (22 individuals)			
ssGTBLUP MF	-177	0.80 (±0.16)	0.60
ssGTBLUP QP	-195	0.92 (±0.17)	0.60
EBV	-203	0.93 (±0.14)	0.69

FIC validation

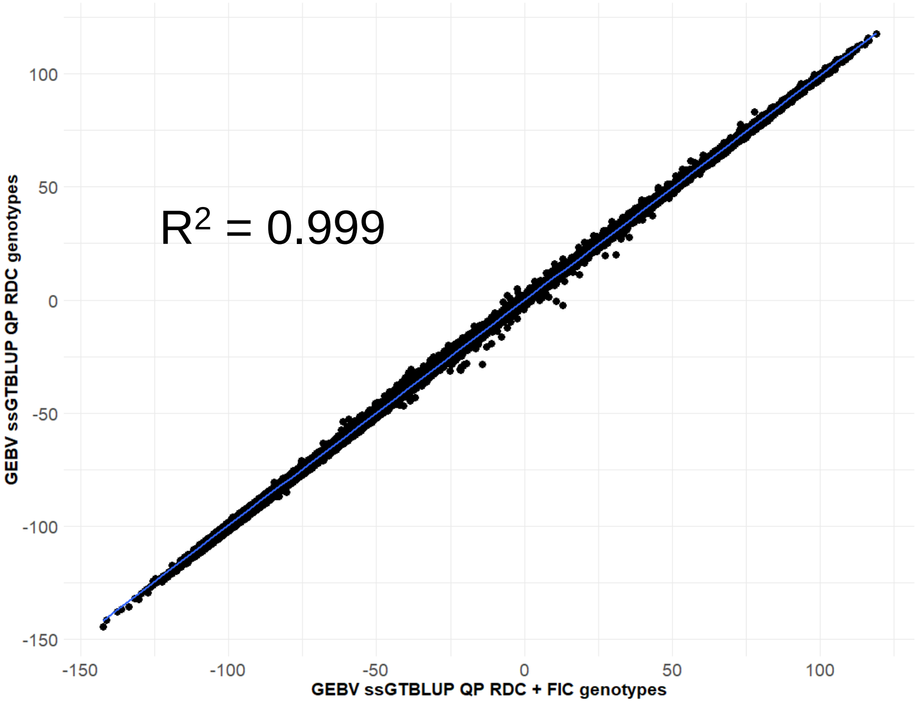
Cows with reliability >50% in full data

Legarra & Reverter (2018) validation test for FIC animals.

Model	m(GEBV)-m(GEBVred)	b_1 (±SE)	R^2
Protein (109 individuals)			
ssGTBLUP MF	3.45	0.83 (±0.08)	0.50
ssGTBLUP QP	3.14	0.89 (±0.09)	0.48
EBV	4.25	0.79 (±0.11)	0.32
Milk (125 individuals)			
ssGTBLUP MF	76	0.99 (±0.07)	0.61
ssGTBLUP QP	66	1.04 (±0.08)	0.59
EBV	90	0.94 (±0.09)	0.48

Influence of FIC genotypes on RDC evaluations

GEBVs of RDC bulls obtained from ssGTBLUP QP model
with and without FIC genotypes



Take home message

- Covariance kernel function could be used to compute large Γ
- Covariable matrix Φ is arbitrary - year-to-year variation is defined by researcher
- RDC MF trends apparently assign too strict trend to FIC MF
- FIC barely harm RDC single-step runs on that level

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Thank you!

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